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GenCore ver Copyright (c) 1993 - 2 OM nucleic - nucleic search, using sw mo	Run on: April 2, 2004, 14:30:56	Title: us-10-006-191-19 Perfect score: 1049 Sequence: 1 ttgaactgattcacatctca	Scoring table: IDENTITY NUC Gapext 0.5	Searched: 501 segs, 8964 residues	Total number of hits satisfying chosen p	Minimum DB seq length: 8 Maximum DB seq length: 50	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 545 summari	Database : rng.seq:*	Pred. No. is the number of results score greater than or equal to the and is derived by analysis of the t	MDS	* Result Query No. Score Match Length DB ID	34.4 3.3 40 1	1 W 4, n	7 23.4 2.2 25 1	8 23.4 2.2 27 1 9 23 2.2 24 1	10 23 2.2 24 1 11 22.2 2.1 27 1	2 22.2 2.1 27 1 3 22.2 2.1 27 1	4 22.2 2.1 27 1 5 22.2 2.1 27 1	5 22.2 2.1 27 1 22.2 7 1	18 22.2 2.1 27 1 19 22 2.1 22 1	20 21.8 2.1 25 1	22 21.8 2.1 25 1	3 21.8 2.1 25 1 4 21.8 2.1 26 1	5 21.8 2.1 26 1	7 21.8 2.1 26 1	8 21.8 2.1 26 1 9 21.8 2.1 27 1	0 21.8 2.1 27 1	21.8 2.1 27 1 27 1 27 1 27 1

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sources, using set of distinct gene specific primers. Example 3; SEQ ID NO 400; 11pp; English SSSSSSSSSSSS

The invention relates to producing a sub-population of labeled nucleic acids (NAs) comprising contacting a NA sample from a physiological source, with a pool of 50 distinct gene specific primers under suitable conditions to enzymatically generate sub-population of NAs, where each gene specific primer has a sequence complementary to a distinct mRNA, an

The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (TG)n >9 microsatellites in the bovine estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the

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Antisense oligo #2
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ABZ60766
AAT27913
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ABZ1102
ABZ11102
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AC AAH77495;	XX DT 20-NOV-2001 (first entry)	AA DE Human zinc finger protein 14 coding sequence probe #1.	XX KW Human; zinc finger protein 14; cancer; haemopathy; HIV infection; KW immunological disease; inflammation; gene therapy; probe; ss.	os Homo sapiens.	PN WO200166583-A1.	PD 13-SEP-2001.	XX PF 26-FEB-2001; 2001MO-CN000187.	XX FR 10-MAR-2600, 2000CN-00111978. XX	PI Mao Y, Xie Y; XX	DR WPI; 2001-565570/63.	PT New human zinc finger protein 14 for diagnosing and treating malignant PT neoplasm, hemopathy, human immunodeficiency virus infection,	- '	CC The present invention provides the protein and coding sequences of human CC zinc finger protein 14. The sequences can be used in the treatment of CC cancer, haemopathy, HIV infection, immunological diseases and CC inflammation. The present sequence is a probe for the coding sequence of	C. the invention XX SQ Sequence 41 BP; 9 A; 0 C; 11 G; 21 T; 0 U; 0 Other;	Query Match 3.2%; Score 33.6; DB 1; Length 41; Best Local Similarity 90.0%; Pred. No. 2.5;	Matches 36; Conservative 0; Mismatches 4;	Db 1 IGTGTGTGTGTGTGTGTGTATATATATATATA 40	RESULT 3	ABK66312 standard; DNA; 32 BP.	AC ABK66312;	AA DT 02-JUL-2002 (first entry) XX	DE Human gene specific PCR primer #400.	KW Primer; ss; DNA microarray; differential expression analysis; human.	OS Homo sapiens.
			····						 - (×	
Oligonucleotide SE							a microsatellite from clone TGLA53.	OPIIPRIM; breeding; cattle; parentage; amplification; ss.					•	genetic identification, gene		of a bovine microsatellite sequence obtd. by of bovine MoD. DNA fragments of between 250 and 500 at a (TC)1s of connected arche one one of se	clones cross-bybridised Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for a 220 mich bowing microsatellites.	Nummarised in the . The sequences upstream and	ion of the corresp.	"microscentify individuals, for parentage testing, and in the genetic	genes involved the determinism of in cattle, to allow selective (Undated on 25-MAR-2003 to correct by	3	0 U; 0 Other;	DB 1; Length 40;

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XX AAQ3

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XX AAQ3

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The present sequence represents an antisense primer which is used to inhibit expression of the rat connective tissue growth factor (CTGF) gene. The polypeptide may play a significant role in the normal development, growth and repair of mammalian tissue. Antisense sequences can be used to inhibit the expression of CTGF in a cell. In particular, the antisense sequences are useful for andiorating cell in particular, the antisense sequences are useful for andiorating cell proliferative tissue cells. The regulation of CTGF e.g. overgrowth of cells, e.g. connective the disorders, which can be treated, are chosen from sclearoderma, arthritis, cirnhosis, hepatic fibrosis, renal fibrosis, atherosclerosis, cardiac fibrosis, adhesions and surgical scarring. The antisense sequences can also be used to detect expression of CTGF in a sample
sequences which can be used as DNA markers. The new method markedly improves the efficiency of isolation of satellite sequences in comparison to prior art methods which are reliant on base sequences. Sequences AA29483-514 represent sequences from Haliotis discus, used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New rat connective tissue growth factor, its related gene and antisense sequences useful for modulating CTGF and treatment of cell proliferative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat; connective tissue growth factor; CTGF; cell proliferative disorder; connective tissue cell; scleroderma; arthritis; cirrhosis; hepatic fibrosis; renal fibrosis; atherosclerosis; cardiac fibrosis; adhesion; surgical scarring; antisense primer; DNA-RNA hybrid; ss.
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                                                                                                                                                                                                                                                                                                    Rat; connective tissue growth factor; CTGF; cell proliferative disorder; connective tissue cell; scleroderma; arthritis; cirrhosis; hepatic fibrosis; renal fibrosis; atherosclerosis; cardiac fibrosis; adhesion; surgical scarring; antisense primer; DNA-RNA hybrid; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FIBR-) FIBROGEN INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200027868-A2
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                                                                                                                                                                                                                                             21-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                         Rattus sp
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Vogel JM;
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                                                                                                21-NOV-1995;
                                                                                                                      28-NOV-1994;
                                                     WO9617082-A2
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                                                                                                                                                                 Morgante M,
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                                                                           06-JUN-1996
                                Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to nucleic acid molecules from regions of the soybean genome which are associated with soybean cyst nematode (SCN) resistance. The nucleic acids are used to transform plants, and can produce soybean plants having an rhgl or an Rhg4 SCN resistant allele. The nucleic acids can be used for investigating rhg1 or Rhg4 haplotypes of soybean plants and for introgressing SCN resistance or partial SCN resistance into soybean plants. They can also be used in plant breeding programmes. The invention also relates to proteins encoded by such nucleic acid molecules, as well as antibodies capable of recognising these proteins. The present sequence is a primer used to amplify a region
                                                                                                                                                                                                                                                                                                                                                                      New purified nucleic acid for producing a soybean plant having soybean cyst nematode resistance and for use in plant breeding programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                    88
                                                                                                                                          Soybean, antihelmintic, gene therapy, soybean cyst nematode, SCN, SCN resistance, rhg1, Rhg4, SCN resistant allele, plant breeding; 240017 region G3, 318013 region A3, 515002 region G2, PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detection; polymorphism; perfect compound simple sequence repeat; adaptor directed primer; genome; genetic; fingerprinting;
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                                                                                                                       Soybean 240017 region G3 DNA forward primer, SEQ ID NO: 601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.2%; Score 23.4; DB 1; Length 27; 96.0%; Pred. No. 30; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Compound simple sequence repeat primer (CA)4.5(TA)7.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 27 BP; 12 A; 11 C; 0 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                            Parnell LD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1795 TGTGTGTGTGTGTGTATATAT 1819
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  GTGAATTTGCCGGTAACAAGCCAGA 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                         05-JAN-2001; 2001WO-US000552.
                                                                                                                                                                                                                                                                                07-JAN-2000; 2000US-0174880P
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                                                                                                   (first entry)
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Les 24; Conservative
                                              AAI61970/c
ID AAI61970 standard; DNA;
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                                                                                                                                                                                                                                                                                                                             Wang ML,
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                                                                                                   16-OCT-2001
                                                                                                                                                                                          Glycine max
                                                                                                                                                                                                                                     19-JUL-2001
                                                                                                                                                                                                                                                                                                                             Hauge BM,
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                                                                              AAI61970;
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Matches
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                                   RESULT 8
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Detecting polymorphisms between 2 nucleic acid samples, esp. in microsatellite regions, comprises digesting the nucleic acid to generate fragments, ligating adaptor segments to their ends, amplifying them using primer directed amplification and comparing the proces. to detect differences. The primers used in the amplification comprise a primer consisting of a perfect cpd. simple sequence repeat (SSR), and an adaptor addrected primer, comprising a sequence complementary to an adaptor segment. The present sequence is an example of a compound SSR primer method represents a modified amplified fragment length polymorphism assay, which is partic, useful for genome fingerprinting, i.e. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis imperfecta; autoimmune disease; acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified amplified fragment length polymorphism assay - for detection of polymorphism esp. in micro:satellite regions.
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amplified fragment length polymorphism assay; microsatellite region; genetic trait marking; germplasm comparisons; compound; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genetic trait marking and germplasm comparisons
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Best Local Similarity 100.0
Matches 23; Conservative
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Georges M, Massey JM;

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primer extension (SNPE) primers, and the sequences of regions flanking stees of single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the includes kits for determining the presence or absence of a SNP, using the cligonucleotides of the invention. The PCR primers are used to amplify a coligonucleotides of the invention. The PCR primers are used to amplify a coligonucleotides are useful for genotyping a nucleic acid sample by performing a single-nucleotide primer extension reaction. The oligonucleotides are useful for determining the presence, absence or dentity of a SNP and for genotyping nucleic acid sample by coligonucleotides are useful for determining the presence, absence or identity of a SNP and for genotyping nucleic acid samples, for e.g. to assess by association analysis the genotype of an individual or group of individuals, having a pathological phenotypic traits include diseases e.g. agammaglobulinaemia, diabetes insipidus, besch Nyhan syndrome, muscular dystrophy, familial hypercholesterolaemia, polycystic kidney disease, osteogenesis imperfecta and caute intermittent porphyria. Phenotypic traits also include symptoms of or susceptibility to wulltifactorial catesase, including, rheumacoid arthritis, multiple sclerosis, contenting and inflammantion, cancer, nervous system diseases and infection and canterinty analysis. The present sequence represents a PCR primer specific contentity annalysis. The present sequence represents a PCR primer specific contents a human SNP containing DNA sequence
                                                                                                                                  New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
genetic mapping; traits; amplification; ss.
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100.0%; Pred. No. 30;
ive 0; Mismatches
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                                                                                                                                                                                                                   Claim 1; Page 59; 83pp; English
                 (ORCH-) ORCHID BIOSCIENCES INC
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                                                       Picoult-Newburg L, Pohl M;
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02-FEB-1993
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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 screening a library of bovine Mbol DNA fragments of between 250 and 500 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information of cor ca. 230 such bovine microsatellites is summarised in the sequence information specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                      Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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(first entry)
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                                              WPI; 1992-284684/34.
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02-FEB-1993
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AAQ33678
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Gaps ö Page 10

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at .300. The sequence information for ca. 230 such bovine microsatellites is summarised in the sequence information of chemicrosatellites sequence were used to generate the sequence PR primers for in vitro amplification of the corresp.

In crosatellite (using the program oPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonuclectide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequence upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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88.9%; Pred. No. 42;
ive 0; Mismatches
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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Best Local Simil
Matches 24, C
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02-FEB-1993
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AAQ33804
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Gaps

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microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polymorphic bovine DNA markers - used in genetic identification, gene
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                                                                                                 2.1%; Score 22.2; DB 1; Length 27; Matches 24; Conservative 0: Min.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Microsatellite sequence from clone TGLA98.
                                                                                                                                                                                                                       1793 TGTGTGTGTGTGTGTGTATAT 1819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cattle, to allow selective breedir
25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mapping, and selective breeding.
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                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
(first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                          AAQ34181;
                                                                                          field.)
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PCR, selection, primers, OPTIPRIM, breeding, cattle, parentage, genetic mapping, traits, amplification, ss.

92WO-US000340. 91US-00642342.

15-JAN-1992; 15-JAN-1991;

06-AUG-1992

WO9213102-A1

Bos taurus.

Sequence of a microsatellite from clone TGLA76.

(revised)
(first entry)

25-MAR-2003 02-FEB-1993

AAQ34143;

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Gaps
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  Indels
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3;
                                                                                                                                                                                                                                                                                                                                                                                                                            Microsatellite sequence from clone TGLA417.
0; Mismatches
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Conservative
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(first entry)
24; Conservative
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les 24; Conserv
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02-FEB-1993
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                                                                                                                                                                                                                                                                                          AAQ34012;
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Matches
  Matches
                                                                                                                                                                                    RESULT 15
                                                                                                                                                                                                              AAQ34012
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Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.

Georges M, Massey JM; WPI; 1992-284684/34.

(GENM-) GENMARK.

Table 7; Page 388; 517pp; English.

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The sequence is that of a bovine microsatellite sequence obtd, by screening a library of bovine MboI DNA fragments of between 250 and 500 by that an (ACI)5 and a (TCI)5 oligomucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information of specification and indexed herein (see below). The sequence information of equivalent of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

The microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economic trait loci, or genes involved the determinism of the correct PN individuals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.1%; Score 22.2; DB 1; Length 27; 88.9%; Pred. No. 42; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat sequence from polymorphic marker clone Mfd31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other;
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Best Local Similarity 88.5
Matches 24; Conservative
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17-JUN-1997
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AAQ34143 ID AAQ34143 standard; DNA; 27 BP.

RESULT 16

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Composition comprising synthetic oligonucleotides which comprise multiple repeats of dinucleotides such as GT, TG useful for treating cancer by inducing cell cycle arrest, inhibiting proliferation, activating
                                          (BION-) BIONICHE LIFE SCI INC.
 13-DEC-1999; 99US-0170325P.
29-AUG-2000; 2000US-0228925P.
                                                                       Phillips NC, Filion MC;
                                                                                                  WPI; 2001-398150/42.
                                                                                                                                                                         caspases.
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                                                                                                                                                                                                                                                                                                                                                       The invention relates to the isolation of polymorphic repeat sequences having the sequence (dc-da)n. (dd-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dc-dh). (dc-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf31 which contains the repeat sequence is from formula: (AC)13A. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                             4
                                                                                                                                                                                                                                                                                        Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic oligonucleotide, dinucleotide repeat, cytostatic, apoptosis, cell cycle arrest, cell proliferation, caspase, cytokine, interleukin, tumour necrosis factor, TNF, cancer, carcinoma, sarcoma, leukemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
linkage analysis, genetic disease, animal; plant, breeding, locus, hybridisation, chromosome; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.1%; Score 22.2; DB 1; Length 27; 88.9%; Pred. No. 42; ive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                Claim 1; Col 9-10; 186pp; English.
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                                                                                                                                                        89US-00341562.
91US-00754351.
                                                                                                                               94US-00222177.
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                                                                                                                                                                                                   (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 88.9
hes 24; Conservative
                                                                                                                                                                                                                                                           WPI; 1997-042299/04.
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                                             Homo sapiens
                                                                                                                               04-APR-1994;
                                                                                                                                                          21-APR-1989;
05-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-SEP-2001
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                                                                       US5582979-A
                                                                                                  10-DEC-1996
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                                                                                                                                                                                                                                Weber JL;
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The present sequence is that of a synthetic oligonucleotide useful to the invention. The invention relates to a composition, comprises multiple base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple repeats of dinucleotides such as GT, TG, etc., according to specific commula and having cytostatic activity. The oligonucleotide compositions are useful for inducing cell cycle arrest, inhibition of profileration, activation of caspases and induction of apoptosis or production of activation of caspases and induction of apoptosis or production of cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour necrosis factor (INF)-alpha by immune system cells, in an animal having cancer such as primary carcinoma, secondary sarcoma such as, leukemia, lymphoma, breast, prostate, colorectal, ovarian or bone cancer. The compositions induce apoptosis independent of Fas, p53/p21, p21/waf-1/CIP, p15(ink4B), p16(ink4), drug resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detection; polymorphism; perfect compound simple sequence repeat; adaptor directed primer; genome; genetic; ingarphinting; amplified fragment length polymorphism assay; microsatellite region; genetic trait marking; germplasm comparisons; compound; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
2.1%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 42;
Matches 24; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1793 TGTGTGTGTGTGTGTGTATATAT 1819
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Example 4; Page 16; 77pp; English.
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                                                                                                          Detecting polymorphisms between 2 nucleic acid samples, esp. in microsatellite regions, comprises digesting the nucleic acid to generate fragments, ligating adaptor segments to their ends, amplifying them using primer directed amplification and comparing the prods. to detect differences. The primers used in the amplification comprise a primer consisting of a perfect cpd. simple sequence repeat (SSR), and an adaptor directed primer, comprising a sequence complementary to an adaptor segment. The present sequence is an example of a compound SSR primer. The method represents a modified amplified fragment length polymorphism assay, which is partic. useful for genome fingerprinting, i.e. for genetic trait marking and germplasm comparisons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bovith an (AC)15 and a (TC)15 oligonuclectide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the
                Modified amplified fragment length polymorphism assay - for detection of polymorphism esp. in micro:satellite regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR; selection; primers, OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                                                                                                                                                                                                                                                                                                                                     Sequence 22 BP; 11 A; 6 C; 0 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Microsatellite sequence from clone TGLA327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1801 TGTGTGTGTGTATATATA 1822
                                                                           Disclosure; Fig 1c; 173pp; English
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(first entry)
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02-FEB-1993
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The sequence is that of a bovine microsatellite sequence obtd. by acceeding a library of bovine Mbol DNA fragments of between 250 and 500 by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information of specification and indexed herein (see below). The sequence information construction and indexed herein (see below). The sequences upstream and construction and indexed herein (see below). The sequence the required PCR primers for in vitro amplification of the corresp.

The microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-WAR-2003 to correct PN
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required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traite sep. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                DB 1; Length 25;
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                                                                                                                                                         Sequence 25 BP; 0 A; 0 C; 12 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                              2.1%; Score 21.8; D 92.0%; Pred. No. 44; ive 0; Mismatches
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Best Local Similarity 92.0
Matches 23; Conservative
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Sequence 25 BP; 0 A; 0 C; 12 G; 13 T; 0 U; 0 Other;

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Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                      Repeat sequence from polymorphic marker clone Mfd32.
           AAT65734 standard; DNA; 25 BP.
                                                                                                                                                                                                                                                                                                           89US-00341562.
91US-00754351.
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                                                               (revised)
(first entry)
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                                                                                                                                                                                                   Homo sapiens.
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17-JUN-1997
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                                      AAT65734;
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 DB 1; Length 25;
                           Indels
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2.1%; Score 21.8; Local Similarity 92.0%; Pred. No. 44; les 23; Conservative 0; Mismatches
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                                                      1793 TGTGTGTGTGTGTGTGTATAT
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                                                                                                                                               AAQ33962 standard; DNA; 25 BP.
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Matches 23, Conservative
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02-FEB-1993
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 Query Match
Best Local Si
Matches 23;
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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used to detect these markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Of ones containing the animal or plant breeding or pedigree analysis of of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated, The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf32 which contains the repeat sequence is from the marker clone Mdf32 which contains the repeat sequence is from the marker clone Mdf32 which contains the repeat sequence is from the marker clone Mdf32 which contains the repeat sequence is from the marker clone Mdf32 which contains the repeat sequence is from the marker clone Mdf32 which contains the repeat sequence is from the marker clone Mdf32 which contains the repeat sequence having the
Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
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                                                                                                                                                Disclosure; Col 9-10; 186pp; English.
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(first entry)
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RESULT 23

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 by with an (AC)15 and a (TC)15 oligomucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100,000. The sequence information of specification and indexed herein (see below). The sequence information specification and indexed herein (see below). The sequences upstream and sommarream of the microsatellite sequence water used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-WAR-2003 to correct PN
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                                                                                                                                                                                         Polymorphic bovine DNA markers - mapping, and selective breeding.
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                   91US-00642342
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                                                                                                          Georges M, Massey JM;
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                                                                (GENM-) GENMARK.
                     15-JAN-1991;
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02-FBB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC1)5 and a (TC)15 oligomuclecited probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information in the bovine genome is estimated at >100, 000. The sequence information conspecification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                           Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.1%; Score 21.8; DB 1; Length 26; 92.0%; Pred. No. 45; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 26 BP; 0 A; 0 C; 13 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Microsatellite sequence from clone TGLA123.
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(first entry)
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Matches 23; Conservative
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                                                                                                                                                                                                                                                                                               (GENM-) GENMARK.
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02-FEB-1993
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                                                                       Bos taurus.
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RESULT 25 AAQ33684

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 by thin an (AC115 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the sequence information for ca. 230 such bovine microsatellites sequence were used to generate the sequence por the microsatellite sequence were used to generate the required por primers for in vitro amplification of the corresp.

The sequence of the microsatellite sequence were used to generate the required por primers for in vitro amplification of the corresp.

The sequence of identify individuals, for parentage testing, and in the genetic used to identify individuals, for parentage testing, and in the genetic economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26 BP; 0 A; 0 C; 13 G; 13 T; 0 U; 0 Other;
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                                         Table 7; Page 211; 517pp; English
mapping, and selective breeding
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(first entry)
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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming in the probe. One out of 50 microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequence upstream and downstream of the microsatellite sequence were used to generate the required PCR primars for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trail loci, or genes involved the determinism of
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for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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(first entry)
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Gaps ; Oligonucleotide clamp 1, containing loop-and-branch forming region. HIV; pol; nef; oligonucleotide clamp; branched; macromolecule; ss.

(revised)
(first entry)

25-MAR-2003 04-OCT-1995

AAQ83951;

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Gaps

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3951/c AAQ83951 standard; DNA; 27 BP.

RESULT 30 AAQ83951,

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 close that ha (ACI)15 and a (TCI)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites and microsatellites is summarised in the powine genome is estimated at >100, 000. The sequence information of for ca. 230 such bowine microsatellites is summarised in the specification and indexed herein (see below). The sequence upstream and downstream of the microsatellite sequence were used to generate the microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                               Query Match 2.1%; Score 21.8; DB 1; Length 26; Best Local Similarity 92.0%; Pred. No. 45; Matches 23; Conservative 0; Mismatches 2; Indels
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              Sequence 26 BP; 0 A; 0 C; 13 G; 13 T; 0 U; 0 Other;
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                                                                                                                                 1793 TGTGTGTGTGTGTGTGTATAT 1817
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                                                                                                                                                                                                                                                                  AAQ33740 standard; DNA; 27 BP.
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(first entry)
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sos taurus.
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This sequence represents an oligonucleotide clamp which was used to bind a target sequence comprising a segment of the HIV pol and nef genes in single stranded or double stranded forms. This molecule forms a loop-and-branch configuration. An oligonucleotide clamp is a compound capable of forming a covalently closed macromolecule or a stable circular complex of forming a covalently closed macromolecule or a stable circular complex clamps generally comprise one or more oligonucleotide moieties capable of specific binding to the target molecule and one or more pairs of binding moieties covalently linked to the oligonucleotide moieties. Upon annealing of the oligonucleotides moieties to the target polynucleotide, the binding moieties of a pair are bought into juxtaposition so that they complex moieties of the binding moieties effectively clamps the specifically interaction of the binding moieties effectively clamps the specifically connealed oligonucleotides moieties to the target polynucleotide. (Updated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthesis of branched polymers and novel branched polymeric structures used as molecular probes esp. for detecting poly-nucleotide(s).
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                                                                                                                                                                                             Location/Qualifiers
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Query Match

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RESULT 31 AAH24300

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The invention relates to compositions for the treatment of cancers, comprising purified hyaluronic acid (HA) and a second antineoplastic comprising purified hyaluronic acid (HA) and a second antineoplastic comprising burified hyaluronic acid (HA) and a second antineoplastic object antineoplastic oligonuclectide. On its own, HA stimulates the production at incertainty of interpretainty of the cytokines interleukin-6 (IL-6) and IL-12 by immune system cells. Or combination, HA and the second antineoplastic agent of the composition act synergistically to potentiate each other's ability to inhibit of proliferation and induce apoptosis in cancer cells. Due to the synergy between the HA and the second antineoplastic agent, a reduced standard cose of the second antineoplastic agent can be used without compromising the therapeutic effectiveness of the cancer treatment. The reduction in cose the patient. In addition, as HA is inexpensive and as most cohemotherapeutic drug are expansive, thereby improving the quality of life chemotherapeutic drug are expansive, the combined use of that an decrease in cost address provide important benefits for mammals, concluding humans. The present sequence repersents a synthetic antineoplastic oligonucleotide which was used in a composition with HA in exemplification of the invention
                                                                                                                                                           Antineoplastic oligonucleotide; hyaluronic acid; HA; cytokine production; interleukin; IL-6; IL-12; synergistic action; standard dose reduction; side-effect reduction; drug resistance reduction; immunosensitisation reduction; cancer; tumour; cytostatic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Symergistic compositions comprising hyaluronic acid and Mycobacterium phlei DNA and cell walls, useful for treating cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 47;
Matches 23; Conservative 0; Mismatches 2; Indels
                                                                                                                       Synthetic antineoplastic oligonucleotide, SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 27 BP; 0 A; 0 C; 14 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 7; Page 23; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BION-) BIONICHE LIFE SCI INC.
AAH24300 standard; DNA; 27 BP
                                                                                                                                                                                                                                                                                                                                                                                               28-DEC-2000; 2000WO-CA001562.
                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0173375P.
                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phillips NC, Filion MC;
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                                                                                                                                                                                                                                                                                                               WO200147561-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                          28-DEC-1999;
                                                                                    21-SEP-2001
                                                                                                                                                                                                                                                                                                                                                          05-JUL-2001
                                                                                                                                                                                                                                                                          Synthetic
                                            AAH24300;
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1793 TGTGTGTGTGTGTGTGTATAT 1817

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AAH46017 standard; DNA; 27 BP.

AAH46017 RESULT 32
AAH46017
ID AAH46
XX
AC AAH46

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The present sequence is that of a synthetic cligonuclectide useful to the invention. The invention relates to a composition, comprising a 2 to 20 base 3'-OH, 5'-OH synthetic oligonuclectide which comprises multiple repeats of dinuclectides such as QT, TG, etc., according to specific formula and having cytostatic activity. The oligonuclectide compositions are useful for inducing cell cycle arrest, inhibition of proliferation, are useful for inducing cell cycle arrest, inhibition of proliferation, cytokines such as interleukin (IL)-1.beta, IL-6, IL-10, IL-12 and tumour necrosis factor (INF)-alpha by immune system cells, in an animal having cancer such as primary carcinoma, secondary carcinoma, primary sarcoma and secondary sarcoma such as, leukemia, lymphoma, breast, prostate, colorectal, ovarian or bone cancer. The compositions induce apportesis induceable apportesis is independent of Fas, p53/p21, p21/waf-1/CIP, p15(ink4B), p16(ink4), drug resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor
                                                                                 Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis; cell cycle arrest; cell proliferation; caspase; cytokine; interleukin; tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Composition comprising synthetic oligonucleotides which comprise multirepeats of dinucleotides such as GT, TG useful for treating cancer by inducing cell cycle arrest, inhibiting proliferation, activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 74; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         (BION-) BIONICHE LIFE SCI INC.
                                                                                                                                                                                                                                                                                                             12-DEC-2000; 2000WO-CA001467.
                                                                                                                                                                                                                                                                                                                                                 13-DEC-1999; 99US-0170325P.
29-AUG-2000; 2000US-0228925P.
                                                      Synthetic oligonucleotide 17.
                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phillips NC, Filion MC;
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                                                                                                                                                                                                                                    WO200144465-A2.
                  12-SEP-2001
                                                                                                                                                          lymphoma; ss
                                                                                                                                                                                                                                                                         21-JUN-2001
                                                                                                                                                                                              Synthetic.
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Gaps ; 0 Query Match

2.1%; Score 21.8; DB 1; Length 27;

Best Local Similarity 92.0%; Pred. No. 47;

Matches 23; Conservative 0; Mismatches 2; Indels 1793 TGTGTGTGTGTGTGTATAT 1817 ð

Sequence 27 BP; 0 A; 0 C; 14 G; 13 T; 0 U; 0 Other;

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0; Gaps

AAH46001 standard; DNA; 27 12-SEP-2001 (first entry) AAH46001; RESULT 33

Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis; cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;

Synthetic oligonucleotide 1.

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12-JAN-1996;
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02-FEB-1993
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                                                    Horn T;
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                                                                                                                                                                                                                      Composition comprising synthetic oligonucleotides which comprise multiple repeats of dinucleotides such as GT, TG useful for treating cancer by inducing cell cycle arrest, inhibiting proliferation, activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
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Pred. No. 47;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                              Example 4; Page 16; 77pp; English.
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                                                                                                                                                       (BION-) BIONICHE LIFE SCI INC
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                                                                                                 12-DEC-2000; 2000WO-CA001467.
                                                                                                                      13-DEC-1999; 99US-0170325P.
29-AUG-2000; 2000US-0228925P.
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Best Local Similarity 92.0%;
Matches 23; Conservative
                                                                                                                                                                            Filion MC;
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                                                      WO200144465-A2
              lymphoma; ss
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                                  Synthetic.
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                                                                                                                                                                                                                                              Synthesizing branched nucleic acids useful as diagnostic and molecular probes, involves combining first units having haloalkylamino groups and second units having thiol or phosphorothicate groups.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 21.8; DB 1; Length 27;
Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 27 BP; 13 A; 14 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Microsatellite sequence from clone TGLA110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genetic mapping; traits; amplification; ss.
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96US-0009918P.
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Best Local Similarity 92.0%;
Matches 23; Conservative
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(first entry)
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                                                                                                                                                                                           WPI; 2001-201911/20
                                                             (FARB ) BAYER CORP.
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screening a library of bovine Mbol DNA fragments of between 250 and 500 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (76)n >9 microsatellites and mbol sites, the frequency of (76)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequence information specification and indexed herein (see below). The sequence upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be microsatellite (using the program OPTIPRIM). The microsatellites may be enonemic trail loci, or genes involved the determinism of economic trails esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                              Score 21.4; DB 1; Length 23;
Pred. No. 46;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                           Seguence 23 BP; 0 A; 0 C; 11 G; 12 T; 0 U; 0 Other;
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Best Local Similarity 95.7%;
Matches 22; Conservative
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(first entry)
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02-FEB-1993
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AAQ33773
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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information of specification and indexed herein (see below). The sequence information of committee for microsatellite sequence were used to generate the cequired PCR primers for in vitro amplification of the corresp. microsatellite (using the program oPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trail loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loot, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct Pl
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                                                                                                                                          Query Match 2.0%; Score 21.4; DB 1; Length 23; Best Local Similarity 95.7%; Pred. No. 46; Matches 22; Conservative 0; Mismatches 1; Indels
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                                                                                                        Sequence 23 BP; 0 A; 0 C; 11 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Microsatellite sequence from clone TGLA304.
                                                                                                                                                                                                                1793 TGTGTGTGTGTGTGTGTAT 1815
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                                                                                                                                                                                                                                                                                                                                            AAQ33885 standard; DNA; 23
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(first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2003
02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                AAQ33885;
                                                                        field.)
                                                                                                                                                                                                                                                                                                        RESULT 37
                                                                                                                                                                                                                                                                                                                           AAQ33885
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Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPB; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis imperfecta; autoimmune disease; acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                               New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic
                            SNP specific upper PCR primer SEQ ID 1801.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 59; 83pp; English.
                                                                                                                                                                                                                                                                                             (ORCH-) ORCHID BIOSCIENCES INC.
                                                                                                                                                                                                                                       13-OCT-2000; 2000WO-US028436.
14-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-290930/30
                                                                                                                                                                                                                                                                                                                         Piccult-Newburg L,
                                                                                                                                                                                  WO200129262-A2
                                                                                                                                                                                                                                                                    15-OCT-1999;
                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                            acid sample.
                                                                                                                                                                                                             26-APR-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic enalysis such as linkage analysis of genetic disease, commercial animal or plant breadthy or pedigree analysis. The sequences AAT66084-166107 represent repeat sequences of low informativeness found in chromosomal clone SW13. The sequence is found in the human chromosomal clone SW13. The sequence is amplified by primers AAT66106-7. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                     Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols, as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.0%; Score 21.4; DB 1; Length 23; llarity 95.7%; Pred. No. 46; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                           Repeat sequence found in the human chromosomal clone SW13.
     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23 BP; 12 A; 11 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 46;
0; Mismatches
     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1793 TGTGTGTGTGTGTGTGTAT 1815
                               1793 TGTGTGTGTGTGTGTGTAT 1815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 9; Col 61-62; 186pp; English.
                                                           rerererererererererer
                                                                                                   RESULT 38
AAT66105/c
ID AAT66105 standard; DNA; 23 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                       89US-00341562.
91US-00754351.
                                                                                                                                                                                   (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MARS-) MARSHFIELD CLINIC
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-042299/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
tes 22; Conserv
                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                       21-APR-1989;
05-SEP-1991;
                                                                                                                                                                                   25-MAR-2003
18-JUN-1997
                                                                                                                                                                                                                                                                                                                                                       JS5582979-A.
                                                                                                                                                                                                                                                                                                                                                                                   10-DEC-1996
    22;
                                                                                                                                                         AAT66105;
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Matches
     Matches
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99US-0160096P.

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primer extension (SNPE) primers, and the sequences of regions flanking sites of single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the oligonucleotides of the invention. The PCR primers are used to amplify a single-nucleotide primer is used as a genotyphing primer. The oligonucleotides are useful for genotyping a nucleic acid sample by performing a single-nucleotide primer extension reaction. The oligonucleotides are useful for determining the presence, absence or identity of a SNP and for genotyping nucleic acid sample by performing a single-nucleotide primer extension reaction. The cligonucleotides are useful for determining the presence, absence or identity of a SNP and for genotyping nucleic acid sample by performing a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic trait suspected of being caused by one or more SNPs. Phenotypic trait suspected of being caused by one or more SNPs. Phenotypic trait suspected of being caused by one or more SNPs. Phenotypic trait suspected of being caused by one or more SNPs. Phenotypic trait suspected of being caused by one or more SNPs. Phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include disease e.g. caterosis imperfects and acute intermittent porphyria. Phenotypic craits also include symptomes of or susceptibility to multifactorial disease of which a component is or may be genetic such as autoimmune configurates also include symptoms of or susceptibility to multifactorial diseases, including, rheumatoid arthritis, multiple sclerosis.

Configurates also include symptoms system diseases and infection by pathogenic microorganism. The method is also useful in forensic investigations and microorganism propertices.
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2.0%; Score 21.4; DB 1; Length 23;.
Best Local Similarity 95.7%; Pred. No. 46;
Matches 22; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 23 BP; 0 A; 0 C; 10 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for a human SNP containing DNA sequence
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AAQ33986 standard; DNA; 24 BP.

AAQ33986;

AAQ33986 ID AAQ3 XX AC AAQ3

AAH39005 standard; DNA; 23

AAH39005

RESULT 39
AAH39005 TD AAH39
XX
AC AAH39

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 screening a library of bovine MboI DNA fragments of between 250 and 500 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100,000. The sequence information of specification and indexed herein (see below). The sequence information constream of the microsatellite sequence ware used to generate the microsatellite sequence ware used to generate the microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                   Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                             PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 21.4; DB 1; Length 24;
Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence of a microsatellite from clone TGLA80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.0%; Score 21.4; DB Best Local Similarity 95.7%; Pred. No. 47; Matches 22; Conservative 0; Mismatches
                                                               Microsatellite sequence from clone TGLA382.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1793 TGTGTGTGTGTGTGTGTAT 1815
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Table 7; Page 324; 517pp; English.
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                                                                                                                                                                                                                                                                         91US-00642342.
                                                                                                                                                                                                                                          92WO-US000340,
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(first entry)
                                  (first entry)
                                                                                                                                                                                                                                                                                                                                       Georges M, Massey JM;
                  (revised)
                                                                                                                                                                                                                                                                                                                                                                        WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                          (GENM-) GENMARK.
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02-FEB-1993
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                                                                                                                                                                          WO9213102-A1
                                                                                                                                                                                                                                          .5-JAN-1992;
                  25-MAR-2003
                                  02-FEB-1993
                                                                                                                                                                                                             06-AUG-1992.
                                                                                                                                             Bos taurus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ34158;
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AAQ34158
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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information of or ca. 230 such bovine microsatellites is summarised in the sequence information of specification and indexed herein (see below). The sequences upstream and specification and indexed herein (see below). The sequences upstream and commistream of the microsatellite sequence were used to generate the required prayments for in vitro amplification of the corresp.

The construction of economic trait loci, or parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective to breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                        - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 47;
Matches 22; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1793 TGTGTGTGTGTGTGTGTAT 1815
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                                                                                                                                                                                                                                                                                           Table 7; Page 394; 517pp; English.
                                                                                                                                                                                                                                           Polymorphic bovine DNA markers - mapping, and selective breeding.
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                                                                           92WO-US000340.
                                                                                                             91US-00642342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first entry)
                                                                                                                                                                          Georges M, Massey JM;
                                                                                                                                                                                                           WPI; 1992-284684/34.
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                                                                                                                                              (GENM-) GENMARK.
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                                                                                                             15-JAN-1991;
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02-FEB-1993
              WO9213102-A1
                                                                           15-JAN-1992;
                                             06-AUG-1992.
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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 by thin an (AC1)5 and a (TC)15 oligomiclecited probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information of cor ca, 230 such bovine microsatellites is summarised in the sequence information of specification and indexed herein (see below). The sequences upstream and specification and indexed herein (see below). The sequences upstream and constructed PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in catelle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                  Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cuery Match 2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 47;
Matches 22; Conservative 0; Mismatches 1. T-2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Microsatellite sequence from clone TGLA444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1793 TGTGTGTGTGTGTGTGTAT 1815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 rerererererererererer 24
                                                                                                                                       Table 7; Page 293; 517pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
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                                                  WPI; 1992-284684/34.
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                             field.)
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92WO-US000340. 91US-00642342

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ine bequence is that on a bovine microsacellite sequence obled. by graceful alphrary of bovine Mbol DNA fragments of between 250 and 500 by with an (AC)15 and a (FC)15 oligomucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of 6 microsatellites and Mbol sites, the frequency of (FG)n >9 microsatellites on the bovine genome is estimated at >100, 600. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequence information for ca. 230 such bovine microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

microsatellite (using the program OPTIPRIM). The microsatellites may be nicrosatellite (using the program oPTIPRIM). The microsatellites may be expensed to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective in the correct PN is presedung. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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0
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sequence is that of a bovine microsatellite sequence obtd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 21.4; DB 1; Length 24;
Pred. No. 47;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Microsatellite sequence from clone TGLA423.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR's selection, primers, OPTIPRIM, breeding genetic mapping, traits, amplification, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1793 TGTGTGTGTGTGTGTGTAT 1815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ34024 standard; DNA; 24 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 95.7%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENM-) GENMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9213102-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-AUG-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ34024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ34024
XXX
AAQ34024
XXX
AAQ34024
DJT 25-P
DJT 02-F
DJT 
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1; Indels

95.7%; Pred. No. 4.7; cive 0; Mismatches

22; Conservative

Best Local Similarity Matches 22; Conserv

1793 TGTGTGTGTGTGTGTGTAT 1815

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to correct PN

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Gaps

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The sequence is that of a bovine microsatellite sequence obtd. by creening a library of bovine MboI DNA fragments of between 250 and 500 cc bp with an (AC)15 and a (TC)15 oligonuclectide probe. One out of 50 cc ones cross-hybridised. Assuming independent distribution of fractions cross-thybridised. Assuming independent distribution of fractions and MboI sites the frequency of (T6)n >9 microsatellites and MboI sites the frequency of (T6)n >9 microsatellites on the bovine genome is estimated at >100, 000. The sequence information of for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the credited PCR primers for in vitro amplification of the corresp.

Trequired PCR primers for in vitro amplification of the corresp.

The microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of connecting important traits esp. in cattle, to allow selective in field.)
microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-WAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                           Query Match 2.0%; Score 21.4; DB 1; Length 24; Best Local Similarity 95.7%; Pred. No. 47; Matches 22; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                        Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Microsatellite sequence from clone TGLA131.
                                                                                                                                                                                                                                                                                 1793 TGTGTGTGTGTGTGTGTAT 1815
                                                                                                                                                                                                                                                                                                         1 TGTGTGTGTGTGTGTGTGTGT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Table 7; Page 213; 517pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ33707 standard; DNA; 24 BP.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JAN-1991;
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ33707;
                                                                                                                                                                                                                                                                                                                                                                                          RESULT 45
AAQ33707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88888888
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2.0%; Score 21.4; DB 1; Length 24;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                     Polymorphism; repeat sequence; genetic marker; primer; amplification;
PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
linkage analysis; genetic disease; animal; plant; breeding; locus;
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                                                                                                                                     Repeat sequence found in the human chromosomal clone JW42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24 BP; 12 A; 12 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 9; Col 61-62; 186pp; English
                                 ВЪ.
                                                                                                                                                                                                                         hybridisation; chromosome; ds
89US-00341562.
91US-00754351.
                                                                                                                                                                                                                                                                                                                                                94US-00222177
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AAH46015
ID AAH46'
XX
AC AAH46
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necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia; lymphoma; ss. Best Local Matches δ g The present sequence is that of a synthetic oligonucleotide useful to the invention. The invention relates to a composition, comprises multiple base 3'-04, 5'-0H synthetic oligonucleotide which comprises multiple repeats of dinucleotides such as GT, TG, etc., according to specific formula and having cytostatic activity. The oligonucleotide compositions are useful for inducing call cycle arrest, inhibition of proliferation, activation of caspases and induction of apoptosis or production of activation of caspases and induction of apoptosis or production of cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour necrosis factor (TNF)-alpha by immune system cells, in an animal having cancer such as primary carcinoma, secondary carcinoma, prostate, and secondary sarcoma such as, leukemia, lymphoma, breast, prostate, colorectal, ovarian or bone cancer. The compositions induce apoptosis independent of Fas, p53/p21, p21/waf-1/CIP, p15(ink4B), p16(ink4), drug resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor Composition comprising synthetic oligonuclectides which comprise multiple repeats of dinuclectides such as GT, TG useful for treating cancer by inducing cell cycle arrest, inhibiting proliferation, activating caspases. Synthetic oligomucleotide; dinucleotide repeat; cytostatic; apoptosis; cell cycle arrest; cell proliferation; caspase; cytokine; interleukin; tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia; Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other; Example 4; Page 17; 77pp; English (BION-) BIONICHE LIFE SCI INC. 13-DEC-1999; 99US-0170325P. 29-AUG-2000; 2000US-0228925P. 12-DEC-2000; 2000WO-CA001467 Synthetic oligonucleotide 15. Phillips NC, Filion MC, WPI; 2001-398150/42. WO200144465-A2. lymphoma, ss 12-SEP-2001 21-JUN-2001 Synthetic.

ö Gaps ô Query Match
2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 47;
Matches 22; Conservative 0; Mismatches 1; Indels

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AAH46016 standard; DNA; 24 AAH46016;

ВР

12-SEP-2001 (first entry)

Synthetic oligonucleotide 16.

Synthetic oligonucleotide, dinucleotide repeat; cytostatic; apoptosis; cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;

The present sequence is that of a synthetic oligomucleotide useful to the invention. The invention relates to a composition, comprises multiple base 3'-OH, 5'-OH synthetic oligomucleotide which comprises multiple repeats of dinucleotides such as GT, TG, etc., according to specific commis and having cytostatic activity. The oligomucleotide compositions are useful for inducing cell cycle arrest, inhibition of proliferation, cutivation of caspases and induction of apoptosis or production of cytokines such as interlenkin (IL) 1-beta, IL-6, IL-10, IL-12 and tumour nerosis factor (TMF)-alpha by immune system cells, in an animal having cancer such as primary carcinoma, secondary carcinoma, present of secondary sarcoma such as, leukemia, lymphoma, breast, prostate, colorectal, ovarian or bone cancer. The compositions induce apported to Fas, p53/p21, p21/waf-1/CIP, p15(ink4B), p16(ink4), drug resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor ö Composition comprising synthetic oligonucleotides which comprise multiple repeats of dinucleotides such as GT, TG useful for treating cancer by inducing cell cycle arrest, inhibiting proliferation, activating 0; Gaps / Match 2.0%; Score 21.4; DB 1; Length 24; Local Similarity 95.7%; Pred. No. 47; les 22; Conservative 0; Mismatches 1; Indels Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other; 1793 TGTGTGTGTGTGTGTGTAT 1815 24 rererererererererererer Claim 6; Page 17; 77pp; English. (BION-) BIONICHE LIFE SCI INC. 12-DEC-2000; 2000WO-CA001467. 13-DEC-1999; 99US-0170325P. 29-AUG-2000; 2000US-0228925P. Phillips NC, Filion MC; WPI; 2001-398150/42 WO200144465-A2. 21-JUN-2001 Synthetic. савравев. Query Match

AAF99862 standard; DNA; 24 BP. RESULT 49

(first entry) 12-JUN-2001 AAF99862;

Immunostimulatory nucleic acid #978.

Vaccine, cytostatic; virucidal, bactericidal, fungicidal, anti-parasitic, immunostimulatory, tumour; viral infection; bacterial infection; fungal infection; parasitic infection; cancer; asthma; infectious disease; allergy; immune deficiency; phosphorothioate; ss.

Synthetic

WO200122972-A2

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Claim 101; Page 59; 338pp; English
                                                            Krieg AM, Schetter C, Vollmer J;
                                                                                                                                                                                                                                                                            ABS78584 standard; DNA; 24 BP.
                     25-SEP-1999; 99US-0156113P.
27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
                                                                                                                                                                                                                                                                                                                                                                                                             14-DEC-2001; 2001WO-US048458.
           25-SEP-2000; 2000WO-US026383.
                                                                                                                                                                                                              Query Match
Best Local Similarity 95,7%;
Matches 22; Conservative
                                           (IOWA ) UNIV IOWA RES FOUND.
(COLE-) COLEY PHARM GMBH.
                                                                                                                                                                                                                                                                                                   (first entry)
                                                                        WPI; 2001-273485/28
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05-APR-2001
                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                       ABS78584;
                                                                                                                                                                                                                                                                 RESULT 50
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The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antianglogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antianglogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid turnour growth, turnour metastasis, precancerous leason, rheumatorid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, evascular glaucoma, retrolental fibroplasia, rubecsis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, your metastasis, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic administration.
                                                                                                                                                                                                                                                                                                           Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunostimulatory, antiinflammatory, dermatological, antipsoriatic; antiulcer; gene therapy, vaccine, non-allergic inflammatory disease; psoriasis, eczema, allergic contact dermatitis, latex dermatitis; inflammatory bowel disease, ulcerative colitis, crohn's disease; ss. inflammatory bowel disease, ulcerative colitis, crohn's disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.0%; Score 21.4; DB 1; Length 24; Best Local Similarity 95.7%; Pred. No. 47; Matches 22; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
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                                                                            (COLE-) COLEY PHARM GROUP INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACH03377 standard; DNA; 24 BP
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14-DEC-2000; 2000US-025534P.
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                                                                                                                                                                                                                                      WPI; 2002-566690/60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2003050268-A1.
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                                                                                                                                                              Bratzler RL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THE STATE OF THE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Th2 to a Th1 immune response and to activate immune cells. Note: the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth; tumour metastasis; psecancerous lesion; rheumatorid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rubeosis; Osler-Webber Syndrome; myocardial anglogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; anglofibroma; wound granulation; intestinal adhebion; atherosclerosis; scleroderma; hypertrophic scar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 21.4; DB 1; Length 24; Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present sequence may have a phosphorothicate backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Angiogenesis inhibitory oligonucleotide #1068.
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Treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic contact dermatitis, latex dermatitis or inflammatory bowel

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Gaps

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1793 TGTGTGTGTGTGTGTGTAT 1815

1 IGRETERGEGEGEGETET 23

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AAQ33861 standard; DNA; 25

25-MAR-2003 02-PEB-1993

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Gaps ò

AAQ33861;

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The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G nucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy especially in a hypo-responsive subject. The present sequence represents an immunostimulatory nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
                                                                   The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing ann-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic contact dermatitis, latex dermatitis or inflammatory bowel disease e.g., ulcerative colitis or Croin's disease. This sequence represents an immunostimulatory nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ds; allergy; asthma; poly-G nucleic acid; aerosol formulation; hypo-responsive subject; immunostimulatory.
                                                                                                                                                                                                                                                                              Query Match
2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 47;
Matches 22; Conservative 0; Mismatches 1; Indels
disease by administering an immunostimulatory nucleic acid.
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                                                                                                                                                                                                                                              Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 20; 221pp; English.
                                      Disclosure; Page 36; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunostimulatory nucleic acid #978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADB37364 standard; DNA; 24 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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(PETE/) PETERSEN D M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-657977/62
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FOUR/) FOURON Y.
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ADB37364
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The sequence is that of a bovine microsatellite sequence obtd, by screening a library of bovine MboI DNA fragments of between 250 and 500 screening a library of bovine MboI DNA fragments of between 250 and 500 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100,000. The sequence information of cor ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequence information committee propries for in vitro amplification of the corresp. microsatellite (using the program oPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trail loci, or general the determinism of economically important trails esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                                                   PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.0%; Score 21.4; DB 1; Length 25; 95.7%; Pred, No. 49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                        Microsatellite sequence from clone TGLA264.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Table 7; Page 274; 517pp; English.
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                                                          (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                 (GENM-) GENMARK.
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AAH40163/c
ID AAH4016
XX
AC AAH4016
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Gaps

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2.0%; Score 21.4; DB 1; Length 24; 95.7%; Pred. No. 47; ative 0; Mismatches 1; Indels

Local Similarity 95.7 tes 22; Conservative

Best Loca Matches

Query Match

14-AUG-2001

SNP specific SNPE primer SEQ ID 2959

Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; Lesch.Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenestecta; autoimmune disease; acute intermittent porphyria; rheumacoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; primer; ss.

Homo sapiens.

WO200129262-A2.

26-APR-2001

13-OCT-2000; 2000WO-US028436.

99US-0160096P. .5-OCT-1999; ORCH-) ORCHID BIOSCIENCES INC.

Pohl M; Picoult-Newburg L,

WPI; 2001-290930/30.

New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic acid sample.

Claim 1; Page 65; 83pp; English.

primer extension (SNPB) primers, and the sequences of regions flanking after extension (SNPB) primers, and the sequences of regions flanking interests are used to said a single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the includes kits for determining the presence or absence of a SNP, using the coligonucleotides are useful for genetyping a mucleic acid sample by performing a single-nucleotide primer extension reaction. The oligonucleotides are useful for genetyping a mucleic acid sample by performing a single-nucleotide primer extension reaction. The cliquoucleotides are useful for determining the presence, absence or identity of a SNP and for genotyping nucleic acid sample by performing a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include diseases e.g. agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, familial hypercholesterolesmia, polycystic kiney disease.

Coffeentophy, familial hypercholesterolesmia, polycystic kiney disease, captering and acute intermittent porphyria. Phenotypic traits also include symptoms of or susceptibility to multifactorial diseases, including, rheumatoid arthritis, multiple sclerosis, inflammation, cancer, nervous system diseases and infection by pathogenic microorganism. The method is also useful in forensic investigations and paternity analysis. The present sequence represents a single nucleotide paterning DNA primer extension (SNPE) primer specific for a human SNP containing DNA

Sequence 25 BP; 12 A; 12 C; 1 G; 0 T; 0 U; 0 Other;

Gaps ô DB 1; Length 25; Indels 2.0%; Score 21.4; D 95.7%; Pred. No. 49; tive 0; Mismatches Conservative Local Similarity es 22; Conserv Query Match Matches

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AAH38303 ID

AAH38303 standard; DNA; 25

AAH38303;

(first entry) 14-AUG-2001 SNPE primer SEQ ID 1099. SNP specific Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteopeesis imperiecta; autoimmune disease; acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; primer; ss.

Homo sapiens.

WO200129262-A2.

26-APR-2001

13-OCT-2000; 2000WO-US028436

99US-0160096P. 15-OCT-1999; (ORCH-) ORCHID BIOSCIENCES INC.

Ξ Pohl Picoult-Newburg L,

WPI; 2001-290930/30

New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic acid sample.

Claim 1; Page 55; 83pp; English

Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide continues that the sequences of regions flanking sites of single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the coligonucleotides of the invention. The PCR primers are used to amplify a coligonucleotides are useful for genotyping a nucleic acid sample by performing a single-nucleotide primer extension reaction. The clientity of a SNP and for genotyping uncleic acid sample by clientity of a SNP and for genotyping nucleic acid sample by clientity of a SNP and for genotyping uncleic acid samples, for e.g. clientity of a SNP and for genotyping nucleic acid samples, for e.g. clientity of a snear SNPs. Phenotypic trait suspected of being caused by one or more SNPs. Phenotypic trait suspected of being agammaqlobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, familial hypercholesterolaemia, polycystic kidney disease, of extended single-fects and acute intermittent porphyria. Phenotypic traits also include symptoms of or susceptibility to multifactorial diseases of which a component is or may be genetic such as autoimmune configuration, cancer, nervous system diseases and infection by pathogenic microrganism. The method is also useful in forensic investigations and microcraganism. The method is also useful in forensic investigations and contraining number of presents a single mucleotide. primer specific for a human SNP containing DNA paternity analysis. The present sequence primer extension (SNPE) primer specific sequence

Sequence 25 BP; 0 A; 0 C; 13 G; 12 T; 0 U; 0 Other;

·. Match 20.0%; Score 21.4; DB 1; Length 25; Local Similarity 95.7%; Pred. No. 49; les 22; Conservative 0; Mismatches 1; Indels Query Match Matches

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Gaps

1793 TGTGTGTGTGTGTGTGTAT 1815 24 rerererererererererer

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The sequence is that of the target sequence #8 which was used in an experiment to determine the in vitro cleavage of target duplaces to evaluate the lengths of purine and pyrimidine tracts which are useful in obtaining oligonuclectides capable of triple helix formation with target nucleic acids. The complementary strand overhangs the 3' and by the sequence CTAG and the sense strand overhangs the complementary strand by the sequence AATT. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                           New oligo:nucleotide(s) forming triple helix with target nucleic acid contain purine and pyrimidine tracts in specific orientations, useful therapeutically or diagnostically e.g. for inactivating HIV RNA, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polymorphic bovine DNA markers - used in genetic identification, gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.0%; Score 21.2; DB 1; Length 26;
88.5%; Pred. No. 53;
ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26 BP; 2 A; 1 C; 11 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Microsatellite sequence from clone TGLA307.
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                                                                                                                                                                                                                                                                                                                                                                                         Example, Fig 14a; 101pp; English
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                                                                                                                                                                                                                                         Johnston BH;
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Best Local Similarity 88.5
Matches 23, Conservative
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                                 WO9312230-A1
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21-JAN-1992;
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02-FEB-1993
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequences given in AAQ41176-77 represent triplex forming oligonatic locals mucleotides which bind to the mRNA sequence of the MHC class II locus DR A structural gene at positions 851-876. The sequences given in AAQ47176-80 represent control oligomers which contain base compositions similar to that around this DR A region but not containing the correct sequences. DR is a transplantation antigen. Binding of this sequence to the DR A gene inhibits antigen production. This method may be used for treating individuals with autoimmune disease, characterised by dysfunctional cappession of a transplantation antigen. It may also be used to produce cells which are more easily transplanted into a recipient. (Updated on 25-003 to correct PN file1d.)
                                                                                                                                                                                   MHC; major histocompatability complex; class II; control oligomers; DR A_i transplantation; antigen; autoimmune disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Depletion of transplantation antigens in donor cells - using anti-sense or triplex-forming oligonucleotide(s), used for treating auto-immune disease and in transplants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Best Local Similarity 95.7%; Pred. No. 50;
Matches 22; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Huey B,
                                                                                                                                                   WHC DR A intron binding oligomer GTcon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 rererererererererererer 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example; Page 22; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hunt A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ44016 standard; DNA; 26 BP
                   AAQ47179 standard; DNA; 26 BP
                                                                                                                                                                                                                                                                                                                                                                                             92US-00830427.
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(first entry)
                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Garovoy MR,
                                                                                             (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1993-258367/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Target sequence #8
                                                                                                                                                                                                                                                                                 WO9314769-A1
                                                                                                                                                                                                                                                                                                                                                           29-JAN-1993;
                                                                                                                                                                                                                                                                                                                                                                                               31-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                 14-SEP-1992;
                                                                                         25-MAR-2003
25-JAN-1994
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28-OCT-1993
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                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ44016;
                                                       AAQ47179;
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 AAQ47179
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AAQ4401

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The sequence is that of a bovine microsatellite sequence obtd, by screening a library of bovine MboI DNA fragments of between 250 and 500 by thin an (AC.)15 and a (TC.)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100,000. The sequence information for ca. 230 such bovine microsatellites is summarised in the sequence information consistence of the microsatellite sequence were used to generate the required pCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits egp. in cattle, to allow selective in the correct PN is in the correct of the correct PN is included the correct of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonuclectide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.0%; Score 21; DB 1; Length 21; 100.0%; Pred. No. 47; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Microsatellite sequence from clone TGLA301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1793 TGTGTGTGTGTGTGTGT 1813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rable 7; Page 281; 517pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21
                                                  Table 7; Page 286; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymorphic bovine DNA markers - mapping, and selective breeding.
mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TGTGTGTGTGTGTGTGTGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JAN-1992;
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ33879;
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          specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIRRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detection of polymorphic genetic markers of the form (dC-dA) n (dG-dT) n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                            Gaps
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such bovine microsatellites is summarised in the
                                                                                                                                                                                                                                                2.0%; Score 21; DB 1; Length 21;
100.0%; Pred. No. 47;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat sequence from polymorphic marker clone Mfd37.
                                                                                                                                                                                                               Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Col 9-10; 186pp; English
                                                                                                                                                                                                                                                                                                                                    1793 TGTGTGTGTGTGTGTGT 1813
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                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-042299/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-APR-1994;
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05-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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17-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT65738;
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The present sequence is that of a synthetic oligonuclectide useful to the invention. The invention relates to a composition, comprising a 2 to 20 base 3 'OH, 5 'OH synthetic oligonucleotide which comprises multiple repeats of dinucleotides such as GT, TG, etc., according to specific formula and having cytostatic activity. The oligonucleotide compositions are useful for inducing cell cycle arrest, inhibition of proliferation, activation of caspases and induction of apoptosis or production of activation of caspases and induction of apoptosis or production of activation of caspases and induction of apoptosis or production of activation of activation of such as interleukin (IL)-1.beta, IL-6, IL-10, IL-12 and tumour necrosis factor (TNF)-alpha by immune system cells, in an animal having cancer such as primary carcinoma, secondary carcinoma, primary sarcoma and secondary sarcoma such as, leukemia, lymphoma, breast, prostate, colorectal, ovarian or bone cancer. The compositions induce apoptosis is independent of Fas, p53/p21, p21/waf-1/CIP, p15(ink4B), p16(ink4), drug resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Composition comprising synthetic oligonucleotides which comprise multiple repeats of dinucleotides such as GT, TG useful for treating cancer by inducing cell cycle arrest, inhibiting proliferation, activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic oligonuclectide; dinuclectide repeat; cytostatic; apoptosis; cell cycle arrest; cell proliferation; caspase; cytokine; interleukin; tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
                                                                                                Gaps
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Conservative 0; Mismatches 0; Indels
                                                  Query Match 2.0%; Score 21; DB 1; Length 21; Best Local Similarity 100.0%; Pred. No. 47; Matches 21; Conservative 0; Mismatches 0; Indels
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               Seguence 21 BP; 11 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                       1793 TGTGTGTGTGTGTGTGT 1813
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                                                                                                                                                                                                                                                                                 AAH46013 standard; DNA; 21 BP
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29-AUG-2000; 2000US-0228925P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-DEC-2000; 2000WO-CA001467.
                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic oligonucleotide 13.
                                                                                                                                                                                                                                                                                                                                                                    12-SEP-2001 (first entry)
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Local Sim.
21;
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                                                                                                                                                                                                                                                                                                                               AAH46013;
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                                                                                                                                                                                                                                                                    AAH46013
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The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects adjanst tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, alleryy or immune deficiency. The present sequence can also be used to redirect a Thi immune response and to activate immune cells. Note: the
                                                                                                                                                                                                                                                                             Vaccine, cytostatic, virucidal, bactericidal, fungicidal, anti-parasitic, immunostimulatory, tumour, viral infection, bacterial infection, fungal infection, parasitic infection, cancer, asthma; infectious disease, allergy, immune deficiency, phosphorothioate, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccinating against tumors, infectious diseases, allergies and asthmausing immunostimulatory Py-rich and TG nucleic acids.
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                                                                                                                                                                                                                                                 Immunostimulatory nucleic acid #818.
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1793 TGTGTGTGTGTGTGTGT 1813
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27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
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                                                                                                                                   AAF99702 standard; DNA; 21
                                                                                                                                                                                                            (first entry)
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Best Local Simil
Matches 21; (
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                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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ID ABS7
                                                                                                   RESULT 62
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Matches

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The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antiangiogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, osler-Webber Syndrome, myocardial angiogenesis plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
                                                                                                                    Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiactasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypertrophic scars. The present sequence is an antianglogenic nucleic acid of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human connective tissue growth factor, RT-PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;
                                                                                       Angiogenesis inhibitory oligonucleotide #907.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1793 TGTGTGTGTGTGTGTGT 1813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 35; 276pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (COLE-) COLEY PHARM GROUP INC
                                                                                                                                                                                                                                                                                                                                                                                                            14-DEC-2001; 2001WO-US048458
                                                                                                                                                                                                                                                                                                                                                                                                                                               14-DEC-2000; 2000US-025534P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK87131 standard; DNA; 21
                                                   (first entry)
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Best Local Similarity
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                                                   13-DEC-2002
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                                                                                                                                                                                                                                                                                               Synthetic.
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                 ABS78423;
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ID ABK8
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AC ABK8
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DE Huma:
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The present invention relates to endothelial cell-specific molecule 4

(ECSM4), and the polynuclectide sequences encoding it. The ECSM4 proteins are deful for imaging vascular endothelium in the body of an individual, and for diagnosing and treating a proliferative disease or condition involving the vascular endothelium (preferably, neovasculature) such as cancer, psoriasis, diabetic retinopathy, atheroscierosis or menorrhagia. The ECSM4 proteins are also useful in the manufacture of diagnostic or prognostic agent for such conditions. The proteins are also useful for detecting endothelial damage or activation, detecting a tumour or neovasculature, cardiac disease, or endometriosis by detecting the amount of ECSM4 present in a sample. The polynuclectide sequences encoding ECSM4 are useful in gene therapy for treating a hypoxic condition such as cancer, cardiac disease, endometriosis or atherosclerosis and in the manufacture of medicaments for treating the above disease. The sequences care useful for modulating angiogenesis in an individual. The present sequence represents a RT-PCR primer for RNA encoding human connective tissue growth factor
                    imaging vascular endothellum, proliferative disease, cancer, psoriasis, dibbetic retinopathy, atherosclerosis, menorrhagia, endothelial damage, tumour neovaeculature, cardiac disease, endometriceis, hypoxic condition, angiogenesis, cytostatic, RT-PCR, connective tissue growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for imaging, diagnosing and treating a condition involving vascular endothelium e.g. cancer, cardiac disease, endometriosis, diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunostimulatory, antiinflammatory, dermatological, antipsoriatic, antiulcer, gene therapy, vaccine, non-allergic inflammatory disease, psoriasis, eczema, allergic contact dermatitis, latex dermatitis; inflammatory bowel disease, ulcerative colitis, Crohn's disease; ss.
molecule 4; ECSM4; neovasculature;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21 BP; 9 A; 4 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LID.
                                                                                                         reverse transcription-PCR; primer; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunostimulatory nucleic acid #876.
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                                                                                                                                                                                                                                                                              06-NOV-2001; 2001WO-GB004906.
                                                                                                                                                                                                                                                                                                                                           07-MAR-2001; 2001US-0273662P.
                                                                                                                                                                                                                                                                                                                       2000US-0245566P
                                                                                                                                                                                                                                                                                                                                                                                                                            Bicknell R, Huminiecki L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-SEP-2003 (first entry)
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Best Local Similarity 100..
East Local Similarity 100..
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                                                                                                                                                                                              WO200236771-A2
                                                                                                                                                                                                                                                                                                                         06-NOV-2000;
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Gaps ö

2.0%; Score 21; DB 1; Length 21; 100.0%; Pred. No. 47; 0; Indels tive 0; Mismatches 0; Indels

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WPI; 2003-657977/62.
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                                                                                                                                                                                                                                                                                                                                                                       WO9213102-A1
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                                                                                                                                                                                                                                                                                25-MAR-2003
02-FEB-1993
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                                                                                                                                                                                                                 The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic contact dermatitis, latex dermatitis or inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease. This sequence represents an immunostimulatory nucleic acid
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                              Treating non-allergic inflammatory diseases, such as psoriasis, ecz allergic contact dermatitis, latex dermatitis or inflammatory bowel disease by administering an immunostimulatory nucleic acid.
                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ds; allergy; asthma; poly-G nucleic acid; aerosol formulation; hypo-responsive subject; immunostimulatory.
                                                                                                                                                                                                                                                                                                                     2.0%; Score 21; DB 1; Length 21; 100.0%; Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                    Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [mmunostimulatory nucleic acid #818.
                                                                                                                                                                                                                                                                                                                                                          1793 TGTGTGTGTGTGTGTGTGT 1813
                                                                                                                                                                                                    Disclosure, Page 32; 229pp; English
                                                                                                                                                                                                                                                                                                                                                                   BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-FEB-2000; 2000US-0179991P.
                                                                 29-MAR-2002; 2002US-00112653.
                                                                                  29-MAR-2001; 2001US-0279642P.
                                                                                                                                                                                                                                                                                                                                                                                                                      ADB37204 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BEAT/) BRATZLER R L.
(PETE/) PETERSEN D M.
(FOUR/) FOURON Y.
                                                                                                                             Krieg AM, Berg DJ;
                                                                                                                                              WPI; 2003-521815/49
                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                   (KRIE/) KRIEG A M. (BERG/) BERG D J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JS2003087848-A1
                              US2003050268-A1
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                                               13-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB37204;
             Synthetic
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Matches
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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage teeting, and in the genetic mapping of economic trait loci, or genes involved the determinism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                    The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G nucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy especially in a hypo-responsive subject. The present sequence represents an immunostimulatory nucleic acid of the invention.
Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.0%; Score 21; DB 1; Length 21;
100.0%; Pred. No. 47;
rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;
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                                                                                                                           Disclosure, Page 17; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1793 TGTGTGTGTGTGTGTGTGT 1813
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(first entry)
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Best Local Similarity 100.
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1813

1 TGTGTGTGTGTGTGTGTGT 21 1793 TGTGTGTGTGTGTGTGTGT

AAQ34038 standard; DNA; 22

RESULT 69 AAQ34038 (first entry)

(revised)

25-MAR-2003 02-FEB-1993

AAQ34038;

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 by with an (AC)15 and a (TC)15 oligomucleotide probe. One out of 50 increatellites and whorl sites, the frequency of (Tc)n >9 microsatellites and MboI sites, the frequency of (Tc)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information of a ca. 230 such bovine microsatellites is summarised in the sequence information of specification and indexed herein (see below). The sequence information of committee for microsatellite sequence were used to generate the microsatellite (using the program of Tthe amplification of the corresp. microsatellite (using the program OFTIPRIN). The microsatellites may be used to identify individuals, for parencage testing, and in the genetic mapping of economic trait lost, or genes involved the determinism of economic trait cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                               Gaps
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                                                                                                       Query Match 2.0%; Score 21; DB 1; Length 22; Best Local Similarity 100.0%; Pred. No. 49; Matches 21; Conservative 0; Mismatches: 0; Indels
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                                                                       Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Microsatellite sequence from clone TGLA117.
                                                                                                                                                                                     rerer 1813
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                                                                                                                                                                                                          2 TGTGTGTGTGTGTGTGTGT 22
                                                                                                                                                                                                                                                                                                                  AAQ33675 standard; DNA; 22 BP
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(first entry)
                                                                                                                                                                                       1793 TGTGTGTGTGTGTGTG
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02-FEB-1993
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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information of co. ca. 230 such bovine microsatellites is summarised in the sequence information of specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the cequired PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                             PCR, selection, primers, OPTIPRIM, breeding, cattle, parentage, genetic mapping, traits, amplification, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other;
                                                                                                Microsatellite sequence from clone TGLA432.
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Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                 (GENM-) GENMARK
                                                                                                                                                                                                                                                                                                                             15-JAN-1991;
                                                                                                                                                                                                                        WO9213102-A1
                                                                                                                                                                                                                                                                                              15-JAN-1992;
                                                                                                                                                                                                                                                           06-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                    Georges M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ34080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 70
AAQ34080
ID AAQ34
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AC AAQ34
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Gaps

The sequence is that of a bovine microsatellite sequence obtd, by screening a library of bovine Mbol DNA fragments of between 250 and 500 by with an (ACL)15 and a (TC)15 oligomucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information of process. The bovine microsatellites is summarised in the sequence information of specification and indexed herein (see below). The sequences upstream and commerceam of the microsatellite sequence ware used to generate the required PCR primers for in vitro amplification of the corresp.

The microsatellite (using the program opripring). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding. PCR; selection; primers, OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss. PCR; selection; primers, OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss. Match 20, Score 21; DB 1; Length 22; Local Similarity 100.0%; Pred. No. 49; of Mismatches 0; Indels es 21; Conservative 0; Mismatches 0; Indels Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other; Microsatellite sequence from clone TGLA39. Microsatellite sequence from clone TGLA48, 1793 TGTGTGTGTGTGTGTGT 1813 Table 7; Page 363; 517pp; English. 1 rererererererererer 21 AAQ33991 standard; DNA; 22 BP 92WO-US000340 91US-00642342 (revised)
(first entry) (revised)
(first entry) Georges M, Massey JM; WPI; 1992-284684/34. (GENM-) GENMARK. .5-JAN-1991; L5-JAN-1992; WO9213102-A1 25-MAR-2003 02-FEB-1993 25-MAR-2003 02-FEB-1993 06-AUG-1992 Bos taurus. Bos taurus AAQ33991; Query Match Best Loca Matches RESULT 71 AAQ33991 ઠે

The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-bybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites and in the bovine microsatellite sequence were used to generate the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required FCP primers for in vitro amplification of the corresp.

Indicosatellite (using the program OPTIPMIM). The microsatellites may be used to identify individuals, for parencage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economic ally important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN field.) ô - used in genetic identification, gene 0; Gaps Query Match
2.0%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 21; Conservative 0; Mismatches 0; Indels Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other; 1793 TGTGTGTGTGTGTGTGT 1813 Table 7; Page 327; 517pp; English. Polymorphic bovine DNA markers - mapping, and selective breeding. Georges M, Massey JM; WPI; 1992-284684/34. ò

rereferererererer AAQ83952/c ID AAQ83952 standard; DNA; 22 BP. (first entry) (revised) 25-MAR-2003 04-OCT-1995 AAQ83952; RESULT 72 g

/*tag= a //note= "Modified with BrCH2(=0)CNH-"
8...9
/*tag= b //note= "C(pnp)A, pnp = a linkage or monomer containing a bromoacetylamino functionality, and p = phosphodiester linkage"
14...15 Location/Qualifiers Key modified_base modified_base THE LEFT TO SERVICE TO THE SERVICE T

modified base

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Gaps

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IIV; pol; nef; oligonucleotide clamp; branched; macromolecule; se. Oligonucleotide clamp n, for producing comb-type brached polymer.

Synthetic.

WO9213102-A1

06-AUG-1992

92WO-US000340 91US-00642342

15-JAN-1992;

(GENM-) GENMARK

15-JAN-1991;

Homo sapiens

US5582979-A

10-DEC-1996

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The sequences given in AAQ81938, AAQ83952 and AAQ83940 are used in the construction of an oligonuclectide clamp. The clamp is a comb-type obtained bolymer which has 3' termini and was used to bind a target sequence comprising a segment of the HIV pol and nef genes in single stranded forms. An oligonuclectide clamp is a compound capable of forming a covalently closed macromolecule or a stable circular complex after specifically binding to the target polymuclectide in one time sequence capable of specific binding to the target molecule and one or more pairs of binding molecties consorted in the oligonuclectide molecties. Upon annealing of the oligonuclectides molecties to the target into juxtaposition so that they form a stable covalent or non-covalent linkage the specifically annealed oligonuclectides molecties to the target the specifically annealed oligonuclectide molecties to the target the specifically annealed oligonuclectide molecties to the target polymuclectide. (Updated on 25-WAR-2003 to correct PM field.)
/*tag= c
brote= "C(pnp)A, pnp = a linkage or monomer containing a
bromoacetylamino functionality, and p = phosphodiester
linkage"
linkage d
/*tag= d
/note= "C(pnp)A, pnp = a linkage or monomer containing a
bromoacetylamino functionality, and p = phosphodiester
linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthesis of branched polymers and novel branched polymeric structures used as molecular probes esp. for detecting poly-nucleotide(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22 BP; 11 A; 11 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 8; Page 33; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                    THERAPEUTICS INC.
                                                                                                                                                                                                                                                                          94WO-US007557.
                                                                                                                                                                                                                                                                                                             93US-00087386
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                                                                               modified base
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Simple Sequence Repeat, SSR; clover; microsatellite; genome mapping;
trait mapping; marker-assisted selection; gene selection; legume;
DNA profiling; breeding; ds.
                    AAI64448 standard; DNA; 22 BP.
                                                                  23-NOV-2001 (first entry)
                                                                                          SSR motif #8.
                                                                                                                                                                                                           25-MAY-2001.
                                                                                                                                                                                    NZ509194-A.
                                             AAI64448;
RESULT 74
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                                 Gaps
                                 .
0
       Query Match 2.0%; Score 21; DB 1; Length 22; Best Local Similarity 100.0%; Pred. No. 49; Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                        Repeat sequence from polymorphic marker clone Mfd25.
                                                       1793 TGTGTGTGTGTGTGTGTGTGT 1813
21 TGTGTGTGTGTGTGTGTGTGT 1
                                                                                                                               5727/c
AAT65727 standard; DNA; 22 BP
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(AGRI-) AGRIC VICTORIA SERVICES PTY LTD.

03-JAN-2001; 2001NZ-00509194. 24-DEC-1999; 99AU-00004907. 28-MAR-2000; 2000AU-00006520.

Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome, ds.

25-MAR-2003 (revised) 17-JUN-1997 (first entry)

AAT65727;

RESULT 73

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0; Gaps

Query Match
2.0%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 21; Conservative 0; Mismatches 0; Indels

1793 TGTGTGTGTGTGTGTGTGT 1813 21 rererererererererer

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Sequence 22 BP; 11 A; 11 C; 0 G; 0 T; 0 U; 0 Other;

The invention relates to the isolation of polymorphic repeat sequences having the sequence (dc-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65794-7647. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence has been determined are shown in Calone the repeat sequence is from the marker clone Mdf25 which contains the repeat sequence is from the marker clone Mdf25 which contains the repeat sequence having the formula: (AC)11. (Updated on 25-MAR-2003 to correct PF field.)

Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.

89US-00341562. 91US-00754351.

21-APR-1989; 05-SEP-1991;

(MARS-) MARSHFIELD CLINIC,

WPI; 1997-042299/04.

Weber JL;

Disclosure; Col 9-10; 186pp; English

37

14:41:45 2004

Fri Apr

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Novel simple sequence repeats in clover species useful for selection of genes in legume breeding, for profiling legume species varieties and for testing the purity of legume seed batches.
                                                                                                                                                                                                                                                                                                                Claim 6; Page 35; 52pp; English
Koelliker R, Forster JW;
                                                                       WPI; 2001-431058/46.
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The present invention relates to Simple Sequence Repeats (SSRs) from clover species. SSRs, also called microsatellites, are based on a 1-7 mucleotide core element which is tandemly repeated. The SSR array is embedded in complex flanking DNA. SSRs are ideal markers for genome mapping, trait mapping and marker-assisted selection. The SSRs may be used in methods for selecting genes in clover/ legume breading. The SSRs are also useful for DNA profiling of clover varieties and for testing the purity of legume seed batches. The present sequence is a SSR motif, which was used in the present invention Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other;

2.0%; Score 21; DB 1; Length 22; 100.0%; Pred. No. 49; iive 0; Mismatches 0; Indels Local Similarity 100. nes 21; Conservative Query Match Matches

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Gaps ò

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AAF60472 standard; DNA; 23 (first entry) 27-APR-2001 AAF60472;

Oligonucleotide clamp #17.

Oligonucleotide clamp; ds.

US6180777-B1 30-JAN-2001 03-JAN-1997;

96US-0009918P 12-JAN-1996;

(FARB) BAYER CORP.

Horn T;

WPI; 2001-201911/20.

Synthesizing branched nucleic acids useful as diagnostic and molecular probes, involves combining first units having haloalkylamino groups and second units having thiol or phosphorothioate groups.

Example 7; Col 19; 20pp; English.

The present invention relates to a method for synthesising a branched or multiply connected macromolecular structure, comprising oligonucleotide clamps (OC). The macromolecular structure is capable of specifically binding to a target molecule, and can therefore be used as probes. At least one OC comprises a target binding sequence that binds specifically and stably with the target molecule, and at least two OCs comprise signal generation moieties capable of generating a detectable signal in the AAF60472/AAF

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                                                                                                                                                                                                                                                                                   Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis imperfecta; autoimmune disease; acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; primer; ss.
  one
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                                                                                         0; Gaps
presence of the target molecule. In addition the OCs are connected tanother by thioalkylamino, or thiophosphorylalkylamino bridges. The present sequence is an OC used in the present invention
                                                               2.0%; Score 21; DB 1; Length 23;
100.0%; Pred. No. 51;
iive 0; Mismatches 0; Indels
                                             Seguence 23 BP; 11 A; 12 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                               SNP specific SNPE primer SEQ ID 2951.
                                                                                                                1793 IGTGTGTGTGTGTGTGT 1813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ORCH-) ORCHID BIOSCIENCES INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0160096P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pohl M;
                                                                                                                                                                                             AAH40155 standard; DNA; 25
                                                                                                                                                                                                                                          14-AUG-2001 (first entry)
                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-290930/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Picoult-Newburg L,
                                                                                Best Local Similarity
Matches 21; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                26-APR-2001.
                                                                                                                                                                                                                     AAH40155;
                                                                                                                                       22
                                                                      Query Match
                                                                                                                                                                                  RESULT 76
    88888
                                                                                                                  8
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Additional Saguences AAH437205 - AAH40944 represent PCR primers, single nuclectide primer extension (SNPB) primers, and the sequences of regions flanking stres of single nuclectide polymorphisms SNPs. The present invention cancel of includes kites for determining the presence or absence of a SNP, using the oligonuclectides of the invention. The PCR primers are used to amplify a cligonuclectide of the SNPE primer is used as a genotyping primer. SNP flanking sequence, the SNPE primer is used as a genotyping primer. The oligonuclectides are useful for genotyping a nucleic acid sample by performing a single-nuclectide primer extension reaction. The cligonuclectides are useful for determining the presence, absence or identity of a SNP and for genotyping nucleic acid samples for e.g. to assess by association analysis the genotype of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include diseases e.g. agammaglobulinaemia, diabetes inspidus, Lesch-Nyhan syndrome, muscular dystrophy, familial hypercholesterolaemia, polycystic kidney disease.

C traits also include symptoms of or susceptibility to multifactorial disease of which a component is or may be genetic such as autoimmune client as including, rheumatoid arthritis, multiple sclerosis, New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polymucleotide polymorphism in a nucleic Claim 1; Page 65; 83pp; English. acid sample.

mcgarry191-19.rng

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Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide primer extension (SNBE) primers, and the sequences of regions flanking sites of single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the oligonucleotides of the invention. The PCR primers are used to amplify a SNP flanking sequence, the SNPE primer is used as a gnotyping primer. The oligonucleotides are useful for genetyping a nucleic acid sample by performing a single-nucleotide primer extension reaction. The oligonucleotides are useful for determining the presence, absence or identity of a SNP and for genotyping nucleic acid samples, for e.g. to assess by association analysis the genotype of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits inspected of being agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, familial hypercholesteroleamia, polycystic kidate disease, osteogenesis imperfects and acute intermittent porphyria. Phenotypic traits also include symptoms of or susceptibility to multifactorial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis imperfecta; autoimmune disease; acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; primer; ss.
    and infection by pathogenic
inflammation, cancer, nervous system diseases and infection by pathogeni microorganism. The method is also useful in forensic investigations and paternity analysis. The present sequence represents a single nucleotide primer extension (SNPE) primer specific for a human SNP containing DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic
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                                                                                                                                                                    2.0%; Score 21; DB 1; Length 25; 100.0%; Pred. No. 54; ative 0; Mismatches 0; Indels
                                                                                                                                  Seguence 25 BP; 11 A; 11 C; 2 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP specific SNPE primer SEQ ID 2955.
                                                                                                                                                                                                                                                              1793 TGTGTGTGTGTGTGTGT 1813
                                                                                                                                                                                                                                                                                     21 TGTGTGTGTGTGTGTGTGT 1
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                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 21; Conservative
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AAH40159/c
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disease of which a component is or may be genetic such as autoimmune diseases, including, rheumatoid arthritis, multiple sclerosis, inflammation, cancer, nervous system diseases and infection by pathogenic microorganism. The method is also useful in forensic investigations and paternity analysis. The present sequence represents a single nucleotide primer extension (SNPE) primer specific for a human SNP containing DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel set of inter-simple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes. The primers of the invention may be useful for genotyping diverse genomes of plant and animal systems, in particular for distinguishing Basmati rice varieties from non-Basmati rice varieties and traditional Basmati rice varieties from evolved Basmati rice varieties. The current sequence is that of the 5' anchored (ISSR)-PCR primer of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inter-simple sequence repeat; ISSR; SSR; PCR; primer; genotyping; plant;
animal; Basmati rice; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New set of inter-simple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes, useful for genotyping diverse genomes of plant
                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                 DB 1; Length 25; 54;
                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               5' anchored (ISSR)-PCR primer - SEQ ID 5 alternative.
                                                                                                                                                Sequence 25 BP; 11 A; 12 C; 2 G; 0 T; 0 U; 0 Other;
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2.0%; Score 20.6; D
Best Local Similarity 95.2%; Pred. No. 57;
Matches 20; Conservative 1; Mismatches
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2.0%; Score 21; DB
Best Local Similarity 100.0%; Pred. No. 54;
Matches 21; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                 ADD69512 standard; DNA; 23
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Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
     PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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(first entry)
                                                                                                                                                                                                           Georges M, Massey JM;
                                                                                                                                                                                                                                    WPI; 1992-284684/34.
                                                                                                                                                                                  (GENM-) GENMARK.
                                                                                                                                                        15-JAN-1991;
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02-FEB-1993
                                                                           WO9213102-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus
                                                  Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ33672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ33672
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 by with an (ACILS and a (TC)15 oligomucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100,000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequence information of commiscrate for in vitro amplification of the corresp.

Trequired PCR primars for in vitro amplification of the corresp.

The microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                          PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 1.9%; Score 20; DB 1; Length 20; Local Similarity 100.0%; Pred. No. 60; Local Soli Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
                                                                                                                    Sequence of a microsatellite from clone TGLA86.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1793 TGTGTGTGTGTGTGTG 1812
                                                                                                                                                                                                                                                                                                                                                                                                                                              Table 7; Page 397; 517pp; English
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                          AAQ34170 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                    92WO-US000340.
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                                                                             (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                  Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                         GENM-) GENMARK
                                                                                                                                                                                                                                                                      LS-JAN-1992;
                                                                               25-MAR-2003
02-FEB-1993
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                                                                                                                                                                                        Bos taurus
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                                                       AAQ34170;
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 RESULT 79
AAQ34170
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ID AAQ3
XX
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AC AAQ3
DT 25-W
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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine Mbol DNA fragments of between 250 and 500
clones cross-hybridised. Assuming independent distribution of
clones cross-hybridised. Assuming independent distribution of
microsatellites and Mbol sites, the frequency of (76)n >9 microsatellites
in the bovine genome is estimated at >100,000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
sepecification and indexed herain (see below). The sequences upstream and
committed PCR primers for in vitro amplification of the corresp.
microsatellite (using the program of THRMM). The microsatellites may be
microsatellite (using the program of PTIPRIM). The microsatellites may be
used to identify individuals, for parentage testing, and in the genetic
capping of economic trait loci, or genes involved the determinism of
connandally important traits esp. in cattle, to allow selective
breeding. See also AAQ33501-34437. (Updated on 25-WAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Microsatellite sequence from clone TGLAll6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1793 TGTGTGTGTGTGTGTGTG 1812
rable 7; Page 256; 517pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 rerererererererere 20
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Microsatellite sequence from clone TGLA22

(revised)
(first entry)

25-MAR-2003 02-FEB-1993

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Detecting polymorphisms between 2 nucleic acid samples, esp. in microsatellite regions, comprises digesting the nucleic acid to generate fragments, ligating adaptor segments to their ends, amplifying them using primer directed amplification and comparing the prods. to detect differences. The primers used in the amplification comprise a primer obsisting of a perfect cpd. simple sequence repeat (SSR), and an adaptor segment. The present sequence complementary to an adaptor segment. The present sequence is an example of a compound SSR primer. The method represents a modified amplified fragment length polymorphism assay, which is partic. useful for genome fingerprinting, i.e. for genetic trait marking and germplasm comparisons
                                            Modified amplified fragment length polymorphism assay - for detection of polymorphism esp. in micro:satellite regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New phospho:di:esteric oligo:nucleotide(s) - which exert a specific and selective cytotoxic effect on tumour cells, for treating both solid and liquid tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antitumoural phosphodiester oligonucleotide 19 with cytotoxic activity.^{\cdot\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phosphodiester; selective binding; cell viability; growth; tumoural cell line; cytotoxic activity; tumour cell; lymphoma; lymphoblastic tumour; ss.
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/note= "phosphodiester oligonucleotide"
                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 10 A; 7 C; 0 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                         Disclosure; Fig 1c; 173pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1799 TGTGTGTGTGTGTATATA 1818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 4; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scaggiante B, Quadrifoglio F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT93829 standard; DNA; 20 BP
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(first entry)
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/*tag=
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              WPI; 1996-277795/28.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-JUN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
24-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT93829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 83
AAT93829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                            The sequence is that of a bovine microsatallite sequence obtd. by screening a library of bovine Mool DNA fragments of between 250 and 500 by thin an (ACI)5 and a (TCI)5 oligomiclecide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mool sites, the frequency of (T5)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the sequence information of specification and indexed herein (see below). The sequence information of downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

Microsatellite (using the program OPTIPRIM). The microsatellites may be required to identify individuals for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective condition and the QTL trait of enhanced milk prodn. in Brown Swiss contitle. See also AAQ33501-34442. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                         - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detection; polymorphism; perfect compound simple sequence repeat; adaptor directed primer; genome; genetic; ingerprinting; amplified fragment length polymorphism assay; microsatellite region; genetic trait marking; germplasm comparisons; compound; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.9%; Score 20; DB 1; Length 20; 00.0%; Pred. No. 60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Compound simple sequence repeat primer (CA)4.5(TA)7.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 Similarity 100.0%; Pred. No. 60; 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DUPO ) DU PONT DE NEMOURS & CO E I.
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                                                                                                                                                                                                                                                  Table 7; Page 198; 517pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymorphic bovine DNA markers - mapping, and selective breeding,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT30427 standard; DNA; 20 BP
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  92WO-US000340.
                                        91US-00642342.
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                                                                                                                Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 20, Conserv
                                                                           (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-NOV-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-NOV-1995;
    15-JAN-1992;
                                        15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JAN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT30427;
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Gaps . 0

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The present phosphodiesteric oligonucleotide is based on the generic formula, in the 3'-5' or 5'-3' direction; (Gara')a'. (GGTD')b'.

(GCTC')c'.-(GGTd')d'.-(GGTB')e'.-(GTTF')f'.- (G-GGTB')b'.'

(GCTC')c'.-(GGTd')d'.-(GGTB')e'.-(GTTF')f'.- (G-GGTB')g'.-N', where: N and clifferent from each other; a, b, c', d', e', f', and g = 0-10, equal or different from each other; a', b', c', d', e', f', and g' = 1-c' different from each other; a', b', c', d', e', f', and g' = 1-c' different from each other; a', b', c', d', e', f', and g' = 1-c' different from each other; a', b', c', d', e', f', and g' = 1-c' different from each other; o', b', c', d', e', f', and g' = 1-c' different from each other; o', b', c', d', e', f', and g' = 1-c' different from each other; o', b', c', d', e', f', and g' = 1-c' different from each other; o' d', e', f', e', f', and g' = 1-c' d', e', d', e', f', e', f', and g' = 1-c' d', e', d', e', f', e',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
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Score 20; DB 1; Length 20; Pred. No. 60; 0; Indels 1.9%; Sco. 100.0%; Pred. No. co. ... 0; Mismatches 1794 GIGIGIGIGIGIGIGI 1813 1 Grererererererer 20 Query Match Best Local Similarity 100. Matches 20; Conservative

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RESULT 84

AAV06824 standard; DNA; 20 BP. AAV06824; AAV06824

01-JUL-1998 (first entry)

Oligonucleotide which binds retroviral nucleocapsid protein.

Retroviral nucleocapsid protein; NC; high affinity; viral replication; gene therapy; retroviral infection; HIV; transduced cell; ss.

99WO-GB003463. 98GB-00022963.

20-OCT-1999; 20-OCT-1998;

27-APR-2000.

(MARS/) MARSDEN J C. (AGNE/) AGNER E.

WPI; 2000-339759/29

Agner E;

Synthetic.

WO9744064-A2

97WO-US008936 19-MAY-1997; 96US-0017128P 20-MAY-1996; (USSH) US DEPT HEALTH & HUMAN SERVICES.

Rein A, Casas-Finet J, Fisher R, Fivash M, Henderson LE WPI; 1998-018230/02 Oligo:nucleotide which binds to retroviral nucleocapsid protein with high affinity - used in targeted molecules, transduced cells and gene therapy vectors for treatment of retroviral infections such as those caused by

Claim 7; Page 56; 70pp; English.

This sequence represents an oligonucleotide which binds to a retroviral nucleocapsid (NC) protein with high affinity. The invention relates to a targeted molecule which binds to a retroviral nucleocapsid protein with high affinity and comprises the oligonucleotide and a fusion partner. Retroviral nucleocapsid proteins, such as NC and the Gag precursors, bind to specific nucleic acid sequences with high affinity. This binding is hydrophobic component. The specific nucleic acid sequences which bind at the sinc Component. The specific nucleic acid sequences which bind or are useful as molecular decoys for retroviral NC proteins, for making

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fusion proteins which inactivate retroviral NC proteins, in screening assays for detecting molecules which inactivate retroviral NC protein nucleic acid binding, and for purification of retroviral NC proteins. In particular, the targeted molecules, the transduced cells and gene therapy vectors based on the oligomucleotides can be used for treatment and prevention of retroviral infections such as those caused by HIV
                                                                                                  Gaps
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0
                                                                                                                                                                                                                                                     Displacement chromatography; purification; separation; ss.
                                                                               DB 1, Length 20;
60;
                                                                                                  0; Indels
                                                                Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
                                                                            1.9%; Scc...
100.0%; Pred. No. c...
... 0; Mismatches
                                                                                                                    1793 TGTGTGTGTGTGTGTGTG 1812
                                                                                                                                  TGTGTGTGTGTGTGTGTG 20
                                                                                                                                                                                                                                       20-mer_oligonucleotide sequence.
                                                                                                                                                                                  AAA39091 standard; DNA; 20 BP
                                                                                                                                                                                                                      (first entry)
                                                                                 Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                           WO200023798-A1.
                                                                                                                                                                                                                                                                           Unidentified.
                                                                                                                                                                                                                      30-AUG-2000
                                                                                                                                                                                                    AAA39091;
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The present invention describes a method (I) for sample displacement chromatography separation. The method comprises applying a multicomponent cample to one end of a chromatography bed, distributing the sample along the bed by passing non-eluting mobile solvent phase over the bed, and recovering a desired component of the sample from at least portion of the bed. The sample components are applied in a non-homogeneous manner to enhance concentration of at least one component with relatively low and/or high affinity for the stationary phase material, respectively, during an earlier and later part of the sample application. The method is useful for chromatographic separation of samples. The method permits recovery of sample components at significantly higher concentrations and generally makes more efficient use of the stationary phase material. The method allows ten-fold greater loading than comparable gradient elution method allows ten-fold greater loading than comparable gradient elution analysis, avoids the use of displacer solution during actual separation analysis, avoids the use of displacer solution during actual separation for the purification of an oligonucleotide by sample displacement Example 2; Page 22; 37pp; English. chromatography

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Displacement chromatography for purification of peptide samples by homogeneous application of sample components to chromatography bed.

Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;

Ouery Match 1.9%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 60; Matches 20; Conservative 0; Mismatches 0; Indels

1793 TGTGTGTGTGTGTGTGTG 1812

1 TGTGTGTGTGTGTGTGTGTG 20

AAS13762 standard; DNA; 20 BP AAS13762; RESULT 86

(first entry) 08-MAY-2002 Simple sequence repeat, SSR, #34.

Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat; cereal profiling; grass profiling; seed batch purity testing.

Lolium perenne

NZ509193-A.

25-MAY-2001

03-JAN-2001; 2001NZ-00509193.

24-DEC-1999; 99AU-00004906. 04-MAY-2000; 2000AU-00007310.

(SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R. (UYSC-) UNIV SOUTHERN CROSS. (VICT-) STATE VICTORIA DEPT NATURAL RES & ENVIRO. (UYAD-) UNIV ADELAIDE. (UYAD-) INIV MAIZE & WHEAT IMPROVEMENT CENT.

Forster JW, Jones ES; WPI; 2001-512563/56. New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species varieties.

Example 1; Fig 6; 72pp; English.

The invention relates to a substantially purified or isolated nucleic acid (I) from ryegrass or fescue species including a simple sequence repeat (SSR), having 2 or more tandemly repeated nuclectide core elements 2-6 nuclectide core elements are included are a nucleic acid primar cuitable for amplifying an SSR, identifying (M1) an SSR by preparing a library of ryegrass or fescue genomic DNA enriched for SSRs and identifying clones in the library containing SSRs, a library of ryegrass or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely associated with the gene such that the SSR and the gene are preferentially co-inherited, and selecting for the SSR in the breeding, a method for DNA profiling grass or cereal species varieties by assessing variation between SSR varieties and testing the purity of grass or cereal seed batches by assessing variation within seed batch of an SSR. The SSRs may be used in the selection of genes in grass or cereal breeding, for profiling grass or cereal species varieties, for testing the purity of grass or cereal seed batches, and for DNA profiling to establish the distinct identity, uniformity and/or stability of a cultivar. The present sequence is a ryegrass or fescue SSR

Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;

ö Gaps ö Length 20; 0; Indels DB 1; 60; 1.9%; Score 20; DB 100.0%; Pred. No. 60; ive 0; Mismatches 1794 GIGIGIGIGIGIGIGIGI 1813 1 Grererereretere Query Match Best Local Similarity 100. Matches 20; Conservative ð

20

RESULT 87

g

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Gaps . 0 3705/c AAS13705 standard; DNA; 20 BP.

08-MAY-2002

AAS13705;

(first entry)

Simple sequence repeat, SSR, #2.

Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat; cereal profiling; grass profiling; seed batch purity testing.

Poeae.

NZ509193-A.

25-MAY-2001.

03-JAN-2001; 2001NZ-00509193

24-DEC-1999; 99AU-00004906. 04-MAY-2000; 2000AU-00007310.

STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R. UNIV SOUTHERN CROSS.
STATE VICTORIA DEPT NATURAL RES & ENVIRO. UNIV ADELAIDE.
INT MAIZE & WHEAT IMPROVEMENT CENT.

(VICT-) (VYAD-)

(ITMA-)

Jones ES; Forster JW,

WPI; 2001-512563/56.

New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species varieties.

Claim 6; Page 51; 72pp; English.

The invention relates to a substantially purified or isolated nucleic acid (I) from ryegrass or fescue species including a simple sequence repeat (SSR), having 2 or morrer tandemly repeated nucleotide core elements 2 or morrer tandemly repeated nucleotide core elements core for amplifying an SSR, identifying (M1) an SSR by preparing a library of ryegrass or fescue genomic DNA enriched for SSRs and core identifying clones in the library containing SSRs, a library of ryegrass or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely core associated with the gene such that the SSR and the gene are core in grass or cereal species writeties by assessing core method for DNA profiling grass or cereal species varieties by assessing core associated batches by assessing variation within seed batch of an SSR. The SSRs core and batches by assessing variation within seed batch of an SSR. The SSRs core as seed batches, and for DNA profiling to establish the core alsered batches, and for DNA profiling to establish the core sequence is a ryegrass or fescue SSR

Sequence 20 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 0 Other;

Query Match

20; DB 1; Length 1.9%; Score 20;

Human, antiinflammatory, cytostatic, antisense gene therapy, phosphoenol pyruvate carboxykinase-cytosolic, PEPCK-cytosolic, infection, inflammation, tumour formation, phosphorothicate, ss.

US6187545-B1

Yeast; Mrell; telomere length; nuclease; gene therapy; melanoma; liver cancer; breast cancer; brain cancer; probe.

(RIKE) RIKEN KK. (NISC-) JAPAN SCI & TECHNOLOGY CORP.

WPI; 2001-541649/60

Ohta K, Shibata T;

14-FEB-2001; 2001WO-JP001024 18-FEB-2000; 2000JP-00041929

40200160996-A1,

Synthetic

Example 3; Page 16; 67pp; Japanese.

Homo sapiens

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Gaps

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Indels

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Pred. No. 60; Mismatches

ilarity 100.0%; Pi Conservative 0;

Best Local Similarity Matches 20; Conserv

1793 TGTGTGTGTGTGTGTG 1812

20 TGTGTGTGTGTGTG 1

셤

AAH75569 standard; DNA; 20 BP.

88 RESULT

(first entry)

06-NOV-2001

AAH75569;

Wrell related probe

rage 12

The present sequence is one of a number of antisense compounds of up to 30 nucleobases in length that are capable of inhibiting the expression of phosphoenom by vivate carboxykinase-cytosolic (FEFCK-cytosolic). The antisense compounds are useful for inhibiting the expression of FEFCK-cytosolic in cells or tissues. They are commonly used as research genes. They are also useful for distinguishing between function of particular various members of a biological pathway and for research use. The antisense compounds are also useful prophylactically, e.g. to redeate of antisense compounds are also useful prophylactically, e.g. to prevent or delay infection, inflammation or tumour formation. The present sequence is a chimeric phosphorothioate oligonucleotide with 2'-MOE wings and a Deoxynucleic S-Methythiourea; DNmt; antisense therapy; cardiovascular disease; neurocellular disease; antiviral therapy; human immunodeficiency virus; human-cytomegalovirus; Antisense compound capable of modulating the expression of phosphoenol pyruvate carboxykinase-cytosolic, useful for preventing or delaying infection, inflammation or tumor formation. Gaps ö DB 1; Length 20; 60; 0; Indels Sequence 20 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 0 Other; 1.9%; Score 20; DB ilarity 100.0%; Pred. No. 60; Conservative 0; Mismatches Cowsert 1794 GIGIGIGIGIGIGIGI 1813 influenza; herpes; infection; ss 20 Grererererererer Wyatt J, Claim 1; Col 43; 64pp; English. 21-JAN-2000; 2000US-00488671. 21-JAN-2000; 2000US-00488671. 99US-00407675 AAF28355 standard; DNA; 20 02-APR-2001 (first entry) (ISIS-)_ISIS PHARM INC. Butler MM, WPI; 2001-190979/19. Local Similarity les 20; Conserv DNA oligomer #5. 28-SEP-1999; US6169176-B1 Unidentified 02-JAN-2001. AAF28355; Mckay R, Query Match Best Loca Matches RESULT 90 AAF28355/ δ 셤 The invention relates to control of telomere length in a cell by andifying the physiological activity of the Mrell protein in the cell, by transformation of the cell with DNA encoding a foreign Mrell protein which may be modified in the C-terminal and/or nuclease domain. The method is useful in gene therapy of telomere length-related diseases such as melanoma, liver cancer, breast cancer, bladder cancer and brain cancer. The present sequence is that of a Mrell related probe of the Controlling telomere length for gene therapy of telomere length related tumors comprises transformation using the modified Mrell protein. Gaps

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0; Indels

1.9%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 60;

llarity 100,0%; Pred. No. 60; Conservative 0; Mismatches

Local Similarity

Query Match

20;

Best Loca Matches

1794 GTGTGTGTGTGTGTGTGT 1813

Grerererererererer

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Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;

invention

Human PEPCK-cytosolic antisense oligonucleotide ISIS 108106

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The present sequence was used to demonstrate the ability of deoxynucleic S-Methythiourea (DNmt) compounds to form triplexes with DNA oligomers. An increase in the C content of the oligor resulted in a large decrease in the C content of the oligor sesulted in a large decrease in binding. This experiment was performed as an example of a method for preparing oligomucleotides comprising a backbone of alkyl or alkoxy continues in antisense or antigene therapy, to inhibit production of proteins associated with genetic diseases, cardiovascular, inflammatory contents associated with genetic diseases, cardiovascular, inflammatory contents in mennodeficiency virus, human-cytomegalovirus, influenza and herpes content the presence or absence of the target DNA content binding contents and content of activity of a target protein, they can be useful in the manipulation of tissue e.g. tissue e.g. tissue differentiation, both in vivo and in ex vivo tissue cultures. The method provides and S-methylthiourea Preparing novel deoxynucleic alkyl thiourea oligonucleotide for use in antisense therapy, by synthesizing oligonucleotides comprising backbone of alkyl or alkoxy thiourea linkages in solution or on solid phase. Sequence 20 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 0 Other; Example 7; Fig 16; 48pp; English. 98US-0091481P. 98US-0111800P. 99US-00347443. (REGC) UNIV CALIFORNIA WPI; 2001-122276/13. Dev AP, Bruice TC; 11-DEC-1998; 02-JUL-1999;

Query Match
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 1793 TGTGTGTGTGTGTGTGTG 1812 ઠે

AAH48201 standard; DNA; 20 AAH48201; RESULT 91

BP

Antibody binding oligonucleotide. (first entry) 20-SEP-2001

Antibody affinity, DNA epitope; anti-DNA antibody; lupus nephritis; systemic lupus erythematosus; immunotolerance; ds.

Synthetic

14-JUN-2001

99US-0167716P 28-NOV-1999;

(LJOL-) LA JOLLA PHARM CO

WPI; 2001-451601/48

Treating systemic lupus erythematosus in individual comprises e.g. administering conjugate comprising non-immunogenic valency platform molecule and double stranded DNA epitopes which specifically bind to antibody from individual.

Claim 4; Page 57; 87pp; English.

The present invention describes a method of treating systemic lupus erythematosus and lupus nephritis, involving administering a conjugate comprising a non-immunogenic valency platform molecule and 2 double stranded DNA epitopes which specifically bind to dsDNA-binding antibodies. Affinity of the epitopes for the antibody is used as a basis for selecting individuals to receive treatment. The present sequence is an antibody binding dsDNA sequence described in the exemplification of the invention

Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;

Gaps ö Query Match
1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels

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1794 GIGIGIGIGIGIGIGIGI 1813 Grerererererererer

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AAI64445 standard; DNA; 20 BP.

(first entry) AAI64445;

23-NOV-2001

SSR motif #5

.; 0

0; Gaps

Simple Sequence Repeat, SSR, clover, microsatellite, genome mapping, trait mapping, marker-assisted selection, gene selection, legume, DNA profiling, breeding, ds.

Unidentified

NZ509194-A.

25-MAY-2001.

03-JAN-2001; 2001NZ-00509194.

24-DEC-1999; 99AU-00004907. 28-MAR-2000; 2000AU-00006520.

(AGRI-) AGRIC VICTORIA SERVICES PTY LTD.

Forster JW; Koelliker R,

WPI; 2001-431058/46.

Novel simple sequence repeats in clover species useful for selection of genes in legume breeding, for profilling legume species varieties and for testing the purity of legume seed batches.

Claim 6; Page 35; 52pp; English.

The present invention relates to Simple Sequence Repeats (SSRs) from clover species. SSRs, also called microsatellites, are based on a 1-7 mucleotided core element which is trandemly repeated. The SSR array is embedded in complex flanking DNA. SSRs are ideal markers for genome mapping, trait mapping and marker-assisted selection. The SSRs may be used in methods for selecting genes in clover/legume breeding. The SSRs are also useful for DNA profiling of clover varieties and for testing the purity of legume seed batches. The present sequence is a SSR motif, which

28-NOV-2000; 2000WO-US042307

Linnik MD,

708 TIS

WO200141813-A2.

Human, endothelial cell-specific molecule 4; ECSM4; neovasculature; imaging vascular endothelium; proliferative disease; cancer; psoriasis; diabetic retinopathy; atherosclerosis; menorrhadia; endothelial damage; tumour neovasculature; cardiac disease; endometriosis; hypoxic condition; angiogenesis; cytostatic; RT-PCR; connective tissue growth factor; reverse transcription-PCR; primer; ss.

WO200236771-A2. Homo sapiens.

10-MAY-2002

Human connective tissue growth factor, RT-PCR primer #2.

(first entry)

07-OCT-2002

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ABK87132;

ABK87132 standard; DNA; 20 BP.

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The present invention relates to Simple Sequence Repeats (SSRs) from clover species. SSRs, also called microsatellites, are based on a 1-7 mucleotide core element which is tandemly repeated. The SSR array is embedded in complex flanking DNR. SSRs are ideal markers for genome mapping, trait mapping and marker-assisted selection. The SSRs may be used in methods for selecting genes in clover/ legume breeding. The SSRs are also useful for DNA profiling of clover varieties and for testing the purity of legume seed batches. The present sequence is a SSR motif, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel simple sequence repeats in clover species useful for selection of genes in legume breeding, for profiling legume species varieties and for testing the purity of legume seed batches.
                                                                                                                                                                                                                                                                                                                                                              Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping;
trait mapping; marker-assisted selection; gene selection; legume;
DNA profiling; breeding; ds.
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                                                       ch 1.9%; Score 20; DB 1; Length 20; 1 Similarity 100.0%; Pred. No. 60; 20; Conservative 0; Mismatches 0; Indels
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                           Sequence 20 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
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was used in the present invention
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28-MAR-2000; 2000AU-00006520.
                                                                                                                                                                                                                                        AAI64449 standard; DNA; 20
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                                                                                                                                                                                                                                                                                                                                       SSR motif #9
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Best Local
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AAI64449
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The present invention relates to endothelial cell-specific molecule 4

(ECSM4), and the polynuclectide sequences encoding it. The ECSM4 proteins
are useful for imaging vascular endothelium in the body of an individual,
and for diagnosing and treating a proliferative disease or condition
involving the vascular endothelium (preferably, neovasculature) such as
cancer, psortiasis diabetic retinopathy, atherosclerosis or menorrhagia.
The ECSM4 proteins are also useful in the manufacture of diagnostic or
prognostic agent for such conditions. The proteins are also useful for
detecting endothelial damage or activation, detecting a tumour or tumour
neovasculature, cardiac disease, or endometriosis by detecting the amount
neovasculature, cardiac disease, or endometriosis by detecting the amount
of ECSM4 present in a sample. The polymucleotide sequences encoding ECSM4
are useful in gene therapy for treating a hypoxic condition such as
cancer, cardiac disease, endometriosis or atherosclerosis and in the
manufacture of medicaments for treating the above disease. The sequences
are useful for modulating angiogenesis in an individual. The present
sequence represents a RT-PCR primer for RNA encoding human connective
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for imaging, diagnosing and treating a condition involving vascular endothelium e.g. cancer, cardiac disease, endometriosis, diabetes.
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tive 0; Mismatches
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Best Local Similarity 100.
Matches 20; Conservative
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Gaps

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Indels

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100.0%; Prec.

Conservative

20;

Best Loca Matches

Local Similarity

Query Match

1794 GIGIGIGIGIGIGIGI 1813

8

Grerererererererer 20

RESULT 94 ABK87132

1.9%; Score 20;

DB 1; Length 20; 60;

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The invention relates to a method for immobilising a molecule on a support comparing reacting a derivatised molecule with a derivatised support capable of reacting with the molecule via a cycloaddition reaction. The method is used for immobilising molecules on a support using cycloaddition reactions such as the Diels-Alder reaction. The method shows better chemoselectivity, functional groups do not need to be protected and it is highly efficient for immobilishing molecules compared to other methods. The present sequence is that of an oligonucleotide, useful to the invention
                                                                                                                                                                                                                                                                               New method for immobilizing a molecule on a support comprises reacting derivatized molecule with a derivatized support via a cycloaddition reaction, shows high selectivity and efficiency.
                                                                                                                                                                                           Leuck M, Latham-Timmons HA;
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100.0%; Pred. No. 60;
tive 0; Mismatches
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30-JAN-2001; 2001US-0265020P.
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30-JAN-2001; 2001US-0265020P.
                                                                   01-MAY-2001; 2001WO-US013956
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Best Local Similarity 100.
Matches 20; Conservative
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Husar GM;
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WO200184234-A1.
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Pilon J, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     Synthesis of polynucleotide useful during fabrication of an array involves coupling nucleoside phosphoramidite and a solid-supported nucleoside and treating the product with an oxidation/deprotection
                                                                       Oligonucleotide synthesis; polynucleotide array; protecting group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 20; DB 1; Length 20;
Pred. No. 60;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                   Caruthers M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
                                      Oligonucleotide synthesis method related DNA #4.
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/mod_base= OTHER
/note= "5' fluorescein label"
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 15; 36pp; English.
                                                                                                                                                                                                                                                                                                            (AGIL-) AGILENT TECHNOLOGIES INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABA96307 standard; DNA; 20 BP
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                                                                                                                                                                                                                                        27-JUL-2001; 2001EP-00118360
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                                                                                                                                                                                                                                                                                                                                                   Perbost MGM,
   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-156732/21
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les 20, Conserv
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modified_base
                                                                                                                                                                                                                                                                                                                                                   Dellinger DJ,
                                                                                             oxidation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             composition.
   24-MAY-2002
                                                                                                                                                                                                   30-JAN-2002
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                                                                                                                             Synthetic.
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Matches

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ABA96307/c RESULT 96

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Indels

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Latham-Timmons HA;

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The invention relates to a method for immobilising a molecule on a support comparing reacting a derivatised molecule with a derivatised support capable of reacting with the molecule via a cycloaddition reaction. The method is used for immobilising molecules on a support using cycloaddition reactions such as the Diels-Alder reaction. The method shows better chemoselectivity, functional groups do not need to be protected and it is highly efficient for immobilising molecules compared to other methods. The present sequence is that of an oligonucleotide, useful to the invention
New method for immobilizing a molecule on a support comprises reacting a derivatized molecule with a derivatized support via a cycloaddition reaction, shows high selectivity and efficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
                                                                                                          Example 6; Page 31; 86pp; English
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Score 20; DB 1; Length 20; Pred. No. 60; 0; Mismatches 0; Indels 1793 TGTGTGTGTGTGTGTGTG 1812 1 rerererererererere 20 Query Match Best Local Similarity 100. Matches 20; Conservative ö

1.9%; 8

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Gaps ; 0

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ABZ24438 standard; DNA; 20 18-MAR-2003 ABZ24438; RESULT 98 ABZ24438/c

BP

(first entry)

Oligonucleotide (CA)10 used in nucleic acid hybridisation.

detection; hybridisation; microarray; thermistor; Nucleic acid detection microcalorimetry; ss

Synthetic

WO200299386-A2.

12-DEC-2002

07-JUN-2002; 2002WO-US018200

07-JUN-2001; 2001US-0296685P.

PROL-) PROLIGO LLC

Roach JS, Wolter A;

WPI; 2003-148685/14.

Detection device useful for detecting binding between members of specific binding pair, and for multiparallel thermal analysis of samples, has an array of addressable thermistors.

Example 2; Page 36; 60pp; English

The present sequence is that of a (CA)10 oligonucleotide used to illustrate the method of the invention. The invention provides methods for detecting specific binding interactions through measuraing the heat of binding generated when members of specific binding pairs interact with each other. The invention also provides methods to detect analytes in a solution through measurement of the heat of binding or reaction generated from the interaction of the analytes with binding or reaction parents. Detection devices are provided that consist of spatially addressable arrays of thermistors, which are useful in the multiparallel thermal analysis of samples. The methods and devices are particularly in the analysis of nucleic acids, especially DNA/DNA, DNA/RNA, DNA/LNA (linear

The present sequence is that of a (TG)10 oligonucleotide used to illustrate the method of the invention. The invention provides methods illustrate the method of the invention. The invention provides methods for for detecting specific binding plants inceract with each other. The invention also provides methods to detect analytes in a solution through measurement of the heat of binding or reaction generated from the interaction of the analytes with binding or reaction partners. Comparise of termistors, which are useful in the multiparallel thermal analysis of thermistors, which are useful in the multiparallel thermal analysis of nucleic acids, especially DNA/DNA, (linear nucleic acid). The binding between the analyte and its binding partner comprises part of an enzymatic amplification reaction, especially PCR or primer extension reaction. The detection device provides a real time, digital profile of the binding or reaction between the analyte and its binding or reaction partner. An example from the invention, using the

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                              ö
nucleic acid), DNA/siRNA (short interfering RNA) and DNA/PNA (peptide nucleic acid). The binding between the analyte and its binding partner comprises part of an enzymatic amplification reaction, especially PCR or primer extension reaction. The detection device provides a real time, digital profile of the binding or reaction between the analyte and its binding or reaction between the analyte and its present oligonucleotide, showed that the thermal detection technique is able to distinguish between perfectly matched and mismatched DNA
                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide (TG)10 used in nucleic acid hybridisation.
                                                                                                                                                         1.9%; Score 20; DB 1; Length 20; llarity 100.0%; Pred. No. 60; Conservative 0; Mismatches 0; Indels
                                                                                                                                  Sequence 20 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                 1793 TGTGTGTGTGTGTGTGTG 1812
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                                                                                                                                                                                                                                                                                                             ABZ24439 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                microcalorimetry; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Roach JS, Wolter A;
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                                                                                                                                                                          Best Local Similarity
Matches 20; Conserv
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Gaps

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This invention relates to novel methods for modulating the expression of connective tissue growth factor (CTGP) by antisense oligonucleotides. CTGF has been mapped to human chromosome region 6q23.1, and is also known as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2, insulin-like growth factor binding protein-related protein 2, IGFBP-FP2, IGSPB-RP 1684 and ecogenin. It is known to stimulate DNA synthesis and promote chemotaxis of fibroblasts, however, it is also upregulated in acute lymphoblastic leukaemia and in tumour or endothelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           insulin-like growth factor binding protein-related protein 2, IGFBP-rP2, IGFBP-8, Hos24, ecogenin, acute lymphoblastic leukaemia, gene therapy, hyperproliferative disorder, cancer, pulmonary fibrosis, renal fibrosis, scleroderma, atherosclerosis, cytostatic, dermatological,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .20
/*tag= a //mod_base= OTHER
/nore= "OTHER phosphorothioate backbone, where 1-5 and /note= "OTHER phosphorothioate backbone, where 1-5 and /note= "OTHER"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                factor expression, particularly useful for treating cancers (e.g. breast or prostate cancer), pulmonary or renal fibrosis, scleroderma or atherosclerosis.
present oligonucleotide, showed that the thermal detection technique is able to distinguish between perfectly matched and mismatched DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                        Human connective tissue growth factor antisense oligo DNA (SeqID 40)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       antisense; human; ss; connective tissue growth factor; CTGF; chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein; fisp-12; NOV2;
                                                                                                        1.9%; Score 20; DB 1; Length 20;
100.0%; Pred. No. 60;
tive 0; Mismatches 0; Indels
                                                                           Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                     1793 TGTGTGTGTGTGTGTGTGTG 1812
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                                                                                                                                                                                                                      rerererererererere 20
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                                                                                                                                                                                                                                                                                                               ADB25647 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                Query Match
Best Local Similarity 100.
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiarteriosclerotic
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                                                                                                                                                                                                                                                                            RESULT 100
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associated with the vasculature. Accordingly, antisense oligonucleotides that inhibit the expression of CTGF in cells or tissues can be used in gene therapy to treat various conditions including hyperproliferative disorders (particularly cancer, e.g. breat, protecte or renal cancer), pulmonary fibrosis, ranal fibrosis, scleroderma and atheroselerosis. As such, the present invention describes these antisense oligos as having cycostatic, dermatological and antiarteriosclerotic activities. This with 2' MOE wings and a deoxy gap, which is used to inhibit expression of human CTGF of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antisense oligonucleotides for modulating connective tissue growth factor expression, particularly useful for treating cancers (e.g. breast or prostate cancer), pulmonary or renal fibrosis, scleroderma or atheroscierosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fisp_12; NOV2; ..., cuguract; indicated inducible secreted protein; fisp_12; NOV2; insulin-like growth factor binding protein-related protein 2; IGFBP-rP2; IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy; hyperprofilferative disorder; cancer; pulmonary fibrosis; renal fibrosis; activateriosclerotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mod_base= OTHER
/note= "OTHER= phosphorothioate backbone, where 1-5 and
16-20 are 2' methoxyethyl nucleotides. All cytidines are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to novel methods for modulating the expression of
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human connective tissue growth factor antisense oligo DNA (SeqID 62)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antisense, human, ss, connective tissue growth factor; CTGF, chromosome 6423.1; ctgrofact; fibroblast inducible secreted protein;
                                                                                                                                                                                                                                                                 ..
                                                                                                                                                                                                                            Query Match
1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                      1724 CTGGACAGCTTGTGGCAAGT 1743
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                                                                                                                                                                                                                                                                                                                           20 CTGGACAGCTTGTGGCAAGT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                               ADB25669 standard; DNA; 20
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modified_base
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ADB25669/c
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mcgarry191-19.rng

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CTGF has been mapped to human chromosome region 6g3.1, and is also known as currently clisted to human chromosome region 6g3.1, and is also known as ctgrofact, fibroblast inducible secreted protein. fisp-12, NOV2, insulin-like growth factor binding protein-related protein 2, IGFBP-FP, IGFBP-8, Hest4 and ecogenin. It is known to stimulate DNA synthesis and promote chemotaxis of fibroblasts, however, it is also upregulated in promote chemotaxis of fibroblasts, however, it is also upregulated in acute lymphoblastic leukaemia and in tumour or endothelial cells associated with the vasculature. Accordingly, antisense oligonucleotides that inhibit the expression of CTGF in cells or tissues can be used in gene therapy to treat various conditions including hyperproliferative disorders (particularly cancer, eg. breast, prostate or renal cancer), conjugnorary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As such, the present invention describes these antisense oligos as having cytostatic, dermatological and antiarteriosclerotic activities. This coligonucleotide sequence is a chimeric phosphorothhoate antisense oligo with 2, MOE wings and a deoxy gap, which is used to inhibit expression of human CTGF of the invention.
   oligonucleotides
connective tissue growth factor (CTGF) by antisense
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Sequence 20 BP; 6 A; 6 C; 2 G; 6 T; 0 U; 0 Other;

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ch 1.9%; Score 20; DB 1; Length 20; 1 Similarity 100.0%; Pred. No. 60; 20; Conservative 0; Mismatches 0; Indels
                                                                                  2206 TIGTIGAGAGIGIGACCAAA 2225
  Query Match
Best Local Similarity
Matches 20; Conserv
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Gaps

20 TTGTTGAGAGTGTGACCAAA 1 셤

ADB25654 standard; DNA; 20 BP. RESULT 102 ADB25654/c

20-NOV-2003 (first entry) ADB25654;

Human connective tissue growth factor antisense oligo DNA (SeqID 47)

insulin.like growth factor binding protein-related protein 2; IGFBP-rP2; IGFBP-8; HGS24; ecogenin; acute lymphoblastic leukaemia; gene therapy; hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis; soleroderma; atherosclerosis; cytostatic; dermatological; antisense; human; ss; connective tissue growth factor; CTGF; chromosome_6q23.1; ctgrofact; fibroblast inducible secreted protein; antiarteriosclerotic. fisp-12; NOV2;

Homo sapiens,

/mod_base= OTHER /note= "OTHER= phosphorothioate backbone, where 1-5 and 16-20 are 2' methoxyethyl nucleotides. All cytidines are 5-methylcytidines" Location/Qualifiers Ø *tag= Key modified_base

WO2003053340-A2

39-DEC-2002; 2002WO-US038618 33-JUL-2003

10-DEC-2001; 2001US-00006191

(ISIS-) ISIS PHARM INC.

Watt AT; Saarde WA,

WPI; 2003-559091/52.

New antisense oligonucleotides for modulating connective tissue growth

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This invention relates to novel methods for modulating the expression of connective tissue growth factor (CTGF) by antisense oligonucleotides.

CTGF has been mapped to human chromosome region 643.1, and is also known as tggrofact, fibroblast inducible secreted protein, fisp-12, NOVZ, insulin-like growth factor binding protein-related protein 2, IGFBF-FP2, CG IGFBF-B, HGSZ4 and ecogenin. It is known to stimulated DNA synthesis and promote chemotaxis of fibroblasts, however, it is also upregulated in acute lymphoblastic leukaemia and in tumour or endothelial cells associated with the various conditions including hyperproliferative associated with the various conditions including hyperproliferative content inhibit the expression of CTGF in cells or tissues can be used in that inhibit the expression of CTGF in cells or tissues can be used in the therapy to treat various conditions including hyperproliferative disonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As such, the present invention describes these antisense oligos as having cytostatic, dermatological and antiarteriosclerotic activities. This collidonucleotide sequence is a chimeric phosphorothicate antisense oligo with 2, MOE wings and a deoxy gap, which is used to inhibit expression of thuman CTGF of the invention.
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ractor expression, particularly useful for treating cancers (e.g. breast or prostate cancer), pulmonary or renal fibrosis, scleroderma or atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 0 Other;
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                                                                                                                                            Claim 3; Page 85; 139pp; English
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RESULT 103 ADB25649,

ADB25649 standard; DNA; 20 BP ADB25649;

(first entry)

20-NOV-2003

Human connective tissue growth factor antisense oligo DNA (SeqID 42)

antisense; human; ss; connective tissue growth factor; CTGF; chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein; fisp-12; NOV2; insulin-like growth factor binding protein-related protein 2; IGFBP-rP2; IGFBP-8; HCS24; ecogenin; acute lymphoblastic leukaemia; gene therapy; hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis; scleroderma; atherosclerosis; cytostatic; dermatological; antiarteriosclerotic.

Homo sapiens

1. .20 /*teg= a OTHER /mod base= OTHER= /note= "OTHER= phosphorothioate backbone, where 1-5 and 16-20 are 2' methoxyethyl nucleotides. All cytidines are 5-methylcytidines" Location/Qualifiers Key modified_base

WO2003053340-A2

03-JUL-2003

09-DEC-2002; 2002WO-US038618

10-DEC-2001; 2001US-0006191

This invention relates to novel methods for modulating the expression of connective tissue growth factor (CTGF) by antisense oligonucleotides.

CTGF has been mapped to human chromosome region 623:1, and is also known as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2, insulin-like growth factor binding protein-related protein 2, IGFBP-rP2, CTG insulin-like growth factor binding protein-related protein 2, IGFBP-rP2, CTG GrBP-B-W Hos24 and ecogenin. It is known to stimulate DNA synthesis and promote chemotaxis of fibroblasts, however, it is also upregulated in acute lymphoblastic leukaemia and in tumour or endothelial cells associated with the vasculature. Accordingly, antisense oligonucleotides that inhibit the expression of CTGF in cells or tissues can be used in that inhibit the expression of CTGF in cells or tissues can be used in gene therapy to treat various conditions including hyperproliferative disorders (particularly cancer, e.g. breast, prostate or renal cancer), culmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As such, the present invention describes these antisense oligos as having cytostatic, dermatological and antiarteriosclerotic activities. This cillonucleotide sequence is a chimeric phosphorothicate antisense oligo with 2, MOE wings and a deoxy gap, which is used to inhibit expression of human CTGF of the invention. New antisense oligonucleotides for modulating connective tissue growth factor expression, particularly useful for treating cancers (e.g. breast or prostate cancer), pulmonary or renal fibrosis, scleroderma or atherosclerosis. Claim 3; Page 85; 139pp; English. (ISIS-) ISIS PHARM INC Gaarde WA, Watt AT; WPI; 2003-559091/52 \$X4X4X4444444

Query Match
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels Seguence 20 BP; 9 A; 2 C; 1 G; 8 T; 0 U; 0 Other;

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Gaps .; 0

Human connective tissue growth factor antisense oligo DNA (SeqID 41).

antisense; human; ss; connective tissue growth factor; CTGF; ctromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein; fisp-12; NOV2; insulin-11ke growth factor binding protein-related protein 2; IGFBP-rP2; IGFBP-RP3; HGS24; ecogenin; acute lymphoblastic leukaemia; gene therapy; hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis; sclearoderma; atheroelerosis; cytostatio; dermatological;

Location/Qualifiers 1.20 /*tag= a

/mod_base= OTHER /note= "OTHER= phosphorothioate backbone, where 1-5 and 16-20 are 2' methoxyethyl nucleotides. All cytidines are 5-methylcytidines"

03-JUL-2003

09-DEC-2002; 2002WO-US038618.

10-DEC-2001; 2001US-0006191

(ISIS-) ISIS PHARM INC

Watt AT; Gaarde WA, WPI; 2003-559091/52

New antisense oligonucleotides for modulating connective tissue growth factor expression, particularly useful for treating cancers (e.g. breast or prostate cancer), pulmonary or renal fibrosis, scleroderma or atherosclerosis.

Claim 3; Page 85; 139pp; English.

This invention relates to novel methods for modulating the expression of connective tissue growth factor (CTGF) by antisense oligonucleotides.

CTGF has been mapped to human chromosome region 643.1, and 18 also known as ctgrofact, fibroblast inducible secreted protein, fisp-12, NoV2, insulin-like growth factor binding protein-related protein 2, IGFBP-rP2, IGFBP-8, Heest and ecogenin. It is known to stimulated DNA synthesis and promote chemotaxis of fibroblasts, however, it is also upregulated in acute lymphoblastic leukaemia and in tumour or endothelial cells associated with the vasculature. Accordingly, antisense oligonucleotides that inhibit the expression of CTGF in cells or tissues can be used in gene therapy to treat various conditions including hyperproliferative disochers (particularly cancer, e.g. breast, prostate or renal cancer), culmonary fibrosis, renal fibrosis, scleroderma and atherosolerosis. As such, the present invention describes these antisense oligos as having cytostatic, dermatological and antiarteriosclerotic activities. This coligonucleotide sequence is a chimaric phosphorothicate antisense oligo with 2, MOB wings and a deoxy gap, which is used to inhibit expression of human CTGF of the invention.

Sequence 20 BP; 8 A; 3 C; 2 G; 7 T; 0 U; 0 Other;

.. 0 Query Match
1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels

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ADB25653 standard; DNA; 20 BP RESULT 105

ADB25653;

(first entry) 20-NOV-2003 Human connective tissue growth factor antisense oligo DNA (SeqID 46)

antisense; human; ss; connective tissue growth factor; CTGF; chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein; fisp-12; NOV2; insulin-like growth factor binding protein-related protein 2; IGFBP-rP2; IGFBP-8; Hcs24; ecogenin; autte lymphoblastic leukaemia; gene therapy; hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis; scleroderma; atherosclerosis; cytostatic; dermatological; ADB25653/ MAC ADB2 MAC A

antiarteriosclerotic

Homo sapiens

Location/Qualifiers Key modified_base

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scleroderma; atherosclerosis; cytostatic; dermatological; antiarteriosclerotic.

This invention relates to novel methods for modulating the expression of connective tissue growth factor (CTGP) by antisense oligonucleotides.

CTGF has been mapped to human chromosome region 6423.1, and is also known as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2, insulin-like growth factor binding protein-related protein 2 IGFBP-rP2, CTGFBP-8, Hosels and promote chemotaxis of fibroblasts, however, it is also upregulated in acute lymphoblastic leukaemia and in tumour or endothelial cells associated with the vasculature. Accordingly, antisense oligonucleotides that inhibit the expression of CTGF in cells or tissues can be used in gene therapy to treat various conditions including hyperproliferative disported (particularly cancer, e.g. breast, prostate or renal cancer), pulmonary fibrosis, renal fibrosis, scleroderma and atherosoclerosis. As such, the present invention describes these antisense oligos as having cytostatic, dermatological and antiarteriosclerotic activities. This colligonucleotide sequence is a chimeric phosphorothioate antisense oligo with 2' MOE wings and a deoxy gap, which is used to inhibit expression of thuman CTGF of the invention. /*tag= a //mod_bage= OTHER /note= "OTHER= phosphorothioate backbone, where 1-5 and 16-20 are 2' methoxyethyl nucleotides. All cytidines are factor expression, particularly useful for treating cancers (e.g. breast or prostate cancer), pulmonary or renal fibrosis, scleroderma or atherosclerosis. New antisense oligonucleotides for modulating connective tissue growth 5-methylcytidines" Claim 3; Page 85; 139pp; English. 10-DEC-2001; 2001US-0006191. 09-DEC-2002; 2002WO-US038618 (ISIS-) ISIS PHARM INC Watt AT; WPI; 2003-559091/52 WO2003053340-A2 03-JUL-2003 Gaarde WA,

Gaps 0 Query Match
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels Sequence 20 BP; 4 A; 7 C; 2 G; 7 T; 0 U; 0 Other;

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ADB25656 standard; DNA; 20 ADB25656;

Human connective tissue growth factor antisense oligo DNA (SeqID 49) 20-NOV-2003 (first entry)

fisp-12; NOV2; Information of the state of t antisense; human; ss; connective tissue growth factor; CTGF; chromosome 6423.1; ctgrofact; fibroblast inducible secreted protein;

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This invention relates to novel methods for modulating the expression of connective tissue growth factor (CTGF) by antisense oligonucleotides.

CTGF has been mapped to human chromedeome region 623.1, and is also known crystofact, fibroblast inducible secreted protein, fisp-12, NOV2, insulin-like growth factor binding protein-related protein 2, IGPBP-rP2, CTG 10FBP-9, Hosey and ecogenin. It is known to stimulate DNA synthesis and promote chemotaxis of fibroblasts, however, it is also upregulated in acute lymphoblastic leukaemia and in tumour or endothelial cells associated with the vasculature. Accordingly, antisense oligonucleotides that inhibit the expression of CTGF in cells or tissues can be used in that inhibit the expression of CTGF in cells or tissues can be used in the therapy to treat various conditions including hyperproliferative disorders (particularly cancer, e.g. breast, prostate or renal cancer), cull monary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As such, the present invention describes these antisense oligos as having cytostatic, dernatological and antiarteriosclerotic activities. This coligonucleotide sequence is a chimeric phosphorothloate antisense oligo with 2, MoE wings and a deoxy gap, which is used to inhibit expression of human CTGF of the invention.
                                                                                                                    1..20
/*tsg= a
/mod_base= OTHER
/note= "OTHER= phosphorothicate backbone, where 1-5 and
16-20 are 2' methoxyethyl nucleotides. All cytidines are
5-methylcytidines"
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                                                                                              Location/Qualifiers
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                                                                                                     Key
modified_base
                                                             Homo sapiens
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Human connective tissue growth factor antisense oligo DNA (SeqID 64). ô 1.9%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 60; tive 0; Mismatches 0; Indels 2242 CTTTCTAGTTGAAATAAAG 2261 20 CTTTCTAGTTGAAATAAAG 1 ADB25671 standard; DNA; 20 BP 20-NOV-2003 (first entry) Best Local Similarity 100. Matches 20; Conservative ADB25671; Query Match RESULT 1 BXHXHXB ò g

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Gaps

ADB25666 standard; DNA; 20 BP.

(first entry)

20-NOV-2003

ADB25666;

This invention relates to novel methods for modulating the expression of connective tissue growth factor (CTGF) by antisense oligonucleotides.

CTGF has been mapped to human chromosome region 6423.1, and is also known as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2, insulin-like growth factor binding protein-related protein 2, IGFBP-FP2, CTGFP-B, RGS4 and ecogenin. It is known to stimulate DNA synthesis and promote chemotaxis of fibroblasts, however, it is also upregulated in acute lymphoblastic leukaemia and in tumour or endothelial cells associated with the vasculature. Accordingly, antisense oligonucleotides that inhibit the expression of CTGF in cells or tissues can be used in gene therapy to treat various conditions including hyperproliferative clascifers fibratis, rehal fibrosis, scleroderma and atherosclerosis. As such, the present invention describes these antisense oligos as having cytostatic, dermatological and antiatraticsclerotic activities. This cligonucleotide sequence is a chimeric phosphorothicate antisense oligo with 2 MOE wings and a deoxy gap, which is used to inhibit expression of human CTGF of the invention. New antisense oligonucleotides for modulating connective tissue growth factor expression, particularly useful for treating cancers (e.g. breast or prostate cancer), pulmonary or renal fibrosis, scleroderma or insulin-like growth factor binding protein-related protein 2; IGFBP-rP2; IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy; hyperprofilerative disorder; cancer; pulmonary fibrosis; renal fibrosis; scleroderma; atherosclerosis; cytostatic; dermatological; antiarteriosclerotic. /note= "OTHER= phosphorothicate backbone, where 1-5 and 16-20 are 2' methoxyethyl nuclectides. All cytidines are 5-methylcytidines" antisense, human; ss; connective tissue growth factor; CTGF; chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein; fisp-12; NOV2; Sequence 20 BP; 6 A; 4 C; 3 G; 7 T; 0 U; 0 Other; Location/Qualifiers Claim 3; Page 85; 139pp; English. /*tag= a /mod base= OTHER 09-DEC-2002; 2002WO-US038618. LO-DEC-2001; 2001US-00006191. 1. .20 /*tag= (ISIS-) ISIS PHARM INC Watt AT; WPI; 2003-559091/52 atherosclerosis. WO2003053340-A2 modified base Homo sapiens 03-JUL-2003 Gaarde WA,

Gaps ö 1.9%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 60; 0; Indels 0; Mismatches 20; Conservative Similarity Query Match Best Local (Matches

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Gaps

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Indels

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0; Mismatches

20; Conservative

Best_Local Similarity Matches 20; Conserv

Query Match

1.9%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 60;

Sequence 20 BP; 4 A; 7 C; 4 G; 5 T; 0 U; 0 Other;

e is a chimeric phosphorothioate antisense oligo deoxy gap, which is used to inhibit expression

oligonucleotide sequence is a chimeric

human CTGF of the invention.

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ઠે 셤 RESULT 108 ADB25666/c

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This invention relates to novel methods for modulating the expression of connective tissue growth factor (CTGF) by antisense oligonucleotides.

CTGF has been mapped to human chromosome region 6q3.1, and is also known as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2, insulin-like growth factor binding protein-related protein 2, IGFBF-FF2, IGFBF-FF2, GTGFBF-F, Hass4 and ecogenin. It is known to stimulate DNA synthesis and promote chemotaxis of fibroblasts however, it is also upregulated in acute lymphoblastic leukaemia and in tumour or endothelial cells associated with the vasculature. Accordingly, antisense oligonucleotides that inhibit the expression of CTGF in cells or tissues can be used in gene therapy to treat various conditions including hyperproliferative disorders (particularly cancer, e.g. breast, prostate or renal cancer), culmonary fibrosis, renal fibrosis, solaroderma and atherosclerosis. As such, the present invention describes these antisense oligos as having cytostatic, dematological and antiarteriosclerotic activities. This entities of the control of t
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                                                                                                                                                                                                      antisense; human; ss; connective tissue growth factor; CTGF; ctgrofact; fibroblast inducible secreted protein; fisp-12; NOV2; NOV2; insulin-11ke growth factor binding protein-related protein 2; IGFBF-rP2; IGFBF-s; HGS24; ecogenin; acute lymphoblastic leukaemia; gene therapy; IGFBF-proliferative disorder; cancer; pulmonary fibrosis; renal fibrosis; scleroderma; atherosclerosis; cytostatic; dermatological;
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16-20 are 2' methoxyethyl nucleotides. All cytidines are
5-methylcytidines"
                                                                                                                                                    Human connective tissue growth factor antisense oligo DNA (SeqID 59)
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Sequence 20 BP; 7 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

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This invention relates to novel methods for modulating the expression of connective tissue growth factor (CTGF) by antisense oligonucleotides.

CTGF has been mapped to human chromosome region 6421, and is also known as crgoridact, fibroblast inducible secreted protein, fisp-12, NOV2.

CTGF has been mapped to human chromosome region 6421, and is also known compared the cogenin. It is known to stimulate DNA synthesis and promote chemotaxis of fibroblasts, however, it is also upregulated in acute lymphoblastic leukaemia and in tumour or endothelial cells associated with the vasculature. Accordingly, antisense oligonucleotides that inhibit the expression of CTGF in cells or tissues can be used in gene therapy to treat various conditions including hyperproliferative disorders (particularly cancer, e.g. breast, prostate or renal cancer), culmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As such, the present invention describes these antisense oligos as having cytostatic, dermatological and antiarteriosclerotic activities. This oligonucleotide sequence is a chimeric phosphorothicate antisense oligo with 2 MoB wings and a deoxy gap, which is used to inhibit expression of tuman CTGF of the invention.
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                                                                                                                                                                                                                                                                                      antisense; human; ss; connective tissue growth factor; CTGF; chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein; fisp-12; NOV2; insulin-like growth factor binding protein-related protein 2; IGFBP-rP2; IGFBP-8; Hos24; ecogenin; acute lymphoblastic leukaemia; gene therapy; hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis; scleroderma; atherosclerosis; cytostatic; dermatological;
                                                                                                                                                                                                                                                       Human connective tissue growth factor antisense oligo DNA (SeqID 95)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
ACTGGACAGCTTGTGGCAAG 1742
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                       20 ACTGGACAGCTTGTGGCAAG 1
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                                                                                                                                       ADB25702 standard; DNA; 20
                                                                                                                                                                                                                   (first entry)
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  1723
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This invention relates to novel methods for modulating the expression of connective tissue growth factor (CTGF) by antisense oligonucleotides. CTGF has been mapped to human chromosome region 623.1, and is also known as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2, insulin-like growth factor binding protein-related protein 2, IGFBP-rP2, IGFBP-R, MOS2, and eogenin. It is known to stimulate DNA synthesis and promote chemotaxis of fibroblasts, however, it is also upregulated in acute lymphoblastic leukeemia and in tumour or endothelial cells associated with the vasculature. Accordingly, antisense oligonucleotides that inhibit the expression of CTGF in cells or tissues can be used in gene therapy to treat various conditions including hyperprollferative
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                                                                                                                                                                                                                                                                                                                                                 insulin-like growth factor binding protein-related protein 2; IGFBP-rP2; IGFBP-B, Ecs4; ecogenin; acute lymphoblastic leukaemia; gene therapy; hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis; scleroderma; atherosclerosis; cytostatic; dermatological;
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                                    Gaps
                                                                                                                                                                                                                                                                                                    antisense; human; ss; connective tissue growth factor; CTGF; chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein;
                                                                                                                                                                                                                                                                       Human connective tissue growth factor antisense oligo DNA (SeqID 45)
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 DB 1, Length 20;
60;
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1.9%; Scor.
100.0%; Pred. No. co.
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                                                                                                 20 AAATTTTAGCGTGCTCACTG
                                                                      1553 AAATTTTAGCGTGCTCACTG
                                                                                                                                                                                ADB25652 standard; DNA; 20 BP.
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disorders (particularly cancer, e.g. breast, prostate or renal cancer), pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As such, the present invention describes these antisense oligos as having cytostatic, dermatological and antiarteriosclerotic activities. This oligonucleotide sequence is a chimeric phosphorothioate antisense oligo with 2' MOE wings and a deoxy gap, which is used to inhibit expression of human CTGF of the invention.
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Sequence 20 BP; 8 A; 6 C; 2 G; 4 T; 0 U; 0 Other;

Gaps .; 0 Score 20; DB 1; Length 20; Pred. No. 60; 0; Indels 1.9%; scc. 100.0%; Pred.No. c. ... 0; Mismatches 20; Conservative Similarity Query Match Best Local S Matches 20 Match

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2203 TATTIGAGAGIGIGACC 2222

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20 TATTTGTTGAGAGTGTGACC 1

RESULT 111 ADB25703/c

ADB25703 standard; DNA; 20 BP

ADB25703

(first entry) 20-NOV-2003 Human connective tissue growth factor antisense oligo DNA (SeqID 96)

antisense; human, ss; connective tissue growth factor; CTGF; chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein;

fisp_12; NOV2; Insular NOV2; Insular like growth factor binding protein-related protein 2; IGFBP-FP2; IGFBP-8; HCS24; ecogenin; acute lymphoblastic leukaemia; gene therapy; hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis; scleroderma; atherosclerosis; cytostatic; dermatological;

antiarteriosclerotic

Homo sapiens

Location/Qualifiers 1. .20 /*tag= a Key modified_base

/mod_base= OTHER /note= "OTHER= phosphorothicate backbone, where 1-5 and 16-20 "methoxyethyl nuclectides. All cytidines are 5-methylcytidines"

WO2003053340-A2

09-DEC-2002; 2002WO-US038618,

.0-DEC-2001; 2001US-0006191

(ISIS-) ISIS PHARM INC

Watt AT; Gaarde WA,

09-DEC-2002; 2002WO-US038618. 10-DEC-2001; 2001US-0006191

03-JUL-2003

(ISIS-) ISIS PHARM INC.

Watt AT;

Gaarde WA,

WPI; 2003-559091/52

WPI; 2003-559091/52

New antisense oligonucleotides for modulating connective tissue growth factor expression, particularly useful for treating cancers (e.g. breast or prostate cancer), pulmonary or renal fibrosis, scleroderma or atherostlerosis.

Example 15; Page 86; 139pp; English.

This invention relates to novel methods for modulating the expression of connective tissue growth factor (CTGF) by antisense oligonuclectides. CTGF has been mapped to human chromosotian region 6q23.1, and is also known as ctgrofact, fibroblast inducible secreted procein, fisp-12, NOV2.

New antisense oligonucleotides for modulating connective tissue growth factor expréssion, particularly useful for treating cancers (e.g. breast or prostate cancer), pulmonary or renal fibrosis, scleroderma or atherosclerosis.

ô insulin-like growth factor binding protein-related protein 2, IGFBP-FP2, IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and promote chemotaxis of fibroblastes, however, it is also upregulated in acute lymphoblastic leukaemia and in tumour or endothelial cells associated with the vasculature. Accordingly, antisense oligomucleotides that inhibit the expression of CTGF in cells or tissues can be used in gene therapy to treat various conditions including hyperproliferative disorders (particularly cancer, e.g. breast, prostate or renal cancer), pullmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As such, the present invention describes these antisense oligos as having cytostatic, dermatological and antiatteriosclerotic activities. This oligomuclocide sequence is a chimeric phosphorothioate antisense oligo with 2, MOE wings and a deoxy gap, which is used to inhibit expression of human CTGF of the invention. /mod_base= OTHER /note= "OTHER= phosphorothicate backbone, where 1-5 and 16-20 are 2, methoxyethyl nucleotides. All cytidines are 5-methylcytidines" Lisp'11, NOV2, including protein-related protein 2; IGFBP-rP2; insulin-like growth factor binding protein-related protein 2; IGFBP-rP2; IGFBP-8; HGPBP-8; HGPBP-8; HGPBP-8; Googenin; acute lymphoblastic leukaemia; gene therapy; hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis; scleroderma; atherosclerosis; cytostatic; dermatological; Human connective tissue growth factor antisense oligo DNA (SeqID 48). antisense; human, ss; connective tissue growth factor; CTGF; chromosome 6423.1; ctgrofact; fibroblast inducible secreted protein; Gaps ö 0; Indels Score 20; DB 1; Length Pred. No. 60; Sequence 20 BP; 7 A; 4 C; 4 G; 5 T; 0 U; 0 Other; 1.9%; Scor. 100.0%; Pred. No. c... Location/Qualifiers 1637 GITGITCCTTAAGTCAGAAC 1656 Н BP. 20 GTIGTICCTTAAGICAGAAC ADB25655 standard; DNA; 20 (first entry) ø Local Similarity 100. nes 20; Conservative /*tag= antiarteriosclerotic. WO2003053340-A2 fisp-12; NOV2; Key modified base Homo sapiens. 20-NOV-2003 ADB25655; Query Match Best Loca Matches RESULT 112 ADB25655, ò

WPI; 2003-559091/52

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This invention relates to novel methods for modulating the expression of connective tissue growth factor (CTGP) by antisense oligonucleotides.

CTGF has been mapped to human chromosome region 6d21, and is also known as etgrofact, fibroblast inducible secreted protein, fisp-12, NoV2, insulin-like growth factor binding protein-related protein, 10 GFBP-rp2, IGFBP-8, HGS24 and ecogenin. It is known to stimulate DNA synthesis and promote chemotaxis of fibroblasts, however, it is also upregulated in carte Inymbholastic leukaemia and in tumour or endothelial cells associated with the vasculature. Accordingly, antisense oligonucleotides that inhibit the expression of CTGF in cells or tissues can be used in the capture various conditions including hyperproliferative disorders (particularly cancer, e.g. breast, prostate or renal cancer), columnnary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As such, the present invention describes these antisense oligos as having cycostatic, dermatological and antiatreriosclerotic activities. This coligonucleotide sequence is a chimeric phosphorothicate antisense oligo the contract of the coligonucleotide acquence is a chimeric phosphorothicate antisense oligo the contract of the coligonucleotide adexy gap, which is used to inhibit expression of the contract of the coligonucleotide acquence o
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                                            Claim 3; Page 85; 139pp; English
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Best Local Similarity
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This invention relates to novel methods for modulating the expression of connective tissue growth factor (CTGF) by antisense oligonucleotides.

CTGF has been mapped to human chromosome region 6423.1, and is also known as ctgrofact, flibroblast inducible secreted protein, fisp-12, NOV2, insulin-like growth factor binding protein-related protein 2, IGFBF-rP2, IGFBF-RP8, SH Hess and cogenin. It is known to sfimulate DNA synthesis and promote chemotaxis of fibroblasts, however, it is also upregulated in acute lymphoblastic leukaemia and in tumour or endothelial cells associated with the vasculature. Accordingly, antisense oligonucleotides that inhibit the expression of CTGF in cells or tissues can be used in gene therapy to treat various conditions including hyperproliferative disorders (particularly cancer, e.g. braast, prostate or renal cancer), culmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As such, the present invention describes these antisense oligos as having cytostatic, dermatological and antiarteriosclerotic activities. This oligonucleotide sequence is a chimaric phosphorothioate antisense oligo with 2 MOE wings and a decxy gap, which is used to inhibit expression of human CTGF of the invention.
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                                                                         factor expression, particularly useful for treating cancers (e.g. breast or prostate cancer), pulmonary or renal fibrosis, scleroderma or atherosclerosis.
                                                          New antisense oligonuclectides for modulating connective tissue growth
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Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels
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connective tissue growth factor (TGTS) by antisense oligonucleotides.

CTGF has been mapped to human chromosome region 693.1, and is also known as ctgrofact, fibroblast inducible screted protein, fish-12, NOV2, insulin-like growth factor binding protein-related protein, 169p-12, NOV3, insulin-like growth factor binding protein-related protein 2, IGFBP-r2, IGFBP-r8, McSt4 and ecogenin. It is known to stimulate DNA synthesis and promote chemotaxis of fibroblasts, however, it is also upregulated in acute lymphoblastic leukaemia and in tumour or endothelial cells associated with the vasculature. Accordingly, antisense oligonucleotides that inhibit the expression of CTGF in cells or tissues can be used in gene therapy to treat various conditions including hyperproliferative disorders (garticularly cancer, e.g. breast, prostate or renal cancer, pulmonary fibrosis, renal fibrosis, scleroderma and atherosoclerosis. As such, the present invention describes these antisense oligos as having cytostatic, dermatological and antiarteriosclerotic activities. This colloquicle sequence is a chimeric phosphorothhoate antisense oligo with 2, Mos wings and a deoxy gap, which is used to inhibit expression of
                                                                                                                                                                                                        New antisense oligonucleotides for modulating connective tissue growth factor expression, particularly useful for treating cancers (e.g. breast or prostate cancer), pulmonary or renal fibrosis, scleroderma or
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/note= "OTHER= phosphorothioate backbone, where 1-5 and
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09-DEC-2002; 2002WO-US038618.
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Matches
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This invention relates to novel methods for modulating the expression of connective tissue growth factor (CTGF) by antisense oligonuclectides.

CTGF has been mapped to human chromosome region 623.1, and is also known as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2, insulin-like growth factor binding protein-related protein, 2, IGFBP-rP2, IGFBP-RP8, Hossy and second protein it is known to stimulate DNA synthesis and promote chemotaxis of fibroblasts, however, it is also upregulated in acute lymphoblastic leukaemia and in tumour or endothelial cells associated with the vasculature. Accordingly, antisense oligonucleotides that inhibit the expression of CTGF in cells or tissues can be used in gene therapy to treat various conditions including hyperproliferative gene therapy to treat various conditions including hyperproliferative planting protein of protein and atherosclerosis. As such, the present invention describes these antisense oligos as having cytostatic, dermatological and antiatteriosclerotic activities. This coligonucleotide sequence is a chimeric phosphorothicate antisense oligo with 2 MoB wings and a deoxy gap, which is used to inhibit expression of human CTGF of the invention.
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                                                                                                                                                                                                                                                                                                                                                                      factor expression, particularly useful for treating cancers (e.g. breast or prostate cancer), pulmonary or renal fibrosis, scleroderma or atherosclerosis.
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16-20 are 2' methoxyethyl nucleotides. All cytidines are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                       New antisense oligonucleotides for modulating connective tissue growth
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100.0%; Pred. No. 60;
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es 20; Conservative 0; Mismatches
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                                                                                                              03-JUL-2003
                                                                                                                                                                                                                                                                             Gaarde WA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 116
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This invention relates to novel methods for modulating the expression of connective tissue growth factor (CTGF) by antisense oligonucleotides.

CTGF has been mapped to human chromosome region 6423.1, and is also known as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2, insulin-like growth factor binding protein-related protein 2, IGF9F-FP2, insulin-like protein 3, IGF9F-FP2, insulin-like 2, IGF9F-FP2, insulin-like 2, IGF9F-FP2, insulin-like 3, IGF9F-FP2, IG /note= "CTHER= phosphorothioate backbone, where 1-5 and 16-20 are 2' methoxyethyl nucleotides. All cytidines are 5-methylcytidines" New antisense oligonucleotides for modulating connective tissue growth factor expression, particularly useful for treating cancers (e.g. breast or prostate cancer), pulmonary or renal fibrosis, scleroderma or atherosclerosis. Sequence 20 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 0 Other; Location/Qualifiers Claim 3; Page 86; 139pp; English OTHER 10-DEC-2001; 2001US-00006191. 09-DEC-2002; 2002WO-US038618. /*tag= a /mod_base= (ISIS-) ISIS PHARM INC Gaarde WA, Watt AT; WPI; 2003-559091/52. WO2003053340-A2 modified base Homo sapiens 03-JUL-2003

Gaps .; 0 Query Match
1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels

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1713 TGTCGATTAGACTGGACAGC 1732

ठ S D

20 TGTCGATTAGACTGGACAGC 1

ADB25667 standard; DNA; 20 RESULT 117 ADB25667/
ID ADB2
XX
AC ADB2
XX
DT 20-N
XX
XX
XX
XX
XX
XX
XX
XX
XX
Anti

ADB25667;

BP.

(first entry) 20-NOV-2003

Human connective tissue growth factor antisense oligo DNA (SeqID 60)

antisense; human; ss; connective tissue growth factor; CTGF; chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein;

insulin-like growth factor binding protein-related protein 2; IGFBP-rP2; IGFBP-8, HGS24; ecogenin; acute lymphoblastic leukaemia; gene therapy; hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis; scleroderma; atherosclerosis; cytostatic; dermatological; antiarteriosclerotic fisp-12; NOV2; insulin-like g Homo sapiens

Location/Qualifiers 1. .20 /*tag= a Key modified base

/mod_base= OTHER /note= "OTHER= phosphorothioate backbone, where 1-5 and 16-20 are 2' methoxyethyl nucleotides. All cytidines are 5-methylcytidines"

WO2003053340-A2

09-DEC-2002; 2002WO-US038618

10-DEC-2001; 2001US-00006191.

(ISIS-) ISIS PHARM INC.

Gaarde WA, Watt AT;

WPI; 2003-559091/52

New antisense oligonucleotides for modulating connective tissue growth factor expression, particularly useful for treating cancers (e.g. breast or prostate cancer), pulmonary or renal fibrosis, scleroderma or atherosclerosis.

Example 15; Page 85; 139pp; English.

This invention relates to novel methods for modulating the expression of connective tissue growth factor (CTGF) by antisense oligonuclocides.

CTGF has been mapped to human chromosome region 6423.1, and is also known as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2, insulin-like growth factor binding protein-related protein. 2 IGFBP-rP2, CTGFBP-8, Growth factor binding protein-related protein. 2 IGFBP-rP2, CTGFBP-8, Growth factor binding protein-related protein. 2 IGFBP-rP2, CTGFBP-8, Growth factor binding protein. This synthesis and promote chemotaxis of fibroblasts, however, it is also upregulated in acute lymphoblastic leukaemia and in tumour or endothelial cells asociated with the vasculature. Accordingly, antisense can be used in that inhibit the expression of CTGF in cells or tissues can be used in genether aparticularly cancer, e.g. breast, prostate or renal cancer), pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As such, the present invention describes these antisense oligos as having cytostatic, dermatological and antiatrenicoclarotic activities. This course of the invention and adexy gap, which is used to inhibit expression of the contract of the human CTGF of the invention. %XGCGGGGGGGGGGGCGX8XBBBBXBXBXBXBXBXBXBXBXBXBXBXBXBX8XXBXBXBX

Seguence 20 BP; 7 A; 3 C; 4 G; 6 T; 0 U; 0 Other;

ö DB 1; Length 20; 0; Indels Query Match
1.9%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches

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Gaps

1752 CIGIAACAAGCCAGAITITI 1771 CTGTAACAAGCCAGATTTT 1

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ADB25672 standard; DNA; 20 BP. RESULT 118
ADB25672/C
ID ADB256
XX
AC ADB256

ADB25672

antisense; human; ss; connective tissue growth factor; CTGF; ctoromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein; fisp.12; NOV2; NOV2; insulin-like growth factor binding protein-related protein 2; IGFBP-rF2; IGFBP-8; Hos24; ecogenin; acute lymphoblastic leuksemia; gene therapy; hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis; scleroderma; atherosclerosis; cytostatic; dermatological; Location/Qualifiers
1. .20
| 1. .20
| *tag= a | mod_base= OTHER | phosphorothicate backbone, where 1-5 and | 16-20 are 2. methoxyethyl nucleotides. All cytidines are 5-methylcytidines" New antisense oligonucleotides for modulating connective tissue growth factor expression, particularly useful for treating cancers (e.g. breast or prostate cancer), pulmonary or renal fibrosis, scleroderma or atherosclerosis. Human connective tissue growth factor antisense oligo DNA (SeqID 65) 09-DEC-2002; 2002WO-US038618. 10-DEC-2001; 2001US-0006191 20-NOV-2003 (first entry) (ISIS-) ISIS PHARM INC Gaarde WA, Watt AT; antiarteriosclerotic WPI; 2003-559091/52. WO2003053340-A2 Key modified_base Homo sapiens 03-JUL-2003

This invention relates to novel methods for modulating the expression of connective tissue growth factor (CTGF) by antisense oligonucleotides.

CTGP has been mapped to human chromosome region 623.1, and is also known as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2, insulin-like growth factor binding protein-related protein 2, IGFBP-rP2, CTG TGFPP- Has decognin. It is known to stimulate DNA synthesis and promote chemotaxis of fibroblasts, however, it is also upregulated in acute lymphoblastic leukaemia and in tumour or endothelial cells associated with the vasculature. Accordingly, antisense oligonucleotides that inhibit the expression of CTGF in cells or tissues can be used in the capter inhibit the expression of CTGF in cells or tissues can be used in gene therapy to treat various conditions including hyperproliferative disorders (particularly cancer, e.g. breast, prostate or renal cancer), pulmonary fibrosis, renal fibrosis, scleroderma and atherosclearis. As such, the present invention describes these antisense oligos as having cycostatic, dermatological and antiatreriosclerotic activities. This clidonucleotide sequence is a chimeric phosphorothicate antisense oligo with 2, MoE wings and a decoy gap, which is used to inhibit expression of human CTGF of the invention. Example 15; Page 85; 139pp; English.

Claim 3; Page 86; 139pp; English.

Sequence 20 BP; 8 A; 3 C; 1 G; 8 T; 0 U; 0 Other;

Gaps .; 0 1.9%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 60; tive 0; Mismatches 0; Indels Local Similarity 100. nes 20; Conservative Query Match Best Loca Matches

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antisense; human; ss; connective tissue growth factor; CTGF; chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein; fisp-12; NOV2; insulin-like growth factor binding protein_related protein 2; IGFBP-RP2; IGFBP-8; HoS24; ecogenin; acute lymphoblastic leukaemia; gene therapy; hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis; acleroderma; atherosclerosis; cytostatic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                   New antisense oligonucleotides for modulating connective tissue growth factor expression, particularly useful for treating cancers (e.g. breast or prostate cancer), pulmonary or renal fibrosis, scleroderma or atherosclerosis.
                                                                                                                                                                                                                                 /mod_base= OTHER
/note= "OTHER= phosphorothioate backbone, where 1-5 and
16-20 are 2' methoxyethyl nucleotides. All cytidines are
5-methylcytidines"
                                                      Human connective tissue growth factor antisense oligo DNA (SeqID 92)
                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                              09-DEC-2002; 2002WO-US038618.
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                                                                                                                                                                                                     Key
modified base
                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                             Gaarde WA,
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ADB25699 standard; DNA; 20

RESULT 119 ADB25699/

ナイナスナナなだくに

(first entry)

20-NOV-2003

ADB25699;

Sequence 20 BP; 9 A; 1 C; 6 G; 4 T; 0 U; 0 Other;

This invention relates to novel methods for modulating the expression of connective tissue growth factor (CTGF) by antisense oligonucleotides.

CTGF has been mapped to human chromosome region 6421, and is also known as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2, insulin-like growth factor binding protein-related protein 2, IGFBP-PP2, IGFBP-RP2, IGFBP-RP3, HGGS4 and ecogenin. It is known to stimulated DNA synthesis and promote chemotaxis of fibroblasts, however, it is also upregulated in acute lymphoblastic leukaemia and in tumour or endothelial cells associated with the vasculature. Accordingly, antisense oligonucleotides that inhibit the expression of CTGF in cells or tissues can be used in the timpist the expression of CTGF in cells or tissues can be used in the timpist the expression of CTGF in cells or tissues can be used in the timpist particularly cancer, e.g. breast, prostate or renal cancer, configurate fibrosis, scleroderma and atherosolerosis. As such, the present invention describes these antisense oligos as having cycestatic, dermatological and antistreriosoleroide activities. The coligonucleotide sequence is a chimeric phosphorothicate antisense oligo with 2, MOE wings and a deoxy gap, which is used to inhibit expression of thuman CTGF of the invention.

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Gaps

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This invention relates to novel methods for modulating the expression of connective tissue growth factor (CTGF) by antiense oligomucleotides.

CTGF has been mapped to human chromosome region 6423.1, and is also known as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2, insulin-like growth factor binding protein-related protein, 1 GFBB-rP2, IGFBB-rP2, IGFBP-rP2, IGFBP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antisense; human; ss; connective tissue growth factor; CTGF; ctbromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein; fisp.12; NOV2; NOV2; insulin-like growth factor binding protein-related protein 2; IGFBF-rP2; IGFBF-rP2; IGFBF-rP2; IGFBF-rP2; IGFBF-rP2; INTROPA; A FOCA94; a coogenin, acute lymphoblastic leukaemia; gene therapy; INTRAPP-R2; INTRAPP-R2; renal fibrosis; colerative disorder; cancer; pulmonary fibrosis; renal fibrosis; scleroderma; atherosclerosis; cytostatic; dermatological;
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DB 1; Length 20; 60;
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0
1.9%; Score 20; DB 100.0%; Pred. No. 60; iive 0; Mismatches
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                                                                                                                                                                           1242 TCACATCTCATTTTCCGTA 1261
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                                                                                                                                                                                                                              20 TCACATCTCATTTTTCCGTA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADB25701 standard; DNA; 20 BP.
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Query Match 1.9
Best Local Similarity 100.
Matches 20; Conservative
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADB25701;
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XX ADB270

XX ADB2570

XX ADB2
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This invention relates to novel methods for modulating the expression of connective tissue growth factor (CTGF) by antisense oligonucleotides. CTGF has been mapped to human chromosome region 6q23.1, and is also known as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2, insulin-like growth factor binding protein-related protein 2, IGFBP-FP2, IGFBP-8, HGS24 and ecogenin. It is known to stimulate DNA synthesis and promote chemotaxis of fibroblasts, however, it is also upregulated in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fisp-12; NOV2; Institute factor binding protein-related protein 2; IGFBP-rP2; insulin-like growth factor binding protein-related protein 2; IGFBP-rP2; IGFBP-RP3; Hos24; ecogenin; acute lymphoblastic leukaemia; gene therapy; hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis; scleroderma; atherosclerosis; cytostatic; dermatological;
cytostatic, dermatological and antiarteriosclerotic activities. This oligomuciectide sequence is a chimeric phosphorothicate antisense oligo with 2' MOE wings and a decxy gap, which is used to inhibit expression chuman CTGF of the invention.
                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             antisense; human; ss; connective tissue growth factor; CTGF; chromosome 6423.1; ctgrofact; fibroblast inducible secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                           Human connective tissue growth factor antisense oligo DNA (SeqID 39)
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                                                                                                                           DB 1; Length 20;
60;
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                                                                                                                           1.9%; Score 20; DB 100.0%; Pred. No. 60; Live 0; Mismatches
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                                                                                                                                                                                                  1371 CCAGACACTGGTTTGAAGAA 1390
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/mod_base= OTHER
                                                                                                                                                                                                                                  20 CCAGACACTGGTTTGAAGAA 1
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                                                                                                                                                                                                                                                                                                                          ADB25646 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                             20-NOV-2003 (first entry)
                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 20, Conservative
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modified_base
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                                                                                                                                                                                                                                                                                            RESULT 121
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acute lymphoblastic leukaemia and in tumour or endothelial cells associated with the vasculature. Accordingly, antisense oligomucleotides that inhibit the expression of CTGF in cells or tissues can be used in gene therapy to treat various conditions including hyperproliferative disorders (particularly cancer, e.g. breast, prostate or renal cancer), pulmonary fibrosis, renal fibrosis, sclockers these and atherosclerosis. As such, the present invention describes these antisense oligos as having cytostatic, dermatological and antiarteriosclerotic activities. This
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                                                                                                                                                                                                                                                                                               Sequence 20 BP; 6 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                             1.9%; Score 20; DB
100.0%; Pred. No. 60;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               1719 TTAGACTGGACAGCTTGTGG 1738
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Best Local Similarity
Matches 20; Conserv
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ADB25668 standard; DNA; 20 BP
RESULT 122
                  ADB25668/
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ADB25668;
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(first entry) 20-NOV-2003

fisp-12; NOVŽ; insuli-like growth factor binding protein-related protein 2; IGFBP-rP2; insulin-like growth factor binding protein-related growth; gene therapy; hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis; scleroderma; atherosclerosis; cytostatic; dermatological; Human connective tissue growth factor antisense oligo DNA (SeqID 61). antisense; human; ss; connective tissue growth factor; CTGF; chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein;

Homo sapiens

antiarteriosclerotic

Location/Qualifiers 1. .20 /*tag= a /mod base= OTHER Key modified_base

/note= "OTHER= phosphorothioate backbone, where 1-5 and 16-20 are 2' methoxyethyl nucleotides. All cytidines are 5-methylcytidines"

WO2003053340-A2

03-JUL-2003

10-DEC-2001; 2001US-00006191. 09-DEC-2002; 2002WO-US038618.

(ISIS-) ISIS PHARM INC

Watt AT;

Gaarde WA,

09-DEC-2002; 2002WO-US038618 10-DEC-2001; 2001US-00006191

(ISIS-) ISIS PHARM INC

WPI; 2003-559091/52.

Gaarde WA,

WPI; 2003-559091/52.

New antisense oligonucleotides for modulating connective tissue growth factor expression, particularly useful for treating cancers (e.g. breast or prostate cancer), pulmonary or renal fibrosis, scleroderma or or prostate cance atherosclerosis.

Example 15; Page 85; 139pp; English

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This invention relates to novel methods for modulating the expression of connective tissue growth factor (CTGF) by antisense oligonucleotides.

CTGF has been mapped to human chromosome region 6421, and is also known as ctgrofact, fisp-12, NOV2.

CTGF insulin-like growth factor binding protein-related protein 2, IGFBF-FP2, insulin-like growth factor binding protein-related protein 2, IGFBF-FP2, CTGF promote chemotaxis of fibroblasts, however, it is also upregulated in acute lymphoblastic leukaemia and in tumour or endothelial cells associated with the vasculature. Accordingly, antisense oligonucleotides that inhibit the expression of CTGF in cells or tissues can be used in CTGF in cells or tissues can be used in CTGF in cells or tissues can be used in CTGF particularly cancer, e.g. breast, profetter or renal cancer, condimonary fibrosis, renal fibrosis, scleroderma and atherosolerosis. As such, the present invention describes these antisense oligos as having cycostatic, dermatological and antiarteriosclerotic activities. This coligonucleotide sequence is a chimeric phosphorothicate antisense oligo with 2, MOE wings and a deoxy gap, which is used to inhibit expression of thuman CTGF of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antisense; human; ss; connective tissue growth factor; CTGF; chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein; fisp-12; NOV2; insulin-like growth factor binding protein-related protein 2; IGFBP-rP2; IGFBP-8; HcG24; ecogenin; acute lymphoblastic ladvaemia; gene therapy; hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis; scheroderma; atherosclerosis; cytostatic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "OTHER= phosphorothioate backbone, where 1-5 and 16-20 are 2' methoxyethyl nucleotides. All cytidines are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                            1.9%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 60; Live 0; Mismatches 0; Indels
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Matches 20; Conservative
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New antisense oligonuclectides for modulating connective tissue growth factor expression, particularly useful for treating cancers (e.g. breast or prostate cancer), pulmonary or renal fibrosis, scleroderma or atherosclerosis.

Claim 3; Page 85; 139pp; English.

This invention relates to novel methods for modulating the expression of connective tissue growth factor (CTGF) by antisense oligonucleotides.

CTGF has been mapped to human chromosome region 6423.1, and is also known as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2, insulin-like growth factor binding protein-related protein. 2 IGFBP-rP2, IGFBP-P8, HCS24 and ecogenin. It is known to stimulate DNA synthesis and promote chemotaxis of fibroblasts, however, it is also upregulated in acute lymphoblastic leukaemia and in tumour or endothelial calls associated with the vasculature. Accordingly, antisense oligonucleotides that inhibit the expression of CTGF in cells or tissues can be used in gene therapy to treat various conditions including hyperprolferative pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As such, the present invention describes these antisense oligons as having cytostatic dermatological and antiarteriosclerotic activities. This oligonucleotide sequence is a chimmeric phosphorothicate antisense oligo with a man and a decxy gap, which is used to inhibit expression of the man of the companient of the contraction of the contrac human CTGF of the invention.

Sequence 20 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 0 Other;

.. 0 1.9%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 60; trive 0; Mismatches 0; Indels Local Similarity 100. 1es 20; Conservative Query Match Best Local Si Matches 20,

2212 AGAGTGTGACCAAAAGTTAC 2231

20 AGAGTGTGACCAAAAGTTAC 1 셤

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ADD26665 standard; DNA; 20 ADD26665; RESULT 124 ADD26665

(first entry) 15-JAN-2004

Polynucleotide (dsDNA) used in treatment of SLE.

Systemic lupus erythematosus, SLE; impaired renal function; LJP 394 conjugate; dermatological; immunosuppressive; antiinflammatory;

Unidentified.

US2003114405-A1

19-JUN-2003

13-AUG-2002; 2002US-00219238

13-AUG-2001; 2001US-0311858P. 22-AUG-2001; 2001US-0314281P.

(LINN/) LINNIK M D. (HEPB/) HEPBURN B.

WPI; 2003-810915/76.

Linnik MD, Hepburn B,

Treating systemic lupus erythematosus comprises selecting an individual having significantly impaired renal function and administering conjugate having non-immunogenic valency platform molecule and double stranded DNA epitopes

Claim 3; Page 18; 22pp; English.

The present invention relates to a method of treating systemic lupus erythematosus (SLE) in an individual. The method comprises selecting an individual having SLE, significantly impaired renal function, and antibodies with high affinity to a polymucleotide epitope by administering a conjugate comprising non-immunogenic valency platform molecules and two or more double stranded DNA (GDNA) epitopes that are polymucleotides. Also disclosed is a kit comprising the conjugate, LJP 394. The conjugate is administered in an amount effective to reduce incidence of renal flares in the individual. A medication chosen from corticosteroids and cyclophosphamide is also administered to the individual. The conjugate is administered in an amount effective to reduce the amount of a corticosteroid or cyclophosphamide administered to the individual. The present sequence represents a polynucleotide (dsbDNA) used in the treatment of SLE.

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Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;

Gaps . 0 Query Match
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels

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1794 GIGIGIGIGIGIGIGIGI 1813

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RESULT 125 AAQ34015

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AAQ34015 standard; DNA; 21 BP.

AAQ34015;

25-MAR-2003 02-FEB-1993

(revised)
(first entry)

Microsatellite sequence from clone TGLA419.

PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.

Bos taurus.

WO9213102-A1

06-AUG-1992.

92WO-US000340. 15-JAN-1992;

15-JAN-1991;

(GENM-) GENMARK.

Georges M, Massey JM;

Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding. WPI; 1992-284684/34.

Table 7; Page 336; 517pp; English.

The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information in the bovine phovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the

Synthetic oligonucleotide, dinucleotide repeat; cytostatic; apoptosis; cell cycle arrest; cell proliferation; caspase; cytokine; interleukin; tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;

lymphoma; ss

Synthetic.

Synthetic oligonucleotide 14.

(first entry)

12-SEP-2001

AAH46014;

AAH46014 standard; DNA; 21 BP.

AAH46014

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required PCR primers for in vitro amplification of the corresp.

microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentese testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective becomeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligo:nucleotide which reduces CD28 gene expression in T cells - for treating immune system diseases, e.g. gráft vs. host disease, septic shock, psoriasis, etc.
                                                                                                                                                                                                             Gaps
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                                                                                                                                                                       1.9%; Score 20; DB 1; Length 21; 100.0%; Pred. No. 62; tive 0; Mismatches 0; Indels
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95US-00529878.
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Matches 20; Conserv
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Best Local Similarity
Matches 20; Conserv
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18-SEP-1995;
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The present sequence is that of a synthetic oligonuclectide useful to the invention. The invention relates to a composition, comprises multiple base 3'-04, 5'-05 synthetic oligonuclectide which comprises multiple repeats of dinuclectides such as GT, TG, etc., according to specific formula and having cytostatic activity. The oligonuclectide compositions are useful for inducing cell cycle arrest, inhibition of proliferation, activation of apoptosis or production of activation of caspases and induction of apoptosis or production of cytokines such as interleukin (IL) 1-beta, IL-6, IL-10, IL-12 and tumour necrosis factor (INF)-alpha by immune system cells, in an animal having cancer such as primary carcinoma, secondary carcinoma, present, prostate, colorectal, ovarian or bone cancer. The compositions induce apoptosis cindependent of Fas, p53/p21, p21/waf-1/CIP, p15(ink4B), p16(ink4), drug resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Composition comprising synthetic oligonucleotides which comprise multi
repeats of dinucleotides such as GT, TG useful for treating cancer by
inducing cell cycle arrest, inhibiting proliferation, activating
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1.9%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 62;
Matches 20; Conservative 0; Mismatches
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29-AUG-2000; 2000US-0228925P.
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Synthetic

Sinha N;

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The present invention describes a phosphoramidite compound (I) comprising two or more nucleoside moieties linked by one or more internucleoside phosphorus atoms, where the internucleoside phosphorus atoms, where the internucleoside phosphorus atoms is toward. Also described: (I) preparing a trivalent phosphorus multimer or its stereoisomer (I); (2) a trivalent phosphorus multimer derivatised solid support (II); and (3) preparing (II). (I) or (II) can be used for the synthesis of oligonucleotides. The present sequence represents a phosphorothioate 21mer oligonucleotide which is synthesised in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, zinc finger protein 9.46; recombinant production, gene therapy, malignant tumnour; cancer; blood disease; human immunodéficiency virus; HIV infection; immune disorder, inflammatory condition; cytostatic; antiinflammatory; immunomodulator; reverse transcription-PCR; RT-PCR;
                                                                                                                                                                                                                                                                                                                                                      Novel phosphoramidite compound, useful for the synthesis of oligonucleotides, comprising nucleoside moieties linked by one or more internucleoside phosphorus atoms.
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/mod_base= OTHER
/note= "phosphorothioate linkages"
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                                                                                                                                         06-SEP-2001; 2001WO-GB003973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel phosphoramidite compound, useful for the synthesis of oligonuclectides, comprising nucleoside moieties linked by one or more internucleoside phosphorus atoms.
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                                                                                  Phosphorothioate; oligonucleotide synthesis; phosphoramidite; ss.
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Best Local Similarity 100.0%; Pred. No. 62;
Matches 20; Conservative 0; Mismatches 0; Indels
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                                            Phosphorothioate 21mer oligonucleotide SEQ ID NO:2.
                                                                                                                                                            Location/Qualifiers
1. .21
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                                                                                                                                                                                                                                                                                                                                                                                                                                               (AVEC-) AVECIA BIOTECHNOLOGY INC.
(AVEC-) AVECIA LTD.
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ID ABN88972 standard; DNA; 21
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        22-AUG-2002 (first entry)
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modified_base
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modified_base
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Synthetic

EXSXEXEXEXEXE

ABN88972;

RESULT 129

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Gaps ó

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonuclectide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the Frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information
                                                                                                                                          The invention relates to human zinc finger protein 9.46 (ABP58904) and nucleic acids encoding it (ABZ57677). The protein has a molecular weight of 9.46 kD. The invention also relates to a method for the recombinant production of the protein, an antagonist of the protein, and the use of the protein gene and antagonist in therapeutic applications. Zinc finger protein 9.46 can be used in the treatment of a variety of diseases such as malignant tumours, blood diseases, HV (human immunodeficiency virus) infection, immune disorders and inflammatory conditions. Sequences ABZ57679 represent reverse transcription-PCR (XT-PCR) primers used in an exemplification of the invention to isolate human zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                          New polypeptide human zinc finger protein 9.46 and polynucleotides encoding this polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                       Sequence 24 BP; 0 A; 0 C; 13 G; 11 T; 0 U; 0 Other;
                                                                                                               Example 2; Page 16 (Disclosure); 31pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                      1.9%; Score 19.8; Local Similarity 91.3%; Pred. No. 73; les 21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Microsatellite sequence from clone TGLA2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92WO-US000340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ33789 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1992-284684/34.
                                WPI; 2003-000239/01.
                                                                                                                                                                                                                                                                                                                         protein 9.46 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENM-) GENMARK
Xie Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JAN-1992;
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Mao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 131
                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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for ca. 230 such bowine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequences given in AATS8071-85 represent oligonucleotides which are antisense to sequences contained in the pre-mRNA or mature mRNA transcript of human intercellular adhesion molecule-1 (ICAM-1). These oligonucleotides may be used for treating septic shock and the manifestations of septic shock, e.g. inflammation, and vascular and tissue defects. They are also useful in the treatment of septic shock associated diseases, e.g. adult respiratory distress syndrome, multiple organ failure etc. (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antisense; pre-mRNA; mature mRNA; vascular defect; tissue defect; human intercellular adhesion molecule-1; ICAM-1; inflammation; adult respiratory distress syndrome; multiple organ failure; GM1594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                               Score 19.4; DB 1; Length 21; Pred. No. 73; 0; Mismatches 1; Indels
                                                                                                                                                                                                                Sequence 21 BP; 0 A; 1 C; 10 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21 BP; 11 A; 9 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Williams TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ICAM-1 antisense oligonucleotide #10.
                                                                                                                                                                                                                                                                                                                               1793 TGTGTGTGTGTGTGTGT 1813
                                                                                                                                                                                                                                                                                                                                                     1 TGTGTGTGTGCGTGTGTGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Col 21; 16pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lee C, Hoke GD, Bradley MO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93US-00136118.
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                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 95.2%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT58080 standard; DNA; 21
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    septic shock; ss.
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18-MAR-1997
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DB 1; Length 24; 2; Indels

1793 TGTGTGTGTGTGTGTGTGT 1813 21 rererererererererer ò 셤

AAV38616 standard; DNA; 21

AAV38616;

(first entry) 13-OCT-1998 Human ICAM-1, E-selectin, VCAM-1 antisense oligonucleotide.

ICAM-1; intracellular adhesion molecule-; B-selectin; VCAM-1; vascular cell adhesion molecule-1; antisense; inflammatory; disease; treatment; septic shock; psoriasis; wounds; burns; acne; arthritis; organ rejection; inhibition; expression; ss.

Homo sapiens. Synthetic

WO9824797-A1

11-JUN-1998

96WO-US019194. 02-DEC-1996;

96WO-US019194. 12-DEC-1996;

(DYAD-) DYAD PHARM CORP

Lee C; Bradley MO, Williams TJ, Hoke GD,

WPI; 1998-333253/29.

Antisense oligonucleotides to ICAM-1, E-selectin or VCAM-1 - useful for treating diseases having an inflammatory component, e.g. psoriasis, wounds and septic shock.

Claim 8; Page 40; 48pp; English.

The sequence is that of an antisense oligonucleotide which is substantially complementary to at least a portion of the pre- or mature start transcript of human intracellular adhesion molecule (ICAM), Eselectin or vascular cell adhesion molecule (VCAM). It can be used to inhibit expression of these proteins. Inhibition of these proteins forms the basis for treatment of conditions and diseases that have an inflammatory component, e.g. acne, postiacis, arthitis, organ rejection, wounds, burns, septic shock or inflammatory complications of septic shock

Sequence 21 BP; 11 A; 9 C; 0 G; 1 T; 0 U; 0 Other;

1.8%; Score 19.4; DB 1; Length 21; 95.2%; Pred. No. 73; tive 0; Mismatches 1; Indels Ouery Match Best Local Similarity 95.2 Matches 20; Conservative

1793 TGTGTGTGTGTGTGTGTGT 1813

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Human NADPH quinone oxidoreductase 2 (NQC2) polymorphic sequence #37 RESULT 134
ABS97829/c
1D ABS97829 standard; DNA; 21 BP.
XX
AC ABS97829;
XX
XX
DT 23-DEC-2002 (first entry)
XX
DE Human NADPH quinone oxidoreducts

Human, ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;

cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

adrenergic receptor beta1; ADBR1; ary1 hydrocarbon, AHR; MR113; NR112;

mary1 hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;

cyclocxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;

cyclocxgenase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;

cyclocxgenase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;

cyclocxdenydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;

cyclocxdenydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;

cyclocxdenydroxylase 2; EPHX2; cyclocransferase; NNMT;

NADPH quinone oxidoreductase 2; NQO2; sulfotransferase; NNMT;

which quinone oxidoreductase 2; NQO2; sulfotransferase; NNMT;

cyclocygenase receptor; UPP-glucuronosyl transferase 2B7;

cyclocygenase receptor; cyclocransferase; CHNR3;

cyclocygenase receptor;

cyclocygenase 2B4; UPP-glucuronosyl transferase;

cyclocygenase receptor;

cyclocygenase receptor;

cyclocygenase 2B7;

cyclocygenase 2B4;

cyclocygenase 2B7;

cyclocygenase 2 single nucleotide polymorphism.

WO200257410-A2

25-JUL-2002.

28-NOV-2001; 2001WO-US044838.

28-NOV-2000; 2000US-00724389

(DNAS-) DNA SCI LAB INC.

Hall J; Guida M, WPI; 2002-698522/75.

Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits.

Example 16; Page 130; 714pp; English.

This invention relates to the sequence of an isolated nucleic acid

molecule comprising at least one base variation from that of a known

CC molecule comprising at least one base variation from that of a known

CC human cytochrome P450 Al (CYP4501A1), adrenergic receptor betal (ADBR1),

cytochrome P450 O2E1 (CYP4501A21), adrenergic receptor betal (ADBR1),

CC (ANNY), cathepsin S (CTSS), cytocoxgenase 2 (CXS), diazepam binding

CC (ANNY), cathepsin S (CTSS), cytocoxgenase 2 (CXS), diazepam binding

CC (ANNY), putathione-S-transferase 12 (GST12), histamine-N-methyl

CC transferase (HNMY), NADPH quinone oxidoreductase 2 (NGO2),

CC (ADBL), putathione-S-transferase 2B7 (UGT2B7), instamine-N-methyl

CC (MRD1), adventione (NRD12B7), untiding resistance associated procein 3

CC (MRD1), actotransferrin (LTF), multidrug resistance associated procein 3

CC (MRD1), orpha nuclear receptor (NRD12B7), untiding resistance

CC (MRD1), orpha nuclear receptor (NRD12B7), untiding resistance

CC (MRD1), orpha nuclear receptor (NRD12B7), chantion receptor (NRD1COT)

CC (MRD1), orpha nuclear receptor (NRD1COT)

CC (MRD1), or realing the dasorders responsible for a variety of disorder-related

CC craits as a result of their e.g., overexpression, constitutive

CC and/Or rreating the disorders. The nucleic acid molecules comprising the

CC ARNI, EPHX2, GST12, NNWT, NQO2, NR112, STM, UGT2B4, UGT2B7, UGT2B15, ARNI, EPHX2, GST12, NNWT, NQO2, NR112, STM, UGT2B4, UGT2B7, CYPP4501A2,

CR ARNI, EPHX2, GST12, NNWT, NQO2, NR112, STM, UGT2B4, UGT2B7, UGT2BB1, UGT2BB1

CC Secptibility to concern polymorphic sequences in ADRAB1 or CHMR2 are

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Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;

cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

adrenargic receptor beta1; ADBR1; aryl hydrocarbon; ARRNY; cathepsin S; CTSS;

cyclooxgenase 2; COX2; diazepam binding inhibitor; DB1; haematological;

cyclooxgenase 2; EPHX2; 5-lipoxygenase activating protein; FiAP;

cyclooxgenase 2; NQO2; sulfotransferase; Day;

cyclooxgenase 2; NQO2; sulfotransferase; Day;

cyclooxgenase 2; NQO2; sulfotransferase; Day;

cyclooxgenase 2; NQO2; cyclooxgenase; Day;

cyclooxgenase;

cycl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits.
nervous system function, in FLAP and HNMT for altered pulmonary, immunological or haematological function, in KLK2 for altered serine protease activity in the prostate, in LTF for altered immunological or haematological function, in CHMR3, CHWR4 or CHMR5 for altered central and peripheral nervous system function. The present sequence represents a polymorphic DNA sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to the sequence of an isolated nucleic acid molecule comparising at least one base variation from that of a known human cytochrome P450 Al (CYP4501Al), cytochrome P450 A2 (CYP4501Al), cytochrome P450 A2 (CYP4501Al), cytochrome P450 02E1 (CYP45002E1), adrenergic receptor betal (ADBRI),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #39
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                                                                                                                                                                                                                                                                 DB 1; Length 21;
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                                                                                                                                                                                                          Seguence 21 BP; 11 A; 9 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                              / Match
Local Similarity 95.2%; Pred. No. 73;
les 20; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                      1793 TGTGTGTGTGTGTGTGTGT 1813
                                                                                                                                                                                                                                                                                                                                                                                                                  21 TATGTGTGTGTGTGTGTGT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABS97831 standard; DNA; 21 BP
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                                                                                                                                                                                                                                                                                                      Best Local
Matches
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aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator (ARNT), cathepsin S (CTSS), cyclooxgenase 2 (CDX2), diazepam binding cinhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating protein (FLAP), glutathione-5-transferase 12 (GST12), histenmine-N-methyl transferase (HNWT), NADH quanno oxidoreductase 2 (NQO2), ctransferase (HNWT), NADH quannon oxidoreductase 2 (NQO2), ctransferase thermolabile (STW), UDP-glucuronosyl transferase (UGT2B4), UDP-glucuronosyl transferase 2BT (UGT2B4), UDP-glucuronosyl transferase 2BT (UGT2B4), UDP-glucuronosyl transferase 2BT (UGT2B4), UDP-glucuronosyl transferase (UGT2B4), uDP-glucuronosyl transferase 2BT (UGT2B4), uDP-glucuronosyl transferase 2BT (UGT2B4), uDP-glucuronosyl transferase (UGT2B4), uDP-glucuronosyl transferase 2BT (UGT2B7), udvaluronosyl transferase (UGT2B4), uDP-glucuronosyl transferase 2BT (UGT2B7), udvaluronosyl transferase (UGT2B4), uDP-glucuronosyl transferase 2BT (UGT2B7), udvaluronosyl transferase 2BT (UGT2B7), udvalurosyl transferase 2BT (UGT2B7), udvaluronosyl transferase 2BT (UGT2B7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%; Score 19.4; DB 1; Length 21; 95.2%; Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21 BP; 11 A; 9 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Microsatellite sequence from clone TGLA135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polymorphic DNA sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peripheral nervous system function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1793 TGTGTGTGTGTGTGTGTGT 1813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 rerarcrerererererer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENM-) GENMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .5-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-AUG-1992.
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02-FEB-1993
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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine Mbol DNA fragments of between 250 and 500
by with an (AC1)5 and a (TC)15 oligomiclecide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100,000. The sequence information
of cr ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
specification and indexed herein (see below). The sequences upstream and
commerced CR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTIPRIM). The microsatellites may be
used to identify individuals, for parentage testing, and in the genetic
mapping of economic trait loci, or genes involved the determinism of
economically important traits esp. in cattle, to allow selective
connecting See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel simple sequence repeats in clover species useful for selection of genes in legume breeding, for profiling legume species varieties and for testing the purity of legume seed batches.
                                Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to Simple Sequence Repeats (SSRs) from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping;
trait mapping; marker-assisted selection; gene selection; legume;
DNA profiling; breeding; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22 BP; 1 A; 0 C; 11 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1793 TGTGTGTGTGTGTGTGT 1813
                                                                                     Table 7; Page 216; 517pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-431058/46.
WPI; 1992-284684/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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AAI64456/
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clover species. SSRs, also called microsatellites, are based on a 1-7 nuclectide core element which is tandemly repeated. The SSR array is embedded in complex flanking DNA. SSRs are ideal markers for genome mapping, trait mapping and marker-assisted selection. The SSRs may be used in methods for selecting genes in clover/ legume breeding. The SSRs may be purity of legume seed barches. The present sequence is and for testing the abuse used in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel set of inter-simple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes. The primers of the invention may be useful for genotyping diverse genomes of plant and animal systems, in particular for distinguishing Basmati rice varieties from non-Basmati rice varieties and traditional Basmati rice varieties from evolved Basmati rice varieties. The current sequence is that of the 5' anchored (ISSR)-PCR primer of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat; ISSR; SSR; PCR; primer; genotyping; plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New set of inter-simple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes, useful for genotyping diverse genomes of plant
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                                                                                                                                                                          Query Match
1.8%; Score 19.4; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 76;
Matches 20; Conservative 0; Mismatches 1; Indels
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                                                                                                                                               Seguence 22 BP; 10 A; 12 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DNAF-) CENT DNA FINGERPRINTING & DIAGNOSTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%; Score 19.4; D
95.2%; Pred. No. 78;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         - SEQ ID 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 5; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1793 TGTGTGTGTGTGTGTGT 1813
                                                                                                                                                                                                                                                1793 TGTGTGTGTGTGTGTGT 1813
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                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ISSR)-PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-APR-2002; 2002IN-CH000260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-JAN-2003; .2003WO-IB000041
                                                                                                                                                                                                                                                                                                                                                            ADD69447 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inter-simple sequence animal; Basmati rice;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-804317/75.
                                                                                                                                                                                                                                                                                                                                                                                                                            (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            animal systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nagaraju JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           5' anchored
                                                                                                                                                                                                                                                                                                                                                                                                                         15-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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ADD69447
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0; Mismatches

Score 19.4; DB 1; Length 22; Pred. No. 76;

ВР.

ABZ70239 standard; DNA; 24

(first entry)

25-APR-2003

ABZ70239;

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RESULT 140
                                ABZ70239,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences AAH17205 - AAH40944 represent PCR primers, single nucleotide polymorphisms SNPs. The present invention sites of single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the includes kits for determining the presence or absence of a SNP, using the oligonucleotides of the invention. The PCR primers are used to amplify a SNP filmling as uncleic acid sample by performing a single-nucleotide primer extension reaction. The oligonucleotides are useful for generation reaction. The oligonucleotide are useful for determining the presence, absence or identity of a SNP and for genotyping nucleic acid sample by consense by association analysis the genotype of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include diseases e.g. agammaglobulinaemia, diabetes insipidus, Lesch Nyhan syndrome, muscular dystrophy, familial hypercholesterolaemia, polycystic kidney disease, osteogenesis imperfecta and acute intermittent porphyria. Phenotypic traits also include symptoms of or susceptibility to multifactorial cates of which a component is or may be genetic such as autoimmune chisaase including, rheumatoid arthritis, multiple sclerosis, incloring and containing DNA sequence represents a PCR primer specific cor a human SNP containing DNA sequence
                                                                                                                                                                                                    Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis imperfecta; autoimmune disease; acute intermittent porphyria; rheumaroid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 24;
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1.8%; Score 19.4; Di
Best Local Similarity 95.2%; Pred. No. 81;
Matches 20; Conservative 0; Mismatches
                                                                                                                                                                  SNP specific upper PCR primer SEQ ID 2153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 60; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ORCH-) ORCHID BIOSCIENCES INC.
                                      AAH39357 standard; DNA; 24 BP
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                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acid sample.
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                           14-AUG-2001
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                                                                                  AAH39357;
RESULT 139
                      AAH393
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                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to murine tricarboxylic acid carrier 13.53 (see ABFS9163). The protein is useful for treating various diseases, such as malignant tumours, haemopathy, HIV infection, immunological diseases and various inflammations. The present sequence is a PCR primer, which was used in an example from the invention
                                                                             Murine, tricarboxylic acid carrier 13.53; tumour, cytostatic; haemopathy;
HIV infection; anti-HIV; immunological disease; inflammation; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR, selection, primers, OPTIPRIM, breeding, cattle, parentage; genetic mapping, traits; amplification; ss.
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0
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                                                                                                                                                                                                                                                                                                                                      New polypeptide murine tricarboxylic acid carrier 13.53 and polynucleotides encoding this polypeptide.
                                                        Murine tricarboxylic acid carrier 13.53 PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 24 BP; 10 A; 12 C; 2 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 17 (Disclosure); 33pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Microsatellite sequence from clone TGLA147.
                                                                                                                                                                                                                                                              (BODE-) BODE GENE DEV CO LTD SHANGHAI.
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nes 20; Conserv
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus
                                                                                                            primer; 88
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Matches
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Best Loca Matches

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WPI; 1996-277795/28.
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                                                                                                                                                                                                                                                                                                                                                                      RESULT 143
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                                                                                                                                                                                                                                                                                                                                                                                                The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 corening a library of bovine MboI DNA fragments of between 250 and 500 core that an a (TC)15 oligonicalectide probe. One out of 50 cores-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information of for ca. 230 such bovine microsatellites is summarised in the sequence information specification and indexed herein (see below). The sequence upstream and specification and indexed herein (see below). The sequences upstream and converted for in vitro amplification of the corresp.

The equired PCR primers for in vitro amplification of the corresp.

Microsatellite (using the program OFTTRRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait losi, or genes involved the determinism of economically important traits esp. in cattle, to allow selective correct PN breeding. See also AAQ33501-34437. (Updated on 25-WAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                     Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detection; polymorphism; perfect compound simple sequence repeat; adaptor directed primer; genome; genetic; fingerprinting, amplified fragment length polymorphism assay; microsatellite region; genetic trait marking; germplasm comparisons; compound; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                1.8%; Score 19; DB 1; Length 19;
100.0%; Pred. No. 75;
rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Compound simple sequence repeat primer (GT)7.5(AT)2.
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19 BP; 0 A; 0 C; 9 G; 10 T; 0 U; 0 Other;
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                                                                                                                                                                           Table 7; Page 221; 517pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1793 TGTGTGTGTGTGTGTGT 1811
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               92WO-US000340.
                                        91US-00642342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Morgante M, Vogel JM,
                                                                                        Georges M, Massey JM;
                                                                                                                 WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                 (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-NOV-1994;
                  15-JAN-1992;
                                         15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          409617082-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT30412;
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                                                                                                                                                                        Detecting polymorphisms between 2 nucleic acid samples, esp. in microsatellite regions, comprises digesting the nucleic acid to generate fragments, ligating adaptor segments to their ends, amplifying them using primer directed amplification and comparing the prods. to detect differences. The primers used in the amplification comprise a primer consisting of a perfect cpd. simple sequence repeat (SSR), and an adaptor segment. The present sequence complementary to an adaptor segment. The prepresents a modified amplified fragment length polymorphism assay, which is partic. useful for genome fingerprinting, i.e. for genetic trait marking and germplasm comparisons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial
Modified amplified fragment length polymorphism assay - for detection of polymorphism esp. in micro:satellite regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mole. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.8%; Score 19; DB 1; Length 19;
100.0%; Pred. No. 75;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat sequence found in the haemoglobin gamma G gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19 BP; 2 A; 0 C; 7 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 9; Col 59-60; 186pp; English.
                                                                                                                       Example 2; Page 84; 173pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1799 TGTGTGTGTGTGTATAT 1817
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91US-00754351.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 19; Conservative
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05-SEP-1991;
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18-JUN-1997
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mcgarry191-19.rng

animal or plant breeding or pedigree analysis. The sequences AAT66084-T66107 represent repeat sequences of low informativeness found in specific human genes. This repeat sequence is found in the haemoglobin gamma G gene located at chromosomal position 11p15.5. The sequence is amplified by primers AAT66094-5. (Updated on 25-MAR-2003 to correct PF 888888888

Sequence 19 BP; 10 A; 9 C; 0 G; 0 T; 0 U; 0 Other;

0; Gaps Query Match
1.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 19; Conservative 0; Mismatches 0; Indels

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1793 TGTGTGTGTGTGTGTGT 1811

19 TGTGTGTGTGTGTGTGT 1

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AAZ89471 standard; DNA; 19 BP. AAZ89471;

16-JUN-2000 (first entry)

SSA primer 3 for amplifying A. thaliana and Z. mays DNA.

Simple sequence repeat; SSR; single site amplification; SSA; disease; primer; ss

Arabidopsis thaliana. Zea mays.

JS6054300-A

25-APR-2000

97US-00915609 21-AUG-1997;

21-AUG-1997;

(USDA) US SEC OF AGRIC.

Mckendree WL;

WPI; 2000-328353/28.

Obtaining unknown DNA sequence flanking a single known sequence for use as PCR templates, involves single site amplification with polymerase having strand displacement capability.

Example 1; Col 9-10; 11pp; English.

This invention describes a novel method for obtaining DNA of unknown sequence flanking a single site of known sequence involves single site amplification of circular DNA template flanking a target DNA of known sequence using a polymerase having strand displacement capability. The method is used for obtaining a particular target DNA sequence that can be useful as templates that contain entire simple sequence repeat (SSR) alleles for amplification (SSA) procedures e.g. PCR or can be employed as molecular markers, e.g. in distinguishing between species, strains or varieties within species or identifying the presence of a disease condition. It also provides a marker for use in areas such as import and export regulation, variety and ecotype identification, marker sequences to see to generate a linear DNA molecule containing two target sequences used to generate a linear DNA molecule containing two target sequences. It can also be used for e.g. for cloning cDNA or genomic DNA which flanks any known short target sequence. The present method can also be used to obtain entire coding regions of genes based upon a known nucleic acid sequence or by using a degenerate nucleic acid sequence or by using a degenerate nucleic acid sequence back translation RESULT 144
AAZ89471/C

ö using a polymerase having strand displacement capability which can synthesize up to 10 kb fragments. This is especially useful for obtaining plant genes which are usually less than 10 kb in length. The method allows accelerated development of high resolution DNA markers that may be used for fingerprinting, mapping etc., using small amounts of tissue (less than 1 mmg). It also allows the production of a PCR template with knowledge of only one region of target equence, the size of which is regulated only by the primer design. The present method also eliminates genomic DNA library preparation and screening which are the most time consuming steps, typically requiring no less than three months, with total time for target DNA development being between 4-6 months. AAZ89469-Z89474 represent primers used to illustrate the method of the invention 0; Gaps Query Match
1.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 19; Conservative 0; Mismatches 0; Indels Sequence 19 BP; 9 A; 10 C; 0 G; 0 T; 0 U; 0 Other; 1794 GIGIGIGIGIGIGIGIG 1812 %\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$ ઠ

19 GIGIGIGIGIGIGIGI 1

RESULT 145 AAZ89472

₽. AAZ89472 standard; DNA; 19

AAZ89472;

16-JUN-2000 (first entry)

SSA primer 4 for amplifying A. thaliana and Z. mays DNA.

Simple sequence repeat; SSR; single site amplification; SSA; disease; primer; 88.

Arabidopsis thaliana Zea mays.

US6054300-A.

25-APR-2000

97US-00915609. 21-AUG-1997;

97US-00915609.

(USDA) US SEC OF AGRIC.

Mckendree WL;

WPI; 2000-328353/28.

Obtaining unknown DNA sequence flanking a single known sequence for use as PCR templates, involves single site amplification with polymerase having strand displacement capability.

Example 1; Col 9-10; 11pp; English.

This invention describes a novel method for obtaining DNA of unknown sequence flanking a single site of known sequence involves single site amplification of circular DNA template flanking a target DNA of known sequence using a polymerase having strand displacement capability. The method is used for obtaining a particular target DNA sequence that can useful as templates that contain entire simple sequence repeat (SSR) alleles for amplification (SSA) procedures e.g. PCR or can be employed as molecular markers, e.g. in distringuishing between species, strains or varieties within species or identifying the presence of a disease condition. It also provides a marker for use in areas such as import and export regulation, variety and ecotype identification, marker development, forensic DNA fingerprinting, etc. The method can also be used to generate a linear DNA molecule containing two target sequences

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from one sequence within a single stranded DNA template and flanking regions for these target sequences. It can also be used for e.g. for cloning CDNA or genomic DNA which flanks any known short target sequence.

The present method can also be used to obtain entire coding regions of genes based upon a known nucleic acid sequence or by using a degenerate nucleic acid sequence back translation using a polymerase having strand displacement capability which can synthesize up to 10 kb fragments. This is especially useful for obtaining plant genes which are usually less than 10 kb in length. The method callows accelerated development of high resolution DNA markers that may be used for fingerprinting, mapping etc., using small amounts of tissue (less than 1 mug). It also allows the production of a PCR template with knowledge of only one region of target DNA sequence, the size of which is regulated only by the primer design. The present method also eliminates genomic DNA library preparation and screening which are the most time consuming steps, typically requiring no less than three months, with total time for target DNA development being between 4-6 months. AAX89469-

Sequence 19 BP; 0 A; 0 C; 10 G; 9 T; 0 U; 0 Other;

Gaps . Score 19; DB 1; Length 19; Pred. No. 75; 0; Indels Ouery Match 1.8%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 75; Best Local Similarity 100.0%; Pred. No. 75; Mismatches 19; Conservative 0; Mismatches

1794 GTGTGTGTGTGTGTGTG 1812 1 Grerererererererere

ઠે 음 RESULT 146

AAC66739

AAC66739 Standard; DNA; 19

AAC66739;

(first entry) 15-FEB-2001

Heterologous insert sequence #2,

Probe; cytostatic; antiviral; gene therapy; ss.

Unidentified.

WO200063365-A1.

26-OCT-2000

21-APR-2000; 2000WO-US010909

99US-0130345P 21-APR-1999;

(PANG-) PANGENE CORP

Zarling Reddy G, Belotserkovskii B,

WPI; 2000-647516/62

Composition for modulating transcription or replication of a pre-selected target sequence and for treating a plant or animal disease, comprises a recombinase and two probes, each containing a homology clamp and an anchoring sequence.

Disclosure, Fig 9; 103pp; English.

The present invention relates to a composition comprising a recombinase and two complementary single stranded probes each containing at least one homology clamp corresponding or complementary to a preselected target nucleic acid sequence and at least one anchoring sequence. The present sequence is a heterologous insert sequence used to generate the probes that can be used in the present invention. The composition of the present invention can be used to modulate transcription or replication of a present elected target sequence, treat a disease state of a plant or animal

caused by expression of a disease gene, detect a double stranded nucleic acid target sequence, isolate either strand of a double stranded target sequence, isolate either strand of a member of a gene family, produce a transgenic non-human organism or plant, determine the function of a double stranded nucleic acid target sequence and inhibit double stranded nucleic acid rotation or branch migration. In addition, the composition may be used to produce animal models for genetic defects

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Sequence 19 BP; 0 A; 0 C; 9 G; 10 T; 0 U; 0 Other;

Gaps ö Query Match
1.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 19; Conservative 0; Mismatches 0; Indels

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ò g RESULT 147 AAC66738/c

BP. AAC66738 standard; DNA; 19

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(first entry) 15-FEB-2001 Heterologous insert sequence #1.

Probe; cytostatic; antiviral; gene therapy; ss.

Unidentified

WC200063365-A1

26-OCT-2000

21-APR-2000; 2000WO-US010909

99US-0130345P 21-APR-1999;

Zarling Belotserkovskii B, Reddy G,

(PANG-) PANGENE CORP

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WPI; 2000-647516/62.

Composition for modulating transcription or replication of a pre-selected target sequence and for treating a plant or animal disease, comprises a recombinase and two probes, each containing a homology clamp and an anchoring sequence.

Disclosure, Fig 9; 103pp; English.

The present invention relates to a composition comprising a recombinase and two complementary single stranded probes each containing at least one homology clamp corresponding or complementary to a preselected target nucleic acid sequence and at least one anchoring sequence. The present sequence is a heterologous insert sequence used to generate the probes that can be used to modulate transcription or replication of the present invention. The composition of the present selected target sequence, treat a disease state of a plant or animal caused by expression of a disease gene, detect a double stranded nucleic acid target sequence, isolate either strand of a double stranded target sequence, isolate either strand of a gene family, produce a transgenic non-human organism or plant, determine the function of a double stranded nucleic acid target sequence and inhibit double stranded obtains. nucleic acid rotation or branch migration. In addition, the composition may be used to produce animal models for genetic defects

Sequence 19 BP; 10 A; 9 C; 0 G; 0 T; 0 U; 0 Other;

DB 1; Length 19; 1.8%; Score 19;

Query Match

RESULT 148 ADD69517

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The present invention relates to measuring the copy number of a locus by amplifying and comparing test and reference loci. The invention is useful as diagnostic and prognostic tools and in correlating abnormal copy number values for specific loci with disease and effectiveness of different treatment options. The present sequence is a CA repeat fluorogenic probe used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
                                                                                                                                                                                                                                                                                                                                                                                                                      Measuring copy number of a polynuclectide locus in sample useful as diagnostic and prognostic tool, comprises quantifying amount of test locus and reference loci in test and control subject.
                                                                          /*tag= a
/mod_base= OTHER
_note= "5' end attached to 6-carboxy fluorescein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 81;
Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human chromosome 1p36-35 PCR primer SEQ ID NO:1418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21 BP; 0 A; 0 C; 10 G; 9 T; 0 U; 2 Other;
                                                                                                                                                                     end attached to TAMRA"
                                                                                                                                                                                                                                                                                                                                                            Gray JW;
                                                                                                                                                                                                                                                                                                                                                              Jensen RH,
                                        Location/Qualifiers
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/mod_base= OTHER
/note= "3' end at
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                                                                                                                                                                                                                                                                                                                                                                Godfrey TE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                              (REGC ) UNIV CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR primer; ss
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                                             Key
modified base
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                                                                                                                         modified base
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               Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel set of inter-simple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes. The primers of the invention may be useful for genotyping diverse genomes of plant and animal systems, in particular for distinguishing Basmati rice varieties from non-Basmati rice varieties and traditional Basmati rice varieties from evolved Basmati rice varieties. The current sequence is that of the ISSR-related PCR primer of the invention.
                                                                                                                                                                                                                                                                              inter-simple sequence repeat; ISSR; SSR; PCR; primer; genotyping; plant; animal; Basmati rice; ss.
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                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19; DB 1; Length 19;
Pred. No. 75;
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                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Scor.
100.0%; Pred. No. '.'
   100.0%; Pred. No. 75; tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CA repeat fluorogenic probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF85976 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                             ADD69517 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 19; Conservative
                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                          ISSR-related PCR primer 4.
                  19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-804317/75.
 Best Local Similarity
Matches 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               animal systems
                                                                                                                                                                                                                                                                                                                                      Unidentified.
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Isolation of satellite sequences from genomic DNA for use as DNA markers
                                                                                                                                                                                                                                                                                                     Satellite sequence; DNA fragmentation; microsatellite DNA; DNA marker;
Haliotis discus; ss.
                                                                                                                                                                                                                                                                                                                                                                               (NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES
                                                                                                                                                                                                                   1793 TGTGTGTGTGTGTGTGT 1811
                                                                                                                                                                                                                                                                                            H. discus derived sequence #21
                                                                                                                                                                                                                                                          AAZ98503 standard; DNA; 20
                                                                                                                                                                                                                                                                                19-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-224692/19.
                                                                                                                                                                                                                                                                                                                        Haliotis discus.
                                                                                                                                                                                                                                                                                                                                   WO200011156-A1.
                                                                                                                                                                                                                                                                                                                                                                                           Pakahashi H,
                                                                                                                                                                                                                                                                                                                                                                     L8-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                         01-JUL-1999;
                                                                                                                                                                                                                                                                                                                                              02-MAR-2000.
                                                                                                                                                                                                                                                                     AAZ98503;
                                                                                                                                                                                                                                              RESULT 151
AAZ98503/c
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99WO-JP003551 98JP-00232153

Sekino M;

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Query Match
Best Local Similarity 95.0 Matches 19, Conservative
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                                                                                                                                                                                                                                                                                 The present invention describes a method of arraying genome clones. The method comprises: (a) clones of the genomic libraries contained in method comprises: (b) a primare designed based on the chromosome marker contrivell plates; (b) a primar designed based on the chromosome marker sequence is added to the mixture to carry out an amplification reaction; (c) a signal corresponding to the marker is detected from the resultant amplified product to specify the discrimination Nos. of the multiwell plates containing the clones having said marker sequence; (d) the order of the markers is changed so that the same discrimination Nos. succeed to the maximum in the specified discrimination Nos. to array the multiwell plates; (e) the clones in the miltiwell plates of the specified discrimination Nos. to array the multiwell conficultures are mixed respectively in each wells of longitudinal and lateral directions; (f) the mixed clones are cultured and the resultant cultures are amplified products; (h) the clones in the multiwell plates are specified from the detected result; and (i) the clones are reconstituted as the positions on the chromosome and arrayed. The mixed suseful for gene analysis. ABM42957 to ABM45321 represent PCR primers for human chromosome 21q22.1, which are specifically claimed for use in the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.8%; Score 19; DB 1; Length 21;
100.0%; Pred. No. 81;
rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21 BP; 0 A; 2 C; 9 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                           Claim 4; Page 32; 528pp; Japanese.
                                     (RIKA ) RIKAGAKU KENKYUSHO.
(GENO-) GENOTEX YG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                      Arraying genome clones.
                                                                                                                       WPI; 2002-144136/19.
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Gaps . 0

Indels

1.8%; Score 18.4; DB 1; Length 20; 95.0%; Pred, No. 92;

0; Mismatches

1793 TGTGTGTGTGTGTGTGTG 1812

Sequence 20 BP; 11 A; 9 C; 0 G; 0 T; 0 U; 0 Other;

of the invention

The invention provides a novel method for isolation of satellite sequences from genomic DNA that comprises fragmentation of the DNA by a method which is not dependent on base sequences. Then selection of the satellite sequences from the obtained genomic library of high homogeneity. The method is useful for the isolation of microsatellite DNA sequences which can be used as DNA markers. The new method markedly improves the efficiency of isolation of satellite sequences in comparison to prior art methods which are reliant on base sequences. Sequences AA29483-514 represent sequences from Haliotis discus, used in the method

comprises isolating a library with high homogeneity by DNA fragmentation

Example 5; Page 14; 35pp; Japanese.

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Human; ds; cytochrome P450 Al; CYP4501Al; UGT2B4; MDR1;

Cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002El; LTF;

Cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002El; LTF;

Adrenatic receptor betal; ADBR1; aryl hydrocarbon; ARNY; Cathepsin S; CTSS;

Aryl hydrocarbon receptor nuclear translocator; ARNY; cathepsin S; CTSS;

Cyclocoxgenase 2; EPRX2; S-lipoxygenase activating protein; FLAP;

Cyclocoxgenase 2; COX2; diagramine-N-methyl transferase;

Cyclocoxgenase 2; NGO2; sulfotransferase thermolabile; STM;

Cyclocoxgenase 2; NGO2; sulfotransferase 2B1;

Cyclocoxgenase 2B2d; UDP SILOCATORS 2; CYMX1;

Cyclocoxgenase 2B2d;

Cyclo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathapsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for
                                                                                                                                                                               Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single nucleotide polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88-NOV-2000; 2000US-00724389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8-NOV-2001; 2001WO-US044838
ABS97833 standard; DNA; 20
                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAB INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PI; 2002-698522/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guida M, Hall J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNAS-) DNA SCI
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                                                                                                                                  23-DEC-2002
                                                                 ABS97833;
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This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known human cytochrome P450 A1 (CY4501A1), adrenargic receptor beta1 (ADBA1), cytochrome P450 A2 (CY4501A1), adrenargic receptor beta1 (ADBA1), cytochrome P450 02E1 (CY45002E1), adrenargic receptor beta1 (ADBA1), cortochrome P450 02E1 (CY45002E1), adrenargic receptor beta1 (ADBA1), cortochrome P450 02E1 (CY45002E1), adrenargic receptor beta1 (ADBA1), cathepsin 8 (CYS2), CYCOXGRAES 2 (CYSY2), diazepam binding cortochrome (TAMY), cathepsin 8 (CYS2), CYCOXGRAES 2 (CYSY2), diazepam binding cortochrome (TAMY), cathepsin 8 (CYS2), cycloxygense 2 (CYSY2), bistamine-N-methyl protein 8 (CYS2), diazepam binding cortochrome (TAMY), which will be a cycloxyderial and cycloxyderial cycloxy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polymorphic DNA sequence of the invention
                                                 Example 16, Page 131; 714pp, English.
disorder-related traits,
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Gaps
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                                1.8%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 92; ive 0; Mismatches 1; Indels
Sequence 20 BP; 10 A; 9 C; 0 G; 1 T; 0 U; 0 Other;
                                               Local Similarity 95.0
                                    Query Match
                                                                  Matches
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Mouse connective tissue growth factor antisense oligo DNA (SegID 153) 1794 GIGIGIGIGIGIGIGIGI 1813 20 Grafererererererer 1 ADB25760 standard; DNA; 20 BP 20-NOV-2003 (first entry) ADB25760 ò 임

fish-12; NOV2; include the factor binding protein-related protein; insulin-like growth factor binding protein-related protein 2; IGFBP-rP2; IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy; hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis; scleroderma; atherosclerosis; cytostatic; dermatological; antiarteriosclerotic. antisense; mouse; murine; ss; connective tissue growth factor; CTGF; chromosome_6q23.1; ctgrofact; fibroblast inducible secreted protein;

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This invention relates to novel methods for modulating the expression of connective tissue growth factor (CTGF) by antisense oligonucleotides.

CTGF has been mapped to human chromosome region 6423.1, and is also known as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2, insulin-like growth factor binding protein-related protein 2, IGFBP-rP2, IGFBP-RP8, HGSZ4 and ecogenin. It is known to stimulate DNA synthesis and promore chemotaxis of fibroblasts, however, it is also upregulated in cute lymphoblastic leukaemia and in tumour or endothelial cells associated with the vasculature. Accordingly, antisense oligonuclectides that inhibit the expression of CTGF in cells or tissues can be used in gene therapy to treat various conditions including hyperproliferative disocuters (particularly cancer, e.g. breast, prostate or renal cancer), culmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As such, the present invention describes these antisense oligos as having cytostatic, dermatological and antiarteriosclerotic activities. This coligonucleotide sequence is a chimeric phosphorothicate antisense oligo with 2 MOE wings and a deoxy gap, which is used to inhibit expression of mouse CTGF of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                           /mod_base= OTHER //notes "OTHER= phosphorothioate backbone, where 1-5 and 16-20 are 2' methoxyethyl nucleotides. All cytidines are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense oligonucleotides for modulating connective tissue growth factor expression, particularly useful for treating cancers (e.g. breast or prostate cancer), pulmonary or renal fibrosis, scleroderma or atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.8%; Score 18.4; DB 1; Length 20; Best Local Similarity 95.0%; Pred. No. 92; Matches 19; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 7 A; 3 C; 0 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence of a microsatellite from clone TGLA69.
                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2247 TAGTIGAAATAAAGTGTAT 2266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 89; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 TAGTTGAAATAAAGTATAT 1
                                                                                                                                                                                                                                            09-DEC-2002; 2002WO-US038618.
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(first entry)
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                                                                                                                                                                                                                                                                                                                      (ISIS-) ISIS PHARM INC.
                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                           Watt AT;
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                                                                                                                                                                  WO2003053340-AZ.
                  Key
modified_base
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02-FEB-1993
                                                                                                                                                                                                         03-JUL-2003
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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine Mbol DNA fragments of between 250 and 500
consisted than (AC)15 and a (TC)15 oligomucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
clones cross-hybridised. Assuming independent distribution of
microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100,000. The sequence information
for 2, 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
specification and indexed herein (see below). The sequences upstream and
commercem of the microsatellite sequence were used to generate the
microsatellite (using the program OPTIPRIM). The microsatellites may be
microsatellite (using the program OPTIPRIM). The microsatellites may be
microsatellity individuals, for parentage resting, and in the genetic
mapping of economic trait loci, or genes involved the determinism of
connect planes. The sequence of the construction o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                          Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPTIPRIM; breeding; cattle; parentage; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 18; 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Microsatellite sequence from clone TGLA346.
                                                                                                                                                                                                                                              Table 7; Page 219; 517pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ33950 standard; DNA; 18 BP.
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(first entry)
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Best Local Similarity 100.0
Matches 18; Conservative
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genetic mapping; traits;
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                                                                   Georges M, Massey JM;
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                                                                                                                 WPI; 1992-284684/34.
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                  (GENM-) GENMARK.
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 correcting a library of bovine MboI DNA fragments of between 250 and 500 corrections at a (AC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information of for ca. 230 such bovine microsatellites is summarised in the sequence information consistent of the microsatellite sequence were used to generate the cequired pCR primers for in vitro amplification of the corresp. microsatellite (using the program OFTPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of preeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                              Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rable 7; Page 381; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1793 TGTGTGTGTGTGTGT 1810
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(first entry)
                                                                                                                                                                                                                                                                                                                                        Georges M, Massey JM;
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                                                                                                                                                                                                                                                                                       (GENM-) GENMARK.
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02-FEB-1993
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                                                                                                                                    06-AUG-1992
                                   Bos taurus.
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AAQ33722
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Gaps

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Table 7; Page 310; 517pp; English.

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The sequence is that of a bovine microsatellite sequence obtd, by screening a library of bovine Mbol DNA fragments of between 250 and 500 by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100,000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequence upstream and specification and indexed herein (see below). The microsatellites may be required PCR primers for in vitro amplification of the corresp.

The microsatellite (using the program OPTPRRM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of connecting important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437? (Updated on 25-MAR-2003 to correct PN field.)
% <del>X G G G G G G G G G G G G G X M</del>
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Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;

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0
1.7%; Score 18; DB 1; Length 18; 100.0%; Pred. No. 94;
                              0; Indels
           Local Similarity 100.0%; Pred. No. 94; nes 18; Conservative 0; Mismatches
                                                             1793 TGTGTGTGTGTGTGTG 1810
Query Match
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Microsatellite sequence from clone TGLA4. 1 rererererererere 18 AAQ33997 standard; DNA; 18 BP (first entry) (revised) 25-MAR-2003 02-FEB-1993 AAQ33997; d

PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.

Bos taurus.

36-AUG-1992.

92WO-US000340, 15-JAN-1992;

91US-00642342. 15-JAN-1991;

(GENM-) GENMARK.

Massey JM; Georges M,

WPI; 1992-284684/34.

Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.

Table 7; Page 329; 517pp; English.

The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and

A (CA)9 simple sequence repeat is used to illustrate the novel method for detecting SSR polymorphisms without the need for direct sequencing or gelectrophoresis. The length of a particular repeat region (i.e. number of repeat sequences can be highly polymorphic; the sequences flanking the repeat region, however, are conserved. Detection of a SSR of a specific length is achieved by successful ligation of two oligonucleotides, one being exactly complementary to the repeat region and one of its conserved flanking sequences (i.e. comprising the sequence (GT)9) and the other being complementary to the other conserved flanking sequence. (Updated on

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downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                    Microsatellite; simple sequence repeat; SSR; polymorphism; variation; genetic marker; human genome; mapping; ligation reaction; ss.
                                                                                                                                                                 Gaps
                                                                                                                                                               0
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                                                                                                                                     Query Match 1.7%; Score 18; DB 1; Length 18; Best Local Similarity 100.0%; Pred. No. 94; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;
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                                                                                                                                                                                        1794 GTGTGTGTGTGTGT 1811
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                                                                                                                                                                                                                                                                                                                                                                              Simple sequence repeat (GT)9.
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/note= "SSR"
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23-DEC-1993
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AAQ46589
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Gaps

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Indels

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0; Mismatches

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18;

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Matches
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10-WAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                  Microsatellite; simple sequence repeat; SSR; polymorphism; variation; genetic marker; human genome; mapping; ligation reaction; ss.
                                                                        Gaps
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                                                  Query Match
1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18 BP; 9 A; 9 C; 0 G; 0 T; 0 U; 0 Other;
                                Seguence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                 /rpt_type= TANDEM
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                                                                                            1794 GTGTGTGTGTGTGTT 1811
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                                                                                                                                                                  AAQ46588 standard; DNA; 18 BP.
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AAQ46588/c
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Query Match .1.7%; Score 18; DB 1; Length 18; Best Local Similarity 100.0%; Pred. No. 94;

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This antisense oligonucleotide is nuclease resistant and can be used in the treatment of animals, including humans, having a bacterial infection. The treatment comprises administration of such nuclease resistant oligonucleotides targeted to a nucleic acid or protein of the bacterium, oligonucleotides targeted to a nucleic acid or protein of the bacterium, and formulated with a carrier. A compound comprising this nuclease content of an articlease and formulated with a carrier. A compound comprising this nuclease and formulated with a carrier. A compound comprising this nuclease of an ethod is used to treat infections by a wide variety of Gram-positive and gram-negative, or acid-fast, bacteria, in human and veterinary medicine. The methods are particularly used in human-and veterinary medicine. Or patients with acquired immunodeficiency syndrome or those receiving chemotherapy or radiation therapy), optionally in combination with, or chemotherapy or radiation therapy), optionally in combination with, or therapeutic use, the oligonucleotides can be used to control bacteria in the construction of the paper of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nuclease resistant; bacterial infection; antibiotic; target; veterinary medicine; treatment; human; industrial process; bacterial control; ss.
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1793 TGTGTGTGTGTGTGTG 1810
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Matches
                                                                                                                                                                                                                                  RESULT 160
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AAX77461;

BP.

This invention describes a novel method for quantitating genetic instability independent of microsatellite alterations by treating a comparison genomic DNA from tumour cells and genomic DNA from the same individual with oligonucleotide primers selected from defanine and x = 3-7 (ii) a nucleotide sequence (CG)xRY, where R is as in (i) and Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii) a nucleotide sequence (CG)xRY, where R is as in (i) and X = 3-7, (iii) a nucleotide sequence (CG)xRY, where R is as in (i) and x = 3-7, (iv) a nucleotide sequence (CG)xRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence (CA)xRY, where R is a purine selected from cytosine, thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where R is a pyrimidine selected from cytosine, thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, (viii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, (viii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, (viii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, (viii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, (viii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, (viii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, (viii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, (viii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, where X is a pyrimidine Primer, quantitation; genetic instability; tumour cell; detection; neoplastic transformation; carcinogenesis; ss. Sequence 18 BP; 9 A; 8 C; 0 G; 1 T; 0 U; 0 Other; Claim 4; Col 17-18; 27pp; English Quantitating genetic instability. Anderson G, Stoler D, Basik M; 18 GIGIGIGIGIGIGIGI 1 96US-00734973. 96US-00734973 AAX77460 standard; DNA; 18 05-AUG-1999 (first entry) (HEAL-) HEALTH RES INC. WPI; 1999-357197/30. USS912147 primer 4. 22-OCT-1996; 22-OCT-1996; JS5912147-A 15-JUN-1999 Synthetic. AAX77460; RESULT 161 AAX77460/ 유

Gaps ö Query Match
1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 0; Indels

1791 ATTGTGTGTGTGTGT 1808

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18 g

RESULT 162 AAX77461/c LD AAX77461 standard; DNA; 18 BP. XX

This invention describes a novel method for quantitating genetic instability independent of microsatellite alterations by treating a comparison pair comparising genomic DNA from tunour cells and cells. The method involves the cells from the same individual cells. The method involves the cells from the same individual comparison plants are selected from cytosine and x = 3-7 (ii) a nucleotide sequence (CG)xRY, where R is as in (i) and X is a nucleotide sequence (CG)xRY, where R is as in (i) and X = 3-7 (iv) a nucleotide sequence (CG)xRY, where R is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7 (iv) a nucleotide sequence (CA)xRY, where R is a purine selected from define and guanine and Y is a pyrimidine selected from adenine and guanine and Y is a pyrimidine selected from adenine and guanine and X = 6-16, (vii) a nucleotide sequence (CA)xRY, where R is a purine selected from adenine and guanine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where R is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where R is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where X is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where X is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where X is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where X is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, und its a pyrimidine selected from cytosine, thymine, and uracil and uracil and x = 6-16, und its a pyrimidine selected from cytosine, thymine, and uracil and uracil and x = 6-16, und its a pyrimidine selected from cytosine, thymine, and ura Primer; quantitation; genetic instability; tumour cell; detection; neoplastic transformation; carcinogenesis; DNA/RNA hybrid; ss. Sequence 18 BP; 9 A; 8 C; 0 G; 0 T; 1 U; 0 Other; Location/Qualifiers Claim 4; Col 17-18; 27pp; English Quantitating genetic instability. Anderson G, Stoler D, Basik M; /*tag= a /note= "uracil" 96US-00734973. 96US-00734973. 05-AUG-1999 (first entry) (HEAL-) HEALTH RES INC. WPI; 1999-357197/30. 22-OCT-1996; 22-OCT-1996; 15-JUN-1999. US5912147-A Synthetic misc RNA

Gaps . 0 Query Match
Best Local Similarity 100.0%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 0; Indels 1791 ATTGTGTGTGTGTGTG 1808

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18 ATTGTGTGTGTGTGTGTG

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AAX76437 standard; DNA; 18 BP. AAX76437; RESULT 163
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ID AAX7643
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AC AAX7643

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cereal profiling, grass profiling, seed batch purity testing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a sequencing reagent (I) comprising: (a) a capture group (CG) that can form a stable complex with a region of a template nucleic acid (II); (b) spacer region (SR); and (c) sequence complementary sequence on (II). Also described are: (I) array comprising a complementary sequence on (II). Also described are: (I) array comprising an arrangement of many (I), immobilized on a solid support; and (2) method of sequencing (II) using a combinatorial array of (I). Arrays of (I) are used for sequencing nucleic acids by a primer extension method, e.g. to scan for mutations (particularly shingle-nucleotide polymorphisms) and for diagnosis of infectious and genetic diseases. Arrays of (I) allow sequencing of templates without any prior knowledge of the wild-type or expected sequence. By separating the capture and of thousands of hybridisation functions, it becomes possible to use smaller primers, simplifying array analysis, reducing costs and allowing thousands of hybridisation reactions to be done simultaneously. Particularly, 4 times fewer primers are required, compared with standard methods, i.e. since primer extension increases the effective as an array of n-mers in usual methods. The method may be applied to single- or double-stranded DNA, AAX76410 to AAX76440 represent sequencing reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                  Sequencing reagent array; primer; capture moiety; hybridisation; detection; mutation; diagnosis; infectious disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                used to detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oligonucleotide primers used in an example from the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.7%; Score 18; DB 1; Length 18; 00.0%; Pred. No. 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reagent for nucleic acid sequencing by primer extension, mutations and to diagnose infectious or genetic diseases.
                                                Sequencing reagent array oligonucleotide primer #28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                         Boyce-Jacino M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Prec. 100.0%; Prec. 100.0%; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 7; Page 27; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1793 TGTGTGTGTGTGTGTG 1810
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                                                                                                                                                                                                                                                                                                                                   (ORCH-) ORCHID BIOCOMPUTER INC.
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                                                                                                                                                                                                                                                                                                                                                                         Karn J,
                                                                                                                                                                                                                                                          98WO-US024966,
                                                                                                                                                                                                                                                                                            97US-00976427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                         Goelet P,
                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-357855/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                          20-NOV-1998;
                                                                                                                                                                               W09927137-A1
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                                                                                                                                                                                                                      03-JUN-1999
                                                                                                      detection;
                                                                                                                                             Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Matches
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The invention relates to a substantially purified or isolated nucleic acid (I) from ryegrass or fescue species including a simple sequence repeat (SSR), having 2 or more tandemly repeated nucleotide core elements or incleotides in length. Also included are a nucleic acid primer outtable for amplifying an SSR, identifying (M1) an SSR by preparing a library of ryegrass or fescue genomic DMA enriched for SSRs and inclentifying clones in the library containing SSRs, a library of ryegrass or fescue genomic DMA enriched for SSRs prepared by the M1, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely associated with the gene such that the SSR and the gene are preferentially co-inherited, and selecting for the SSR in the breeding, a preferentially co-inherited, and selecting for the SSR in the breeding, a method for DNA profiling grass or cereal species varieties by assessing variation between SSR varieties and testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of sequence its a ryegrass or fescue SSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species
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                                                                                                                                                                                                                                                                                                                             STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R. UNIV SOUTHERN CROSS.
STATE VICTORIA DEPT NATURAL RES & ENVIRO. UNIV ADELALDE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             INT MAIZE & WHEAT IMPROVEMENT CENT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Fig 6; 72pp; English.
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                                                                                                                                                                          03-JAN-2001; 2001NZ-00509193
                                                                                                                                                                                                                                      24-DEC-1999; 99AU-00004906
04-MAY-2000; 2000AU-00007310
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AAS13732/c
ID AAS13732 standard; DNA; 18
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Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Forster JW, Jones ES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-512563/56.
Lolium multiflorum
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                                                                                                                      25-MAY-2001
                                                         NZ509193-A.
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                                                                                                                                                                                                                                                                                                                                                                                          (VICT-)
(UYAD-)
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Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat;

Simple sequence repeat, SSR, #37.

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NZ509193-A.

Poeae.

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The invention relates to a substantially purified or isolated nucleic acid (I) from ryegrass or fescue species including a simple sequence crepeat (SSR), having 2 or more tandemly repeated nucleotide core elements 2-6 nucleotides in length. Also included are a nucleic acid primer cultable for amplifying an SSR, identifying (M1) an SSR by preparing a library of ryegrass or fescue genomic DNA enriched for SSRs and identifying clones in the library containing SSRs, a library of ryegrass or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely associated with the gene such that the SSR and the gene are contained, and selecting for the SSR in the breeding, a preferentially co-linerited, and selecting for the SSR in the breeding, a correct box profiling grass or cereal species varieties by assessing variation within seed batch of an SSR. The SSRs may be used in the selection of genes in grass or cereal breeding, for profiling grass or cereal seed batches, and for DNA profiling to establish the creal seed batches, and for DNA profiling to establish the selection of secue SSR secue according to establish the sequence is a ryegrass or fescue SSR
                                                                                                                                                                                                                                                                                                                                                                                                                   New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Simple sequence repeat, plant, ds, SSR, ryegrass, fescue, tandem repeat, cereal profiling, grass profiling, seed batch purity testing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.7%; Score 18; DB 1; Length 18;
llarity 100.0%; Pred. No. 94;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18 BP; 9 A; 9 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                        STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
UNIV SOUTHBRN CROSS.
STATE VICTORIA DEPT NATURAL RES & ENVIRO.
UNIV ADELAIDE.
                                                                                                                                                                                                                                                                                                    INT MAIZE & WHEAT IMPROVEMENT CENT.
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                                                                                                                              3-JAN-2001; 2001NZ-00509193.
                                                                                                                                                                   24-DEC-1999; 99AU-00004906.
04-MAY-2000; 2000AU-00007310.
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                                                                                                                                                                                                                                                                                                                                               Forster JW, Jones ES;
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-512563/56
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les 18; Conserv
                                                                                              25-MAY-2001
                                                       NZ509193-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  varieties.
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                                                                                                                                                                                                                               (SAUS-)
(UYSC-)
                                                                                                                                                                                                                                                                                                          (ITMA-)
                                                                                                                                                                                                                                                                 (VICT-)
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Matches
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The invention relates to a substantially purified or isolated nucleic acid (I) from ryegrass or fescue species including a simple sequence repeat (SSR), having 2 or more tandemly repeated nucleotide core elements core repeat (SSR) in a nucleic acid primer and length. Also included are a nucleic acid primer centrable for amplifying an SSR, identifying (M1) an SSR by preparing a library of ryegrass or fescue genomic DNA enriched for SSRs and dentifying clones in the library containing SSRs, a library of ryegrass or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely associated with the gene such that the SSR and the gene are preferentially co-inherited, and selecting for the SSR in the breeding, a method for DNA profiling grass or cereal species varieties by assessing variation within seed batch of an SSR. The SSRs core as beection of genes in grass or cereal breeding, for may be used in the selection of genes in grass or cereal breeding, for profiling grass or cereal species varieties, for testing the purity of grass or cereal seed batches, and for DNA profiling to establish the confidentity, uniformity and/or stability of a cultivar. The present sequence is a ryegrass or fescue SSR
                                                                                                                                                                                                                                                                                                                                                                                  New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species varieties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat; cereal profiling; grass profiling; seed batch purity testing.
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100.0%; Pred. No. 94;
vative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18 BP; 9 A; 9 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                               STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R. UNIV SOUTHERN CROSS.
STATE VICTORIA DEPT NATURAL RES & ENVIRO. UNIV ADELAIDE.
                                                                                                                                                                                                                                                                         INT MAIZE & WHEAT IMPROVEMENT CENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Page 51; 72pp; English.
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                                                                                                         03-JAN-2001; 2001NZ-00509193.
                                                                                                                                             24-DEC-1999; 99AU-00004906.
04-MAY-2000; 2000AU-00007310.
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                                                                                                                                                                                                                                                                                                                   Jones ES;
                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-512563/56.
                                                                                                                                                                                                                                                                                                                   Forster JW,
                                                                         25-MAY-2001.
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                                                                                                                                                                                                                         (UYSC-)
(VICT-)
(UYAD-)
                                                                                                                                                                                                                                                                                 (ITMA-)
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The invention relates to a substantially purified or isolated nucleic acid (I) from ryegrass or fescue species including a simple sequence repeat (SSR), having 2 or more tandemly repeated mucleotide core elements or enclocide or amplifying an SSR, identifying are a nucleic acid primer suitable for amplifying an SSR, identifying (M1) an SSR by preparing a library of ryegrass or fescue genomic DNA enriched for SSRs and clentifying clones in the library containing SSRs, a library of ryegrass or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for fescue genomic DNA enriched for SSRs prepared by the M1, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely a secentially co-inherited, and selecting for the SSR in the breeding, a method for DNA profiling grass or cereal species varieties by assessing variation between SSRs varieties and testing the purity of grass or cereal species varieties, for tering the purity of grass or cereal species varieties, for tering the purity of grass or cereal species varieties, for tering the purity of grass or cereal species varieties, for tering the purity of grass or cereal species varieties, for tering the purity of grass or cereal species varieties, for tering the purity of grass or cereal species varieties, for tering the purity of grass or cereal section of genes in grass or cereal section of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species
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1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                          STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R. UNIV SOUTHERN CROSS. STATE VICTORIA DEPT NATURAL RES & ENVIRO.
                                                                                                                                                                                                                                                                                                                                              (UYAD-) UNIV ADELAIDE.
ITMA-) INT MAIZE & WHEAT IMPROVEMENT CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1794 GTGTGTGTGTGTGTGT 1811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Page 51; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH46012 standard; DNA; 18 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic oligonucleotide 12.
                                                                                                                                 03-JAN-2001; 2001NZ-00509193.
                                                                                                                                                                                  24-DEC-1999; 99AU-0004906.
04-MAY-2000; 2000AU-00007310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Grererererererer
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Forster JW, Jones ES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-512563/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lymphoma; ss
                                                                             25-MAY-2001
                         NZ509193-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       varieties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH46012;
                                                                                                                                                                                                                                                                (SAUS-)
(UYSC-)
(VICT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
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The present sequence is that of a synthetic oligonuclectide useful to the invention. The invention relates to a composition, comprising a 2 to 20 has a 3-04, 3-04 synthetic oligonucleotide which comprises multiple base 3-04, 3-04 synthetic oligonucleotide which comprises multiple formula and having cytostatic activity. The oligonucleotide compositions are useful for inducing cell cycle arrest, inhibition of proliferation, are useful for inducing cell cycle arrest, inhibition of proliferation, activation of caspases and induction of apoptosis or production of cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour necrosis factor (INF)-alpha by immune system cells, in an animal having cancer such as primary carcinoma, secondary carcinoma, primary sarcoma and secondary sarcoma such as, leukemia, lymphoma, breast, prostate, colorectal, cvarian or bone cancer. The compositions induce apoptosis independent of Pas, p53/p21, p21/waf-1/CIP p15(ink4B), p16(ink4), drug resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor Gaps 0 1.7%; Score 18; DB 1; Length 18; 100.0%; Pred. No. 94; rative 0; Mismatches 0; Indels Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other; 1794 GIGIGIGIGIGIGIGI 1811 Query Match
Best Local Similarity 100...
Local Similarity
Local Similarity
Local Similarity හි

18 Grererererererer g

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AAH46011 standard; DNA; 18 12-SEP-2001 (first entry) AAH46011; RESULT 169

Synthetic oligonucleotide 11.

ВP

Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis; cell cycle arrest; cell proliferation; caspase; cytokine; interleukin; tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia; Іутрьота; вв

WO200144465-A2. 21-JUN-2001 Synthetic

WO200144465-A2. Synthetic.

12-DEC-2000; 2000WO-CA001467. 21-JUN-2001

13-DEC-1999; 99US-0170325P. 29-AUG-2000; 2000US-0228925P.

(BION-) BIONICHE LIFE SCI INC.

Phillips NC, Filion MC;

WPI; 2001-398150/42.

Composition comprising synthetic oligonucleotides which comprise .multiple repeats of dinucleotides such as GT, TG useful for treating cancer by inducing cell cycle arrest, inhibiting proliferation, activating саѕравев.

Claim 5; Page 17; 77pp; English.

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0; Gaps

18

12-DEC-2000; 2000WO-CA001467.

Page

Page 82

of for

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Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping;
trait mapping; marker-assisted selection; gene selection; legume;
DNA profiling; breeding; ds.
                                                                                                                                                                                                                                                                                                                                                             (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
                                                                                                                                                                                                                                                                                                                                   03-JAN-2001; 2001NZ-00509194
                                                                                                                                                                                                                                                                                                                                             24-DEC-1999; 99AU-00004907
28-MAR-2000; 2000AU-00006520
                                                                                                                                                                                                                                                                      SSR motif #14.
                                                                                                                                                                                                                                                                                                                                                                       Koelliker R,
                                                                                                                                                                                                                                                                                                     Jnidentified.
                                                                                                                                                                                                                                                                                                                         25-MAY-2001
                                                                                                                                                                                                                                                                                                                NZ509194-A.
                                                                                                                                                                                                                                                   AAI64454;
                                                                                                                                                                                 Query Match
                                                                caspases
                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                               RESULT 170
                                                                                                                                                                                                                                  AA164454/
                                                                                                                                                                                                                                         임
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The present invention relates to Simple Sequence Repeats (SSRs) from clover species. SSRs, also called microsatellites, are based on a 1-7 nucleotide core element which is tendenly repeated. The SSR array is embedded in complex flanking DNA. SSRs are ideal markers for genome mapping, trait mapping and marker-assisted selection. The SSRs may be used in methods for selecting genes in clover/ legume breeding. The SSRs may be are also useful for DNA profiling of clover varieties and for testing the purity of legume seed batches. The present sequence is a SSR motif, which was used in the present invention Primer for detecting polymorphisms among highly related plant species Novel simple sequence repeats in clover species useful for selection genes in legume breeding, for profiling legume species varieties and testing the purity of legume seed batches. Detection; polymorphism; genetic fingerprinting; primer; ss. Match 1.7%; Score 18; DB 1; Length 18; Local Similarity 100.0%; Pred. No. 94; Conservative 0; Mismatches 0; Indels Sequence 18 BP; 9 A; 9 C; 0 G; 0 T; 0 U; 0 Other; 1793 TGTGTGTGTGTGTG 1810 Claim 6; Page 35; 52pp; English. 18 TGTGTGTGTGTGTGTG 1 AAQ49455 standard; DNA; 20 (first entry) WPI; 2001-431058/46. 24-SEP-1991; 24-SEP-1991; JP05244995-A 06-MAY-1994 24-SEP-1993 Synthetic. AAQ49455; Query Match Best Loca Matches RESULT 171 AAQ49455 B ð The present sequence is that of a synthetic oligonucleotide useful to the invention. The invention relates to a composition, comprises multiple base 3'-04, 5'-0H synthetic oligonucleotide which comprises multiple repeats of dinucleotides such as GT, TG, etc., according to specific formula and having cytostatic activity. The oligonucleotide compositions are useful for inducing cell cycle arrest, inhibition of proliferation, cutivation of caspases and induction of apoptosis or production of activation of caspases and induction of apoptosis or production of cytokines such as interleukin (II)-1-beta, IL-6, IL-10, IL-12 and tumour necrosis factor (INP)-alpha by immune system cells, in an animal having cancer such as primary carcinoma, secondary carcinoma, precondary sarcoma such as, leukemia, lymphoma, breast, prostate, colorectal, ovarian or bone cancer. The compositions induce apoptosis induce apoptosis is transforming growth factor (TGP)-beta I receptor and hormone dependence ö Composition comprising synthetic oligonucleotides which comprise multiple repeats of dinucleotides such as GT, TG useful for treating cancer by inducing cell cycle arrest, inhibiting proliferation, activating Gaps ; 0 1.7%; Score 18; DB 1; Length 18; 100.0%; Pred. No. 94; ive 0; Mismatches 0; Indels Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other; 1793 TGTGTGTGTGTGTGTG 1810 Claim 5; Page 17; 77pp; English 1 TGTGTGTGTGTGTGTG 18 AAI64454 standard; DNA; 18 BP. (BION-) BIONICHE LIFE SCI INC. 13-DEC-1999; 99US-0170325P. 29-AUG-2000; 2000US-0228925P. 23-NOV-2001 (first entry) Local Similarity 100. nes 18; Conservative Filion MC; WPI; 2001-398150/42. Phillips NC,

BP

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Gaps

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                                                                                                                                                                                                                                                                                                                                         The PCR primers (See also AAQ49449-54, AAQ49456) are used to detect polymorphisms among highly interrelated rice plants or among plants of family Brassicae. They can also be used for genetic fingerprinting of plants, allowing detection of polymorphism within one or the same species
                                                                                                                                                                                                                                                                            Primer - for detecting polymorphism in DNA among highly interrelated rice plants or plants of family Brassicae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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0
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Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 0 A; 2 C; 9 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                       Disclosure; Page 5; 6pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1793 TGTGTGTGTGTGTGTG 1810
                                                                                                                                                                                                                                   (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                       91JP-00243122
                                                                                                                                                                                                              91JP-00243122
                                                                                                                                                                                                                                                            WPI; 1993-338949/43
                                                                                                                                                                                                                                                                                                                                                                                             of plant
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Forster JW;

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New set of inter-simple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes, useful for genotyping diverse genomes of plant and animal systems. inter-simple sequence repeat; ISSR; SSR; PCR; primer; genotyping; plant; animal; Basmati rice; ss. (DNAF-) CENT DNA FINGERPRINTING & DIAGNOSTICS (ISSR)-PCR primer - SEQ ID 26 Claim 1; SEQ ID NO 26; 60pp; English Grererererererar 18 85 09-JAN-2003; 2003WO-IB000041. 38-APR-2002; 2002IN-CH000260 AAQ75727 standard; DNA; 21 ADD69468 standard; DNA; 20 Query Match Best Local Similarity 100. Matches 18; Conservative (first entry) WPI; 2003-804317/75. 402003085133-A2 Nagaraju JG; 15-JAN-2004 3' anchored 16-OCT-2003 Synthetic. ADD69468; à 쉽

ö The invention relates to a novel set of inter-simple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes. The primers of the invention may be useful for genotyping diverse genomes of plant and animal systems, in particular for distinguishing Basmati rice varieties from non-Basmati rice varieties and traditional Basmati rice varieties from evolved Basmati rice varieties. Gaps .. 0 1.7%; Score 18; DB 1; Length 20; 100.0%; Pred. No. 1e+02; tive 0; Mismatches 0; Indels Sequence 20 BP; 1 A; 2 C; 8 G; 9 T; 0 U; 0 Other; 3' anchored (ISSR)-PCR primer of the invention.

1798 GTGTGTGTGTGTAT 1815

BP

(first entry) 04-AUG-1995

AAQ75727;

Reverse transcription primer used in cDNA analysis technique.

Analysis, gene expression, reverse transcription, primer; cDNA, aggregate, restriction enzyme; ss.

28-NOV-2001; 2001WO-US044838

Homo sapiens

Synthetic

Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;

cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR112;

adventage acceptor nuclear translocator; ARNT; cathepsin S; CTSS;

cyclooxgenase 2; COXZ; diazepam binding inhibitor; DB1; haematological;

cyclooxgenase 2; COXZ; diazepam binding inhibitor; DB1; haematological;

cyclooxgenase 2; EPHXZ; 5-lipoxygenase activating protein; FLAP;

cyclooxgenase 2; EPHXZ; 5-lipoxygenase activating protein;

cyclooxgenase 2; EPHXZ; 5-lipoxygenase activating protein;

cyclooxgenase 2; EPHXZ; 5-lipoxygenase activating protein;

cyclooxgenase 2; NGC, inicotinamide-N-methyl transferase;

cyclooxgenase 2; NGC, inicotinamide-N-methyl transferase;

cyclooxgenase 2; NGC; sulfotransferase; NNMT;

cyclooxgenase 2; NGC; sulfotransferase; NNMT;

cyclooxgenase 2; NGC; sulfotransferase; NNMT;

cyclooxgenase;

cyclooxgenase 2; NGC; sulfotransferase; NNMT;

cyclooxgenase;

cycloox - by amplification of mRNA followed A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #38. Gaps .. 1.7%; Score 17.8; DB 1; Length 21; 90.5%; Pred. No. 1.1e+02; ative 0; Mismatches 2; Indels Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other; (NITE) NIPPON TELEGRAPH & TELEPHONE CORP Analysis of cDNA and gene expression - by digestion with restriction enzymes. 1865 TITITATITITITATIC 1885 Disclosure; Page 8; 11pp; Japanese. 1 rrrrrrrrrrrrrrrrrrahig 21 ABS97830 standard; DNA; 21 BP 93JP-00112515 93JP-00112515 (first entry) Query Match Best Local Similarity 90.5° WPI; 1995-018287/03. 23-DEC-2002 JP06303997-A 16-APR-1993; 16-APR-1993; 01-NOV-1994. ABS97830; RESULT 174 ABS97830/c 셤 ð

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28-NOV-2000; 2000US-00724389.
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(DNAS-) DNA SCI LAB INC.

Guida M, Hall J;

WPI; 2002-698522/75.

Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits.

Example 16; Page 130; 714pp; English.

This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known human cytcohrome P450 A1 (CPP4501A1), cytcohrome P450 A2 (CPP4501A1), cytcohrome P450 A2 (CPP4501A2), cytcohrome P450 A2 (CPP4501A1), cytcohrome P450 A2 (CPP4501A2), cytcohrome P450 A2 (CPP4501A1), cytcohrome P450 A2 (CPP4501A2), cytcohrome P450 A2 (CPP4501A2), adrenegic receptor beta1 (ADBR1), cytcohrome P450 A2 (CPP4501A2), adrenegic receptor beta1 (ADBR1), cytcohrome P450 A2 (CPP4501A2), and base acid with a control (ARN), cathegein S (CTSS), cyclooxgenae 2 (CPPA2), diazapam binding protein (PLAP), glutathione-S-transferase 2 (CPPA2), histohrome-N-methyl cransferase (MNMT), MADBH quinone-S-transferase 2 (MNQZ), culfortansferase (MNMT), MADBH quinone-S-transferase 2 (MNQZ), culfortansferase (MNMT), MADBH quinone-S-transferase 2 (MNQZ), culfortansferase (MNZ), or copy of transferase (MNZ), or copy of transferase (MNZ), or copy of transferase (MNZ), copy of transferase (MNZ), and the copy of transferase (MNZ), or copy of transferase (MNZ), and the copy of transferase (MNZ), or copy of transferase (MNZ), cythan unclear receptor (MNZ), multidrug resistance 1 (MNZ), or copy of transferase (MNZ), and the copy of transferase (MNZ), cythan and copy of transferase copy of the property in the protein in the protein in the protein in the peripheral nervous system function. The present sequence represents a polymorphic DNA sequence of the invention

Sequence 21 BP; 10 A; 9 C; 1 G; 1 T; 0 U; 0 Other;

. ch 1.7%; Score 17.8; DB 1; Length 21; 1 Similarity 90.5%; Pred. No. 1.1e+02; 19; Conservative 0; Mismatches 2; Indels Query Match Best Local Similarity Matches

1793 TGTGTGTGTGTGTGTGTGT 1813 21 rargrererecerererer

g

ABS97832; BXXXXXB

ABS97832 standard; DNA; 21

RESULT 175 ABS97832/c

23-DEC-2002 (first entry)

Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #40.

Human, ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;

Cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

Cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

Adrenergic receptor beta1; ADBR1; aryl hydrocarbon, AHRP; NR112;

W adrenergic receptor nuclear translocator; ARNT; cathepsin S; CTSS;

Cyclooxgenase 2; COX2; diazepam binding inhibitor; DB1; haematological;

W epoxide hydroxylase 2; EPHX2; S-11poxygenase activating protein; FLAP;

Gultathione-S-transferase 12; GGT12; histamine-N-methyl transferase;

W HNMT; kallikrain 2; KLKZ; nicotinanide-N-methyl transferase; NNMT;

W HNMT; kallikrain 2; KLKZ; nicotinanide-N-methyl transferase 2B7;

W HDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;

W multidrug resistance 1; lactotransferase; UGT2B15; urokinase receptor; UPA;

multidrug resistance associated protein 3; cancer; prostate;

M cetylcholine muscarinic receptor; CHWR1; CHWR2; CHWR3;

A altered drug metabolism; cardiovascular function; colorectal tumour;

CM single nucleotide polymorphism.

Homo sapiens.

WO200257410-A2.

25-JUL-2002.

28-NOV-2001; 2001WO-US044838.

28-NOV-2000; 2000US-00724389

(DNAS-) DNA SCI LAB INC.

Guida M, Hall J;

WPI; 2002-698522/75.

Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits.

Example 16; Page 131; 714pp; English.

This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known concurred to the sequence of a variation from that of a known concurred to the sequence page 20 A2 (CTP4501A2), advencency correctione P450 O2E1 (CYP4501A1), advencency correctione P450 O2E1 (CYP4500A2), advencency correctione P450 O2E1 (CYP4500A2), advencency correctioned P450 O2E1 (CYP4500A2), advencency correctioned P450 O2E1 (CYP4500A2), advencency correctioned P450 O2E1 (CYP5), advencency correction (FAB1), approximate a correction (FAB1), epoxyde phydroxylase 2 [EPHX2), 5-lipoxygenase activating inhibitor (DB1), beoxyde phydroxylase 2 [EPHX2), 5-lipoxygenase activating corresponding from the correction (FAB1), NADPH quinone oxidoreductase 2 (NDO2), transferase (NNWT), NADPH quinone oxidoreductase 2 (NDO2), transferase (NOTEN), NADPH quinone oxidoreductase 2 (NDO2), transferase (UGT2B15), uroxinase receptor (URP1), unitiding resistance associated protein 3 (NDP3), lactoriansferase (UGT2B15), uroxinase receptor (URP12), unitiding resistance associated protein 3 (NDP3), lactoriansferase (NDMP1), lactoriansferase (CHWR1), chwR2, CHWR3, CHWR3, CHWR3, CHWR3) chwR4 or CHWR5) sequence. The polymorphisms in the human genes cited in the invention are useful as genetic linkage markers for locating and characterising the genes responsible for a variety of disorder-related comprision or underexpression, which may be used in diagnosing and characterising the disorders. The nucleic acid molecules comprising the polymorphic sequences conteained in CYP4501A1, CYP4501A1, CYP4501A2, CYP4501A2, MWR1 and/or MDR3 are useful for screening individuals for altered central custom conteained in CYP4501A1, CYP4501A1, CYPA501A1, CYPA501A1, CYPA501A1, CYPA501A1, CYPA501A1, CYPA501A1, CYPA501A1, CYPA501A1, CYPA501A2, CAPACA1A1, C

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Gaps

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Indels

90.5%; Pred. No. 1.2e+02; tive 0; Mismatches 2;

1793 TGTGTGTGTGTGTGTGT 1813

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19; Conservative

Best Local Similarity Matches 19; Conserv

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information of for ca, 230 such bovine microsatellites is summarised in the sequence information specification and indexed herein (see below). The sequence information of required PCR primers for in vitro amplification of the ogenerate the microsatellite (using the program OPTIRRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economic trait leads of the catefinism of conomic trait leads in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
nervous system function, in FLAP and HNWT for altered pulmonary, immunological or haematological function, in KLK2 for altered serine protease activity in the prostate, in LTF for altered immunological or haematological function, in CHWR3, CHWR4 or CHWR5 for altered central and peripheral nervous system function. The present sequence represents a polymorphic DNA sequence of the invention
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - used in genetic identification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                             ö
                                                                                                                                                                 Ouery Match
1.7%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22 BP; 1 A; 0 C; 11 G; 10 T; 0 U; 0 Other;
                                                                                                                                    Sequence 21 BP; 10 A; 9 C; 1 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Microsatellite sequence from clone TGLA306.
                                                                                                                                                                                                                                                   1793 TGTGTGTGTGTGTGTGTGT 1813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rable 7; Page 285; 517pp; English
                                                                                                                                                                                                                                                                     21 TGTATGTGTGCGTGTGTGT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphic bovine DNA markers - mapping, and selective breeding.
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                                                                                                                                                                                                                                                                                                                                                                                  AAQ33888 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JAN-1991;
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3os taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ33888;
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                                                                                                                                                                                                                                                                                                                                                  RESULT 176
                                                                                                                                                                                                                                                                                                                                                                      AAQ33888
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DB 1; Length 22;

1.7%; Score 17.8;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to Simple Sequence Repeats (SSRs) from clover species. SSRs, also called microsatellites, are based on a 1-7 nucleotide core element which is tandemly repeated. The SSR array is embedded in complex flanking DNA. SSRs are ideal markers for genome mapping, trait mapping and marker-assisted selection. The SSRs may be used in methods for selecting genes in clover/ legume breeding. The SSRs are also useful for DNA profiling of clover varieties and for testing the purity of legume seed batches. The present sequence is a SSR motif, which was used in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel simple sequence repeats in clover species useful for selection of genes in legume breeding, for profiling legume species varieties and for testing the purity of legume seed batches.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                         Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping;
trait mapping; marker-assisted selection; gene selection; legume;
DNA profiling; breeding; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.7%; Score 17.8; DB 1; Length 22; ilarity 90.5%; Pred. No. 1.2e+02; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22 BP; 10 A; 10 C; 2 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                               PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1793 TGTGTGTGTGTGTGTGT 1813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 19; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                               (AGRI-) AGRIC VICTORIA SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 rererererecerererer
                                                                                                                                                                                                                                                                                                                                                                                   24-DEC-1999; 99AU-00004907.
28-MAR-2000; 2000AU-00006520.
                                                                                                                                                                                                                                                                                                                                                      03-JAN-2001; 2001NZ-00509194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                            AAI64468 standard; DNA; 22
                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Koelliker R, Forster JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-431058/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                   SSR motif #18.
                                                                                                                                                                                                                                                             Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-DEC-2002
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                                                                                                                                      23-NOV-2001
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                                                                                                                                                                                                                                                                                            NZ509194-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABS97834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                         AA164468;
                                             RESULT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABS 97834/c
ID ABS 97
XX
AC ABS 97
XX
DT 23-DE
g
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Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;

Cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

Cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

Cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

Cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

Cytochrome Cytochrome Cytochrome Cytochrome P48; MRP3; CYTS;

Cytochrome Cytochro Human NADFH quinone oxidoreductase 2 (NQO2) polymorphic sequence #42. single nucleotide polymorphism

WO200257410-A2.

25-JUL-2002

28-NOV-2001; 2001WO-US044838.

28-NOV-2000; 2000US-00724389

DNAS-) DNA SCI LAB INC.

Hall J; Guida M,

WPI; 2002-698522/75.

Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits.

Example 16; Page 131; 714pp; English.

This invention relates to the sequence of an isolated nucleic acid
molecule comprising at least one base variation from that of a known
human cytochrome P450 Al (CYP4501Al), cytochrome P450 A2 (CYP4501A2),
cytochrome P450 02E1 (CYP45002E1), adrenergic receptor betal (ADBR1),
aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
(ARNY), cathepsin S (CYP56), cytlocxgenase 2 (CPT2), joint binding
inhibitor (DB1), epoxide hydroxylase 2 (EPHZ2), 5-lipoxygenase activating
cinhibitor (DB1), poxide hydroxylase 2 (EPHZ2), 5-lipoxygenase activating
cinhibitor (DB1), plutathione-S-transferase 12 (GST12), histamine-N-methyl
transferase (NNMY), (KA11krein 2) KLK2, nicotinamide -N-methyl
transferase thermolabile (STM), UDP-glucuronosyl transferase 28 (UGT2B1), uncethyl
curronsyl transferase 28 (UGT2B1), uncethyl
transferase (UGT2B15), urckinase receptor (UPA), multidrug resistance associated protein 3
(UMR1), lactotransferrin (LTF), multidrug resistance associated protein 3
(WRR1), orphan nuclear receptor (NR12), or acceptor (UPA), multidrug resistance
creeptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
The polymorphisms in the human genes cited in the invention are useful are responsible for specific traits within the genome and eventually
care responsible for specific traits within the genome and eventually
creeptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR3, CHMR3, CAPA501A1, CYPP4501A2,
craits as a result of their e.g., overexpression, which may be used in diagnosing
creepton mutation or underexpression, which may be used in diagnosing
creptonics equences contained in CYP4501A1, CYPP4501A2,
creptonics and/or treating the disorders. The nucleic acid molecules comprising the
composition of their eagen of their eagen of the composity of their eagen ea

ö used to screen for altered cardiovascular function, in COX2 for altered susceptibility to colorectal tumours, in DBI or CHWR1 for altered central nervous system function, in FLAP and HNWT for altered pulmonary, immunological or haematological function, in KLK2 for altered serine protease activity in the prostate, in LTF for altered immunological or haematological cunction, in CHWR3, CHWR4 or CHWR5 for altered central and peripheral nervous system function. The present sequence represents a polymorphic DNA sequence of the invention Mouse, antiinflammatory, cytostatic; antisense gene therapy; phosphoenol pyruvate carboxykinase-cytosolic; PEPCK-cytosolic; infection; inflammation; tumour formation; phosphorothicate; ss. Antisense compound capable of modulating the expression of phosphoenol pyruvate carboxykinase-cytosolic, useful for preventing or delaying infection, inflammation or tumor formation. . 0 Mouse PRPCK-cytosolic antisense oligonucleotide ISIS 113342. Local Similarity 90.5%; Pred. No. 1.2e+02; Length. 19; Conservative 0; Mismattle. Sequence 22 BF; 10 A; 10 C; 1 G; 1 T; 0 U; 0 Other; Cowsert LM; 1793 TGTGTGTGTGTGTGTGT 1813 21 rardrererecerererer 1 Wyatt J, AAF62964 standard; DNA; 20 BP. 21-JAN-2000; 2000US-00488671. 21-JAN-2000; 2000US-00488671. 08-MAY-2001 (first entry) (ISIS-) ISIS PHARM INC. Mckay R, Butler MM, WPI; 2001-190979/19. Mus musculus US6187545-B1 13-FEB-2001. AAF62964; Query Match Matches RESULT 179 AAF62964 8888888888 à g

Example 17; Col 44; 64pp; English.

The present sequence is one of a number of antisense compounds of up to 30 nucleobases in length that are capable of inhibiting the expression of phosphoenon pyruvate carboxykinase-cytosolic (PEPCK-cytosolic). The antisense compounds are useful for inhibiting the expression of PEPCK-cytosolic in cells or tissues. They are commonly used as research capagnes and in diagnostics, e.g. to elucidate the function of particular genes. They are also useful for distinguishing between functions of various members of a biological pathway and for research use. The dalay infection, inflammation or tumour formation. The present or dalay infection, inflammation or tumour formation. The present or inflammation or tumour formation. The present or himmeric phosphorothioate oligonucleotide with 2'-MOE wings and a

deoxy gap

Sequence 20 BP; 2 A; 0 C; 10 G; 8 T; 0 U; 0 Other;

Score 17.4; DB 1; Length 20; Pred. No. 1.2e+02; 1.7%; Query Match Best Local Similarity ABS97835 standard; DNA; 20 BP.

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The invention relates to antisense oligonucleotides targeted to a nucleic acid molecule encoding human Survivin, where the antisense oligonucleotides inhibits the expression of human Survivin. These catisense oligonucleotides are used in the treatment of an animal antisense oligonucleotides are used in the treatment of an animal so suffering from a disease or condition associated with Survivin, e.g. a hyperprofilerative condition such as cancer, and comprises administering a therapeutically or prophylactically effective amount of the animatering at the approciate so that expression of Survivin is inhibited. The collyonucleotides can also be used to treat a human suffering from a disease or condition characterised by a reduction in apoptosis comprising administering the antisense oligonucleotide to a human. In addition, the antisense oligonucleotide modulate apoptosis, cytokinesis or the call cycle, or inhibit the proliferation in a cancer cell by contacting the cile and antisense oligonucleotide. AAS21521-AAS21768 represent Survivin used in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel antisense compounds for modulating the expression of Survivin and treatment of cancer.
Gaps
                                                                                                                                                                                                                                                                                          Survivin, human; mouse; cytostatic; antisense oligonucleotide; hyperproliferative condition; cancer; apoptosis; cytokinesis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1,7%; Score 17.4; DB 1; Length 20; 94.7%; Pred. No. 1.2e+02; tive 0; Mismatches 1; Indels
Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 11 A; 2 C; 0 G; 7 T; 0 U; 0 Other;
 ..
                                                                                                                                                                                                                                                            Mouse Survivin antisense oligonucleotide #57.
 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 18; Page 62; 120pp; English.
                                   1794 GIGIGIGIGIGIGIGIG 1812
                                                                   1 Grererereadrerere 19
                                                                                                                                                         AAS21755 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US002939.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ackermann EJ,
                                                                                                                                                                                                                             (first entry)
 Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ISIS-) ISIS PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                         WO200157059-A1
                                                                                                                                                                                                                                                                                                                                                      musculus.
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                                                                                                                                                                                                                                                                                                                                                                       Synthetic
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                                                                                                                                                                                             AAS21755;
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This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known molecule comprising at least one base variation from that of a known molecule comprising at least one base variation from that of a known than oylochrome P450 Al (CYP4501Al), cytochrome P450 A2 (CYP4501Al), cytochr Example 16; Page 131; 714pp; English.

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Gaps

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1811 TGTATATATATATGT 1829

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Conservative

Best Local Similarity Matches 18; Conserv

TGTTTATATATATATGT 1

19

RESULT 181 ABS97835/c

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Human, ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;

cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

cytochrome P450 A2; CYP4501A2; cytochrome P450 D2E; CYP45002E1; LTF;

cytochrome Carbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;

cyclocoxgenase 2; COX2; diazepam binding inhibitor; DB1; haematological;

cyclocoxgenase 2; EPRX2; 5-lipoxygenase activating protein; FLAP;

cyclocoxgenase 2; EPRX2; 5-lipoxygenase activating protein; FLAP;

cyclocoxgenase 2; EPRX2; 5-lipoxygenase activating protein; FLAP;

cyclocoxgenase 2; EPRX2; 1 incotinamide-N-methyl transferase;

cyclocoxgenase 2; NGV2; sulfotransferase thermolabile; STM;

cyclocoxgenase 2; NGV2; sulfotransferase thermolabile; STM;

cyclocoxgenase 2; NGV2; sulfotransferase 187;

cyclocoxgenase 2; NGV2; sulfotransferase 187;

cyclocoxgenase 2; NGV2; sulfotransferase 287;

cyclocoxgenase 2; NGV2;

cyclocoxgenase 287;

cyclocoxgenas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits.
                                                                                                                            quinone oxidoreductase 2 (NQO2) polymorphic sequence #43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single nuclectide polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-NOV-2001; 2001WO-US044838.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-NOV-2000; 2000US-00724389
                                                                                         23-DEC-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hall J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200257410-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                       Human NADPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guida M,
                                             ABS97835;
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economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN field.)

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ARNT, EPHX2, GST12, NRWT, NQO2, NR112, STW, UGT2B4, UGT2B15, AJR, MDR1 and/or MDR3 are useful for screening individuals for altered drug metabolism. The polymorphic sequences contained in CYPF301A1, CYPP4501A2, AJR, MDR1 and/or MDR3 may also be used to screen individuals for susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are used to screen for altered cardiovascular function, in COX2 for altered necrous system function, in FLAP and HNMT for altered pulmonary, immunological or haematological function, in KLK2 for altered serine procease activity in the prostate, in LTF for altered immunological can hematological function, in CHMR3, CHMR4 or CHMR5 for altered central hematological function, in CHMR3, CHMR4 or CHMR5 equence represents a polymorphic DNA sequence of the invention
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Sequence 20 BP; 10 A; 8 C; 0 G; 2 T; 0 U; 0 Other;

Query Match
1.7%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 1793 TGTGTGTGTGTGTGT 1811 19 rerarerererererer ઠે

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Gaps

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AAQ34164 standard; DNA; 17 BP RESULT 182 AAQ34164

(revised)
(first entry) 25-MAR-2003 02-FEB-1993 AAQ34164;

Sequence of a microsatellite from clone TGLA84.

PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.

Bos taurus.

WO9213102-A1

36-AUG-1992.

92WO-US000340. 15-JAN-1992;

91US-00642342 15-JAN-1991;

(GENM-) GENMARK.

Massey JM; Georges M,

WPI; 1992-284684/34.

Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.

Table 7; Page 396; 517pp; English.

The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleocide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (TG)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the septence information specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPPIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of

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Gaps

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Query Match
1.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels

Sequence 17 BP; 0 A; 0 C; 8 G; 9 T; 0 U; 0 Other;

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The sequence is that of a bovine microsatellite sequence obtd. by

screening a library of bovine MDOI DNA fragments of between 250 and 500

considerable and a (TC)15 oligomucleotide probe. One out of 50

clones cross-hybridised. Assuming independent distribution of

microsatellites and MDOI sites, the frequency of (T6)n >9 microsatellites

con the bovine genome is estimated at >100, 000. The sequence information

con 230 such bovine microsatellites is summarised in the

specification and indexed herein (see below). The sequences upstream and

consomitation and indexed herein (see below). The sequences upstream and

consomitation of the microsatellite sequence water used to generate the

confirmed PCR primers for in vitro amplification of the corresp.

microsatellite (using the program OPTIPRIM). The microsatellites may be

used to identify individuals, for parentage testing, and in the genetic

consomically important traits esp. in cattle, to allow selective

connectly see also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                       .
                                                                                        Length 17;
                                                                                                                      0; Indels
                                                         Sequence 17 BP; 0 A; 0 C; 8 G; 9 T; 0 U; 0 Other;
                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                     Microsatellite sequence from clone TGLA188.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Table 7; Page 242; 517pp; English
                                                                                                                                                         1793 TGTGTGTGTGTGT 1809
                                                                                                                                                                                                                                                                    AAQ33783 standard; DNA; 17 BP.
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                                                                                                                                                                                                                                                                                                                                        (revised)
(first entry)
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus.
                                                                                                                                                                                                                                                                                                         AAQ33783;
                                                                                                                                                                                                                                          RESULT 183
                                                                                                                                                                                                                                                            AAQ33783
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AAT66099 standard; DNA; 17

AAT66099;

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This invention describes novel oligonucleosides that causes RNaseH-
mediated cleavage of target RNA comprising (a) an RNaseH-activating
region (R1) of at least 3 consecutive 2 unaubstituted nucleosides
connected by charged internucleoside links and (b) a non-RNase activating
region (R2) of at least 2 nucleoside links and (b) a non-RNase activating
selected internucleoside link. The oligonucleosides of the invention have
base sequences complementary to that of target RNA. The products of the
invention are used to inhibit transcription of target RNA in a cell or
corganism, they are antisense molecules that also activate RNAseH.
Particularly the oligonucleosides are used in diagnosis and treatment of
disease associated with endogenous or foreign gene expression. Use
against human papilloma vitus is exemplified. The modified
internucleoside links improve target specificity, potency and binding
affinity (Ra) compared with racemic analogues. They are also more
resistant to nuclease and so have better in-vivo lifetimes. The chirally
selected linkages in R2 allow control of binding affinity. AAXS68SS-
X56881 represent oligonucleosides used in the method of the invention
                                                                                                                                                                                                                                                                         Oligonucleoside; RNaseH-mediated cleavage; target; RNaseH; inhibitor; internucleoside linkage; antisense; diagnosis; treatment; disease; binding affinity; Ka; nuclease resistance; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New oligo:nucleotide(s) causing cleavage of target RNA - with RNaseH activated segment having charged inter-nucleoside links and second segment with chirally selected links.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.6%; Score 17; DB 1; Length 17;
100.0%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17 BP; 1 A; 0 C; 8 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Giachetti C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 137; 165pp; English
1793 TGTGTGTGTGTGTGT 1809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93US-00154013.
93US-00154014.
94US-00233778.
94US-00238177.
                   WO9513834 oligonucleoside 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94WO-US013387
                                                                                                                             AAX56865 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arnold LJ, Reynolds MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-254769/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENT-) GENTA INC.
                                                                                                                                                                                                                                                                                                                                                                                           WO9513834-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-NOV-1994;
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26-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6-NOV-1993
                                                                                                                                                                                                     16-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAY-1995
                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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                                                                                                                                                                 AAX56865;
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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. The sequences AAT66084-T66107 repeats sequences of low informativeness found in specific human genes. This repeat sequence is found in the angiogenin gene located at chromosomal position 14q11-q13. The sequence is amplified by primers AAT66100-1. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phosphonate internucleosidyl linkage; chirality; hybridization; racemic; binding affinity; 88.
                                                                                                               Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detection of polymorphic genetic markers of the form (dC-dA) n(dG-dT)\,n using novel nucleic acid mols. as primers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17 BP; 9 A; 8 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . Match 1.6%; Score 17; DB 1; Le Local Similarity 100.0%; Pred. No. 1.2e+02; les 17; Conservative 0; Mismatches 0;
                                                                                     Repeat sequence found in the angiogenin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 9; Col 61-62; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methylphosphonate oligomer 2517-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1793 IGEGIGIGIGIGIGIGI 1809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX91062 standard; DNA; 17 BP
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                                                                                                                                                                                                                                                                                                                      89US-00341562.
91US-00754351.
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                                            (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                      (MARS-) MARSHFIELD CLINIC
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-042299/04.
                                                                                                                                                                                                                                                                                          04-APR-1994;
                                                                                                                                                                                                                                                                                                                        21-APR-1989;
05-SEP-1991;
                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                               US5582979-A.
                                                                                                                                                                                                                                                              10-DEC-1996.
                                            25-MAR-2003
18-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX91062;
                                                                                                                                                                                                                                                                                                                                                                                                     Weber JL;
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Matches
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Gaps

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0; Indels

0; Mismatches

100.08;

Local Similarity les 17; Conserv

Best Loca Matches

1798 GIGIGIGIGIGIA 1814

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Van Haringen WA;

Van Haringen H,

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The invention provides methods for preparing oligomers having phosphonate internucleosidyl linkages of a preselected chirality which hybridize to a target RNA sequence. The method of making comprises: (a) synthesizing a nucleoside dimer, trimer, or tetramer with racemic internucleosidyl phosphonate linkages; (b) purifying the racemic nucleoside to a chirally pure nucleoside; and (c) sequentially linking at least 2 of the chirally pure nucleosides to form a synthetic oligomer that is enriched for phosphonate internucleosidyl linkages of a preselected chirality and is complementary to an RNA target sequence. The methods are useful for providing chirally enriched synthetic oligomers have enhanced binding affinities for RNA compared to oligomers with racemic all methylphosphonate internucleosidyl linkages. Sequences AAX91054-75 represent oligomers chemically synthesised using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomic DNA analysis; 5' variation generator; 3' fragment generator; endangered animal identification; PCR primer; 88.
                                                                                                                                                                                                                                                              Oligomers made using chirally pure nucleoside dimers, trimers, tetramers with enhanced binding affinities.
                                                                                                                                                                                                    Schwartz DA, Vaghefi MM, Riley TA, Arnold LJ, Reynolds MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.6%; Score 17; DB 1; Length 17;
100.0%; Pred. No. 1.2e+02;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5' variation generator oligonucleotide PCR primer #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 1 A; 0 C; 8 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                               Example 19; Col 39-40; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1798 GTGTGTGTGTGTA 1814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (VHAE-) VAN HAERINGEN LAB BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-MAR-2000; 2000EP-00200757
                                                                                                                        93US-00154013.
                                                                                          97US-00885126
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                                                                                                                                                                                                                                WPI; 1999-539600/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                     (GENT-) GENTA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP1130114-A1
                                                                                                                          16-NOV-1993;
                                                                                                                                         21-NOV-1994;
                                                                                            30-JUN-1997;
                              USS955597-A
                                                             21-SEP-1999
Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD17594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 187
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cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss; primer; probe; tumour suppression; tumour reversion; apoptosis; virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
                                                                                                                                                                                    The patent discloses a method and associated kit for analysing genomic DNA in a sample. The method comprises conducting a nucleic acid second oligonucleotide primer to produce DNA fragments based on repeat sequences on at least one end of the genomic DNA. The first and sequences on at least one end of the genomic DNA. The first primer is a solution generator including a repeat sequence and at least one nonsepart nucleotide. The second oligonucleotide primer is a 3' fragment generator starting within such a genetic distance that amplification of the genomic DNA can be performed and preferably includes inosine. The method is useful for the genetic analysis of an individual organism, particularly of species or individual. It is also useful for the rapid and straight forward identification of endangered animals or plants. The present DNA sequence is a 5' variation generator oligonucleotide PCR
                                                    Analyzing genomic DNA in a sample, useful for analyzing genes of organisms (e.g. a species or individual) or identifying endangered animals or plants, by using oligonucleotide primers comprising universal variable fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
1.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumour suppression/reversion associated nucleotide #6051.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17 BP; 0 A; 0 C; 8 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 739; 771pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tuijnder M;
                                                                                                                                                         Example 1; Page 6; 23pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1792 TIGIGIGIGIGIGIG 1808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB45728 standard; DNA; 17 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 Trerererererere 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-SEP-2002; 2002WO-IB004219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           API; 2003-441574/41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful e.g.
polypeptide
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The invention relates to the isolation of 6327 nucleotide sequences, fragments of at least 15 consecutive nucleotides of these nucleotides, a sequence having at least 80% identity, after optimal alignment, with the nucleotides, a sequence that hybridizes under stringent conditions with the nucleotides, or the complement, or corresponding RNA, of the nucleotides, The nucleotides are used as probes or primers for detecting, dentifying quantifying and/or amplifying nucleic acids, as in vitro sense and antisenes sequences, of nucleotides involved in tumour suppression or reversion, apoptosis and or viral resistance, to produce recombinant polypeptides, and to prepare transgenic animals, as experimental models. The nucleotides [also vectors containing them and calls containing the vectors), the encoded polypeptides and antibodies or viral infections or diseases characterized by development of tumours or viral infections or diseases characterized by development of tumours and/or prognosis of these diseases. The nucleotides and polypeptides can and/or prognosis of these diseases. The nucleotides and polypeptides can also be used to screen for their specific interactive molecules. expression of the nucleotides. \$

Sequence 17 BP; 3 A; 4 C; 2 G; 8 T; 0 U; 0 Other;

0; Gaps Query Match 1.6%; Score 17; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 17; Conservative 0; Mismatches 0; Indels 2141 GATCAGTTTTTCACCT 2157 ઠે

1 GATCAGTTTTTCACCT 17 d

AAX77487 standard; DNA; 18 BP RESULT 189 AAX77487/c

(first entry) 05-AUG-1999 AAX77487;

USS912147 primer 31.

Primer, quantitation, genetic instability; tumour cell; detection; neoplastic transformation; carcinogenesis; ss.

Synthetic.

US5912147-A

15-JUN-1999

96US-00734973, 22-OCT-1996;

96US-00734973. 22-OCT-1996;

(HEAL-) HEALTH RES INC.

WPI; 1999-357197/30.

Anderson G,

Stoler D, Basik M;

Quantitating genetic instability.

Claim 4; Col 29-30; 27pp; English.

This invention describes a novel method for quantitating genetic instability independent of microsatellite alterations by treating a comparison pair comprising genomic DNA from tumour cells and genomic DNA from normal cells. The method involves the cells from the same individual with oligonuclectide primers selected from (i) a nuclectide sequence (CG) xRG, where R is a purine selected from adenine and guanine and x = 3-7, (ii) a nuclectide sequence (CG) xRY, where R is as in (1) and Y is a

pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii) a nucleotide sequence (CG)xRR, where R is as in (1) and x = 3-7, (iv) a nucleotide sequence (CG)xYY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (V) a nucleotide sequence (CA)xXY, where R is a purine selected from adenine and guanine and x = 6-6, (V) a nucleotide sequence (CA)xXY, where R is a purine selected from adenine and guanine and Y is a pyrimidine selected from cytosine, thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xXY, where X is a pyrimidine selected from dynosine, thymine, and uracil and x = 6-16, (viii) a nucleotide sequence (CA)xYY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination of the primers. The method is useful for detecting genomic instability which are commonly associated with the various stages of neoplastic transformation and carcinogenesis. The method is rapid and simple

Sequence 18 BP; 8 A; 9 C; 0 G; 1 T; 0 U; 0 Other;

Gaps ö 1.6%; Score 17; DB 1; Length 18; 100.0%; Pred. No. 1.2e+02; ative 0; Mismatches 0; Indels 1.64
Best Local Similarity 100.0
Matches 17; Conservative

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1794 GTGTGTGTGTGTGTG 1810 ò

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RESULT 190 AAX77486/c

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AAX77486 standard; DNA; 18

AAX77486;

(first entry) 05-AUG-1999

genetic instability; tumour cell; detection; Primer, quantitation; genetic instability; tum neoplastic transformation; carcinogenesis; ss. US5912147 primer 30.

Synthetic.

US5912147-A.

15-JUN-1999.

96US-00734973. 22-OCT-1996; 96US-00734973. 22-OCT-1996;

(HEAL-) HEALTH RES INC.

Basik M; Stoler D, Anderson G,

WPI; 1999-357197/30.

Quantitating genetic instability.

Claim 4; Col 29-30; 27pp; English.

This invention describes a novel method for quantitating genetic instability independent of microsacellite alterations by treating a domparison pair comprising genomic DNA from tumour cells and genomic DNA from normal cells. The method involves the cells from the same individual with oligonucleotide primers selected from (1) a nucleotide sequence (CG)xRX, where R is a purine selected from adenine and guanine and x = 3-7, (ii) a nucleotide sequence (CG)xRX, where R is as in (i) and Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii) anucleotide sequence (CG)xRX, where R is as in (i) and x = 3-7, (iii) nucleotide sequence (CG)xXX, where R is a purinidine selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence (CG)xXY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence (CA)xRX, where R is a purine and guanine and X = 6-16, (xi) a nucleotide sequence (CA)xRX, where R is a purine selected from adenine and guanine and Y is a pyrimidine selected from cytosine,

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thymine, and uracil, and x=6-16, (vii) a nucleotide sequence (CA)xRR, where R is a purine selected from adenine and quantine and a = 6-16, (viii) a nucleotide sequence (CA)xYY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x=6-16, and (ix) a combination of the primers. The method is useful for detecting genomic instability which are commonly associated with the various stages of neoplastic transformation and carcinogenesis. The method is rapid and simple
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Sequence 18 BP; 8 A; 10 C; 0 G; 0 T; 0 U; 0 Other;

Gaps ö Match 10.08; Score 17; DB 1; Length 18; Local Similarity 100.08; Pred. No. 1.2e+02; es 17; Conservative 0; Mismatches 0; Indels Query Match Matches

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1794 GTGTGTGTGTGTGTG 1810

17 Grerererererere a

AAX77484 standard; DNA; 18 BP 05-AUG-1999 (first entry) JS5912147 primer 28 AAX77484; RESULT 191 AAX77484/c

Primer; quantitation; genetic instability; tumour cell; detection; neoplastic transformation; carcinogenesis; ss.

Synthetic.

JS5912147-A

15-JUN-1999

96US-00734973 22-OCT-1996; 96US-00734973 22-OCT-1996;

(HEAL-) HEALTH RES INC

Stoler D, Anderson G,

WPI; 1999-357197/30.

Quantitating genetic instability.

Claim 4; Col 27-28; 27pp; English

This invention describes a novel method for quantitating genetic instability independent of microsatellite alterations by treating a comparison pair comparising genomic DNA from tumour cells and sequence (CG)xRY, where R is as in (i) and x = 3-7 (ii) a nucleotide sequence (CG)xRY, where R is as in (i) and x = 3-7, (iii) a nucleotide sequence (CG)xRY, where R is as in (i) and x = 3-7, (iii) a nucleotide sequence (CG)xRY, where R is a sin (i) and x = 3-7, (iv) a nucleotide sequence (CG)xRY, where R is a purime selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence (CA)xRY, where R is a purime selected from definic and guanine and x = 6-16, (vi) a nucleotide sequence (CA)xRY, where R is a purime selected from definic and guanine and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where X is a purime selected from definic and guanine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where X is a purime selected from definic and guanine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where X is a purime selected from definic and guanine, and uracil and x = 6-16, (viii) a nucleotide sequence (CA)xRY, where X is a pyrimidine selected from dytosine, thymine, and uracil and x = 6-16, (viii) a nucleotide sequence (CA)xRY, where X is a pyrimidine selected from dytosine, thymine, and uracil and x = 6-16, and yet is compination of the primers. The method is useful for detecting genomic instability which are commonly associated with the various stages of nopplastic transformation and carcinogenesis. The method is rapid and simple

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Gaps

.. 0

Query Match
1.6%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels

Sequence 18 BP; 9 A; 9 C; 0 G; 0 T; 0 U; 0 Other;

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This invention describes a novel method for quantitating genetic instability independent of microsatellite alterations by treating a comparison pair comprising genomic DNA from tumour cells and genomic DNA in the oligonucleotide primers selected from adenine and yearine and x = 3-7 (ii) a nucleotide sequence (CG)xRY, where R is as in (i) and X = 3-7 (ii) a nucleotide sequence (CG)xRY, where R is as in (i) and x = 3-7 (iii) a nucleotide sequence (CG)xRY, where R is a primidine selected from cytosine, thymine, and uracil and x = 3-7, (iv) a nucleotide sequence (CG)xRY, where R is a primidine selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence (CA)xRY, where R is a purine selected from adenine and guanine and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where R is a purine selected from adenine and guanine and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, (viii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, (viii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, (viii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, (viii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, thyminer, and uracil and x = 6-16, (viii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, thyminer, and uracil and x = 6-16, (viii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, thyminer, and uracil and carcines stages of neoplastic transformation and carcinosensis. The method is rapid and simple
                                                                                              Gaps
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                                           Query Match
1.6%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels
Sequence 18 BP; 10 A; 8 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                    17 TTGTGTGTGTGTGTGTGTG
                                                                                                                                                                                                                                                                                                                                   AAX77459 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                    05-AUG-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HEAL-) HEALTH RES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-357197/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JS5912147 primer 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                      AAX77459;
                                                                                                                                                                                                                                                                                  RESULT 192
                                                                                                                                                                                                                                                                                                           AAX77459/
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Primer; quantitation; genetic instability; tumour cell; detection; neoplastic transformation; carcinogenesis; ss.

AAX77457 standard; DNA; 18 BP

AAX77457/C RESULT 194

05-AUG-1999 (first entry)

AAX77457;

US5912147 primer 1.

17 GTGTGTGTGTGTG 1

В

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This invention describes a novel method for quantitating genetic instability independent of microsatellite alterations by treating a comparison pair comparison genomic DNA from tumour cells and genomic DNA from tumour cells. The method involves the cells from the same individual with oligonucleotide primers selected from adenine and x = 3-7 (Ii) a nucleotide sequence (CG)xRY, where R is as in (i) and x = 3-7, (ii) a nucleotide sequence (CG)xRY, where R is as in (i) and x = 3-7, (ii) a nucleotide sequence (CG)xRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence (CG)xXY, where R is a pyrimidine selected from adenine and guanine and x = 6-16, (vi) a nucleotide sequence (CA)xRY, where R is a purine selected from adenine and ynamine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where R is a purine selected from adenine and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from formine and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination continuous stages of neoplastic transformation and carcinogenesis. The method is rapid and simple
                                                                                                                                                                                     Primer; quantitation; genetic instability; tumour cell; detection; neoplastic transformation; carcinogenesis; DNA/RNA hybrid; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.6%; Score 17; DB 1; Length 18; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 BP; 8 A; 9 C; 0 G; 0 T; 1 U; 0 Other;
                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Col 29-30; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quantitating genetic instability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anderson G, Stoler D, Basik M;
                                                                                                                                                                                                                                                                                                                         /*tag= a
/note= "uracil"
                                     AAX77488 standard; DNA; 18 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-00734973
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                                                                                                               05-AUG-1999. (first entry)
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                                                                                                                                                    US5912147 primer 32.
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                                                                                                                                                                                                                                                                                      Key
misc_RNA
                                                                                                                                                                                                                                                     Synthetic
                                                                          AAX77488;
RESULT 193
AAX77488/c
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Quantitating genetic instability

Basik M;

Anderson G, Stoler D, (HEAL-) HEALTH RES INC

WPI; 1999-357197/30.

96US-00734973. 96US-00734973.

22-OCT-1996; 22-OCT-1996;

US5912147-A. L5-JUN-1999.

Synthetic.

This invention describes a novel method for quantitating genetic instability independent of microsatellite alterations by treating a comparation pair comprising genomic DNA from tumour cells and genomic DNA comparation pair comparation is a purine selected from admine and x = 3-7 (ii) a nucleotide sequence (CO)xRY, where R is as in (i) and Y is a primidine selected from cytosine, thymine, and uracil and x = 3-7, (iii) a nucleotide sequence (CO)xRY, where R is as in (i) and X = 3-7, (iii) a nucleotide sequence (CO)xRY, where R is as in (i) and x = 3-7, (iv) a nucleotide sequence (CO)xRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence (CA)xRY, where R is a purine selected from adenine and guanine and Y is a pyrimidine selected from cytosine, thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where R is a purine selected from adenine and x = 6-16, (viii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil, and x = 6-16, (viii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, (viii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected comparation contraction and carcinogenesis. The method is rapid and simple 1.6%; Score 17; DB 1; Length 18; 100.0%; Pred. No. 1.2e+02; tive 0; Mismatches 0; Indels Sequence 18 BP; 9 A; 8 C; 1 G; 0 T; 0 U; 0 Other; Claim 4; Col 15-16; 27pp; English 1792 TIGIGIGIGIGIGIG 1808 17 Trgrererererere AAQ75581 ID AAQ75581 standard; DNA; 20 XX Best Local Similarity 100. Matches 17; Conservative Query Match RESULT 195 ઠે ö Gaps ö

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Gaps

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WPI; 2000-485552/43

mcgarry191-19.rng

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
                                                                                                                                                                                                                                                                                                                           Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; melanocortin-1 receptor; MCIR; promoter; regulation; detection;
                                                                            Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human MC1R gene related TATA box oligonucleotide SEQ ID NO:15
                                                     Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 1.6%; Score 16.8; DB 1; Length 20; Best Local Similarity 90.0%; Pred. No. 1.46+02; Matches 18; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 2 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                        (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 5; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1865 TTTTTATTTTTAAT 1884
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                           (first entry)
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                                                                                                                                                                                                                                                                                                     WPI; 1995-018287/03
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                             04-AUG-1995
                                                                                                                              Synthetic
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AAQ75581
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                                                                                                                The present invention describes a control-active polynucleotide derived from the human melanocortin-1 receptor (MC1R) gene upstream controlling sequence. Also described is a method for detecting a substance affecting synthesis of melanin in which a host transformed by an expression vector, comprising a control active polynucleotide darived from MC1R, is cultured in the presence of a sample to be tested and a signal formed by the expression of said reporter gene is detected. The control-active polynucleotide is used for the detection of a substance affecting synthesis of melanin. The present sequence represents a human melanocortin-1 receptor gene TMTA box oligonucleotide, which is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; melanocortin-1 receptor; MCIR; promoter; regulation; detection;
melanin; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human MC1R gene related TATA box oligonuclectide SEQ ID NO:15.
                             Upstream controlling sequence of melanocortin1 receptor and
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 10 A; 0 C; 0 G; 10 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           1811 TGTATATATATATATGTA 1830
                                                                                       Disclosure; Page 4; 21pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ratatatatatatata 20
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                                                       application
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(first entry)

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Human uridine diphosphate glucuronosyltransferase gene polymorphism #1.
                                                                                     Human, polymorphism, TA repeat; ds; UGT; thymidine-adenine repeat; uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1; drug dosage optimisation; xenobiotic sensitivity.
                                       16-JAN-2003
             AAL50667;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention comprises a method for detecting polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter (preferably CMCTAAL). The method involves determining the number of thymidiahe-adenine (TA) repeats in the promoter - as the number of TA repeats correlates with expression of the UGT gene. The method of the invention is useful for detecting polymorphisms in a UGT gene promoter. The method of the invention is also useful in optimising drug dosages and predicting an individual's sensitivity to xenobiotics for drugs and xenobiotics that are glucuronidated by UGT. The present DNA sequence represents a UGT gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, involves determining number of thymidine-adenine repeats in the promoter.
                                                                                                                                                                                                                                                                       Human uridine diphosphate glucuronosyltransferase gene polymorphism #1
                                                                    Gaps
                                                                                                                                                                                                                                                                                              Human, polymorphism, TA repeat, ds, UGT; thymidine-adenine repeat,
uridine diphosphate glucuronosyltransferase gene promoter; UGTIA1,
drug dosage optimisation; xenobiotic sensitivity.
                                                                    ;
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                                     Query Match
1.6%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.46+02;
Matches 18; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 10 A; 0 C; 0 G; 10 T; 0 U; 0 Other;
              Sequence 20 BP; 10 A; 0 C; 0 G; 10 T; 0 U; 0 Other;
                                                                                              1811 TGTATATATATATGTA 1830
                                                                                                                      20 TATATATATATATATATA 1
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                                                                                                                                                                                          BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-2002; 2002US-00061693
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                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-740095/80.
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Iyer L, Ratain MJ;

Rienzo AD,

(ARCH-) ARCH DEV CORP

99US-00251274.

16-FEB-1999;

01-FEB-2002; 2002US-00061693

US2002115097-A1.

22-AUG-2002

Homo sapiens

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                                                                                                                                                                                      The invention comprises a method for detecting polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter (preferably UGTAAL). The method involves determining the number of thymidine-adenine (TA) repeats in the promoter - as the number of TA repeats correlates with expression of the UGT gene. The method of the invention is useful for detecting polymorphisms in a UGT gene promoter. The method of the invention is useful in optimising drug dosages and predicting an individual's sensitivity to xenobiotics for drugs and xenobiotics that
                                                                 gene promoter, useful for optimizing drug dosages for a patient, involves determining number of thymidine-adenine repeats in the promoter.
                                                                                                                                                                                                                                                                                                                                                                                          are glucuronidated by UGT. The present DNA sequence represents a UGT gene
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                                           glucuronosyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 10 A; 0 C; 0 G; 10 T; 0 U; 0 Other;
                                              Detecting polymorphisms in uridine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1811 TGTATATATATATGTA 1830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATATATATATATATA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human oligonucleotide sequence.
                                                                                                                                                     Claim B; Page 9; 13pp; English.
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Matches 18; Conservative
WPI; 2002-740095/80.
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Gaps

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1.6%; Score 16.8; DB 1; Length 20; 90.0%; Pred. No. 1.48+02; Live 0; Mismatches 2; Indels

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Local Similarity 90.0 nes 18; Conservative

Best Loca Matches

Query Match

1811 TGTATATATATATGTA 1830

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ratararararara 20

AAL50667 standard; DNA; 20

RESULT 199 AAL50667/c ID AAL506

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the invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonuclectide antisense to the initiation codon, coding region, 5' or 3' end genemic flanking regions, 5' and 3' intron-exon junctions or regions within 2-10 nucleotides of junctions of genee encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an entilnflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallargic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of biquinone or lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed approach of the printed or form the printed or 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pharmaceutical composition for treating allments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                                            Katz E, Pabalan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
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i, Shahabuddin S;
                                                                                                                                                                                                               24-APR-2001; 2001US-0286137P.
                                                                                                                                                    23-APR-2002; 2002WO-US013135
                                                                                                                                                                                                                                                                       (EPIG-) EPIGENESIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                  Li Y, Sar
Tang L,
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                                WO200285308-A2
                                                                                        31-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                   Miller S,
                                                                                                                                                                                                                                                                                                                                      Nyce JW,
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1.6%; Score 16.8; DB 1; Length 20; 90.0%; Pred. No. 1.4e+02; ive 0; Mismatches 2; Indels Sequence 20 BP; 1 A; 2 C; 7 G; 10 T; 0 U; 0 Other; Ouery Match

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Gaps

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IGTGTA 1814 rererererererere 20 1795 TGTGTGTGTGTGTGTGT

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Local Similarity 90.0%; es 18; Conservative

Best Loca Matches

RESULT 201

ВЪ

EST polymorphic DNA repeat polynucleotide #337.

EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat; polymorphic marker prediction of ubiquitous simple sequences; POMPC Rep-X; human; genetic disease; drug-treatment; Machado-Joseph; Haw River syndrome; Huntington's disease; fragile-X syndrome; Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia; spinal atrophy; bulbar atrophy; spinocerebellar ataxia. AXX80012/C
ID ABX80012 standard; CDNA; 20 BP
AC ABX80012;
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XX
I7-APR-2003 (first entry)
XX
XX
XX
EST polymorphic DNA repeat pol.
XX
XX
KW EST; expressed sequence tag; s
XW RSPx; human; genetic disease;
XW Rep.x; human; genetic disease;
XW Rapx; human; genetic disease;
XW Predreich's ataxis; myotonic d
XX
Homo sapiens.

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The invention discloses a method for identifying a candidate polymorphic repeat within a coding sequence (expressed sequence tag, EST), which comprises detecting tandem repeats in a target coding sequence, scoring the repeats for polymorphic probability and generating a dataset correlating the repeats with polymorphic probability to identify a correlating the repeats. The computational methods (polymorphic repeat. The computational methods (polymorphic repeat. The computational methods (polymorphic repeat in a marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are useful for identifying and detecting candidate polymorphic repeats in human genes, which can be used to understand, treat or eliminate genetic diseases linked to nucleotide repeats are Machado-Joseph, Haw River syndrome, Hautington's disease, fragile-X syndrome, Fredieich's atexais, myctonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and spinocereballar ataxia. The sequences presented in ABX79676-ABX80022 are the polymorphic repeats identified for a search of human ESTS
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                                                                                                                                                                                                                                                                                                                  Identifying a candidate polymorphic repeat within a coding sequence, funderstanding or treating genetic disease, comprises detecting tandem repeats in a target coding sequence and scoring the repeats for polymorphic probability.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; Col 1165; 588pp; English.
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Best Local Similarity 90.0
Matches 18; Conservative
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Fondon JW;

Garner HR, Wren JD, Minna JD,

Aguilar D;

(TEXA) UNIV TEXAS SYSTEM

99US-00475947. 99US-00475947

31-DEC-1999; 31-DEC-1999;

US6472154-B1 29-OCT-2002 1792 TIGIGIGIGIGIGIGIGI 1811 Н rececrererererererer 셤 à

figp-12; NOV2; 10829-rP2; insulin-like growth factor binding protein-related protein 2; IGFBP-rP2; Insulin-like growth factor binding protein-related protein 2; IGFBP-rP2; IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy; hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis; scleroderma; atherosclerosis; cytostatic; dermatological; Mouse connective tissue growth factor antisense oligo DNA (SegID 135) antisense; mouse; murine; ss; connective tissue growth factor; CTGF; chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein; ADB25742 standard; DNA; 20 BP. 20-NOV-2003 (first entry) antiarteriosclerotic ADB25742; RESULT 202

Location/Qualifiers 1. .20 /*tag= modified_base Mus sp.

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A method for the analysis of cDNA comprises (a) preparing an aggregate double-stranded cDNAs by using an aggregate of mRNAs and a plural type labelled reverse transcription primers (GRNESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 8; 11pp; Japanese.
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                                          93JP-00112515.
                                                                                 93JP-00112515
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Matches 18; Conservative
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                                          16-APR-1993;
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01-NOV-1994.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to novel methods for modulating the expression of connective tissue growth factor (CTGF) by antisense oligonucleotides.

CTGF has been mapped to human chromosome region 6423.1, and is also known as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2, insulin-like growth factor binding protein-related protein 2, IGFBF-FP2, CTGFBF-8, Heast and ecogenin. It is known to stimulate DNA synthesis and promote chemotaxis of fibroblasts, however, it is also upregulated in acute lymphoblastic lenkaemia and in tumour or endothelial cells associated with the vasculature. Accordingly, antisense oligonucleotides that inhibit the expression of CTGF in cells or tissues can be used in gene therapy to treat various conditions including hyperproliferative disorders (particularly cancer, e.g. breast, prostate or renal cancer), pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As such, the present invention describes these antisense oligos as having cycostatic, dermatological and antiatteriosclerotic activities. This oligonucleotide sequence is a chimeric phosphorothioate antisense oligo with 2, MOE wings and a deoxy gap, which is used to inhibit expression of mouse CTGF of the invention.
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                      /note= "OTHER= phosphorothioate backbone, where 1-5 and 16-20 are 2' methoxyethyl nucleotides. All cytidines are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                         New antisense oligonucleotides for modulating connective tissue growth factor expression, particularly useful for treating cancers (e.g. breast or prostate cancer), pulmonary or renal fibrosis, scleroderma or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 89; 139pp; English.
    mod_base= OTHER
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                                                                                                                                                                                                                                                                                                                        Gaarde WA, Watt AT;
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                                                                                                                                         expression - by amplification of mRNA followed
                                                                                                                                                                                                                                                                                                                         A method for the analysis of cDNA comprises (a) preparing an aggregate of double stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEO files AAC75547-075798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The
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(NITE ) NIPPON TELEGRAPH & TELEPHONE CORP
                                                                                                                                             alysis of cDNA and gene expression - digestion with restriction enzymes.
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JP06303997-A.

Synthetic

AAQ75729;

RESULT 203

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Query Match Best Local S: Matches 18

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16-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   - by amplification of mRNA followed
electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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                                                                                                                                                                                                                                 Reverse transcription primer used in cDNA analysis technique
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                                                   Length 21;
                                                 Score 16.8; DB 1; Length 2
Pred. No. 1.4e+02;
0; Mismatches 2; Indels
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                              Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
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by digestion with restriction enzymes.
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Matches 18; Conservative
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Matches
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This sequence represents a PCR primer used to amplify the chemokine macrophage inflammation protein 3 beta (MIP 3beta) coding sequence. The PCR product is used in the analysis of dendritic cell response to different chemokines. The invention relates to the use of chemokines which are capable of directing dendritic cells, in the manufacture of a medicament for the treatment of a disease state. Methods are included for treatment to the disease state. Methods are included for crivation of antigen-presenting dendritic cells. The chemokines can be used to initiate, amplify or modulate an immune response. The chemokines use useful for the treatment of disease states e.g. a bacterial, viral, fungal or parasitic infection, cancer (especially melanomal, breast, pancreatic, colon, lung, glioma, hepatocellular, endometrial, gastric, intestinal, renal, prostate, thyroid, ovarian, testicular, liver, head and neck, colorectal, oseophagus, stomach, eye, bladder, glioblastoma and neck, colorectal, oseophagus, stomach, eye, bladder, glioblastoma and incential and control and
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                                                                                                            Chemokine, PCR primer, macrophage inflammation protein 3beta; dendritic cell, disease treatment, MIP-3beta; infection; cancer; allergy; immune response initiation; autoimmune disease; tissue rejection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of chemokines capable of directing migration of dendritic cells, useful for treating microbial infections, cancer and autoimmune diseases
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Reverse PCR primer ~439/MIP-3beta used to amplify MIP-3beta ORF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1794 GTGTGTGTGTGTGTGT 1813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Col 13; 16pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABK47993 standard; DNA; 21 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98EP-00401799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vanbervliet B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SCHE ) SCHERING-PLOUGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-118300/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                  site of
                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method for enhancing an immune response in a mammal, comprising administering chemokine MCP-4 or 6Ckine or their biologically active fragments. The chemokines are capable of directing the migration of dendritic cells to manufacture a medicament for a disease state. The invention is used to treat disease states, including an autoimmune disease, tissue rejection or an allergy, or a cancer, particularly melanoma, breast, pancreatic, colon, lung, glioma, hepatocellular, endometrial, gastric, intestinal, renal, prostate, thyroid, ovarian, testicular, liver, head and neck, colorectal, thyroid, ovarian, eye or bladder cancer, glioblastoma or metastatic carcinoma. This sequence represents an RT-PCR primer for macrophage inflammatory protein 3 beta (MIP-3 beta), used in analysis of responsiveness to chemokines
                                                                                                                                                                                                                                                                                                                                  Using chemokine MCP-4 or 6Ckine to attract dendritic cells to the situan an antigen is useful to treat disease states, particularly autoimmune disease, tissue rejection, allergy and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detection; polymorphism; perfect compound simple sequence repeat; adaptor directed primer; genome; genetic; fingerprinting; amplified fragment length polymorphism assay; microsatellite region; genetic trait marking; germplasm comparisons; compound; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90.0%; Pred. No. 1.46+02;
Matches 18; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Compound simple sequence repeat primer (CA)4.5(TA)7.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21 BP; 8 A; 11 C; 0 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1794 GTGTGTGTGTGTGTGTGT 1813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 GTGTGTGAGTGTGAGTGT 2
                                                                                                                                                                                                                                                                                                                                                                                                      Example, Page 7; 29pp; English
                                                                                                                                                                                                                                                                    Laface D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT30425 standard; DNA; 24 BP
                                                                                                                                                                  24-JAN-2001; 2001US-00768917.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-NOV-1995; 95WO-US015150
                                                                                                                                24-JAN-2001; 2001US-00768917.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JAN-1997 (first entry)
                                                                                                                                                                                                                                                                  Vicari AP, Caux C,
                                                                                                                                                                                              (VICA/) VICARI A P.
(CAUX/) CAUX C.
(LAFA/) LAFACE D.
                                                                                                                                                                                                                                                                                                WPI; 2002-351086/38
                                                                US2002034494-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9617082-A2
                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36-JUN-1996
                                                                                                21-MAR-2002
MIP-3 beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 208
AAT30425
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                                                                                                                                                                                                    Detecting polymorphisms between 2 nucleic acid samples, esp. in microsatellite regions, comprises digesting the nucleic acid to generate fragments, ligating adaptor segments to their ends, amplifying them using primer directed amplification and comparing the prods. to detect differences. The primers used in the amplification comprise a primer directed primer, comprising of a perfect capt. Sequence repeat (SSR), and an adaptor segment. The present sequence is an example of a compound SSR primer. The method represents a modified amplified fragment length polymorphism assay, which is partic. useful for genome fingerprinting, i.e. for genetic trait marking and germplasm comparisons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New set of inter-simple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes, useful for genotyping diverse genomes of plant and
                                                                                                                           Modified amplified fragment length polymorphism assay - for detection of polymorphism esp. in micro:satellite regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inter-simple sequence repeat; ISSR; SSR; PCR; primer; genotyping; plant;
animal; Basmati rice; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel set of inter-simple sequence repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                    o;
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
1.6%; Score 16.8; DB 1; Length 24;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 24 BP; 12 A; 4 C; 0 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DNAF-) CENT DNA FINGERPRINTING & DIAGNOSTICS
                                          (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 19; 60pp; English.
                                                                                                                                                                            Disclosure, Fig 1c; 173pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1813 TATATATATATATGTACA 1832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADD69518 standard; DNA; 17 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JAN-2003; 2003WO-IB000041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-APR-2002; 2002IN-CH000260
           94US-00346456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISSR-related PCR primer 5.
                                                                       Vogel JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-804317/75
                                                                                                    WPI; 1996-277795/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003085133-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                animal systems.
              28-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nagaraju JG;
                                                                         Morgante M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADD69518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 209
ADD69518
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Gaps

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Indels

Pred. No. 1.4e+02; 0; Mismatches 1;

1794 GTGTGTGTGTGTGTGT 1811

l Similarity 94.4%; 17; Conservative

Best Local Similarity Matches 17; Conserv

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Grerereaerererer

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BP.

AAX19941 standard; DNA; 18

RESULT 21

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Gape ő

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MooI DNA fragments of between 250 and 500 concenting a library of bovine MooI DNA fragments of between 250 and 500 by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 concers cross-tybridised. Assuming independent distribution of 50 microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites and mooI sites, the frequency of (T6)n >9 microsatellites of for ca. 230 such bovine microsatellites is summarised in the cyperification and indexed herein (see below). The sequence upstream and downstream of the microsatellite sequence were used to generate the crossatellite (using the program OPPIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective field.)
(ISSR)-PCR primers for genotyping eukaryotes. The primers of the invention may be useful for genotyping diverse genomes of plant and animal systems, in particular for distinguishing Basmati rice varieties from non-Basmati rice varieties and traditional Basmati rice varieties from evolved Basmati rice varieties. The current sequence is that of the ISSR-related PCR primer of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cattle; parentage;
                                                                                                                                                                Ouery Match 1.6%; Score 16.6; DB 1; Length 17; Best Local Similarity 94.1%; Pred. No. 1.38+02; Matches 16; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 18 BP; 1 A; 0 C; 9 G; 8 T; 0 U; 0 Other;
                                                                                                                                  Sequence 17 BP; 0 A; 0 C; 8 G; 8 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR; selection; primers; OPTIPRIM; breeding; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Microsatellite sequence from clone TGLA189.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Table 7; Page 244; 517pp; English.
                                                                                                                                                                                                                                                1794 GTGTGTGTGTGTGTG 1810
                                                                                                                                                                                                                                                                                  1 Grerererererers 17
                                                                                                                                                                                                                                                                                                                                                                               AAQ33786 standard; DNA; 18 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92WO-US000340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09213102-A1
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02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Georges M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ33786;
                                                                                                                                                                                                                                                                                                                                              RESULT 210
                                                                                                                                                                                                                                                                                                                                                                AAQ33786
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A method has been developed for labelling an oligonucleotide having a repeated sequence of (XY)n (where X and Y consists of a combination of adenine and thymine or uracil or guanine and cytosine, and n is an integer of 1 or more ) at the 3'-terminal side in which the repeated sequence is added and extended using a labelled body of the nucleotide constituting the repeated sequence and a DNA polymerase lacked in 5' to 3' exonuclease activity. The method can be used for detecting a gene. The method can detect a gene in a sensitivity up to ten times higher than prior art methods. The present sequence represents a primer used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                             Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                     Labelling of an oligonucleotide - useful for detecting genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.6%; Score 16.4; DB 1; Length 18; 94.4%; Pred. No. 1.4e+02; ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18 BP; 9 A; 0 C; 0 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                              (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer SEQ ID NO:1 from JP11075880
                                                                                Primer SEQ ID NO:1 from JP11075880.
                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 7; 10pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1813 TATATATATATATGTA 1830
                                                                                                                                                                                                                                                                 97JP-00205378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TATATATATATATATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX19941 standard; DNA; 18
                                                     14-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                            NPI; 1999-257710/22.
                                                                                                                                                                                                                                                                   14-JUL-1997;
                                                                                                                                                                                                                                      10-JUL-1998;
                                                                                                                                                                              JP11075880-A
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                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX19941
                              AAX19941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 21
AAX19941/
임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SXXXXXXXXXX
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1.6%; Score 16.4; DB 1; Length 18;

.. 0 A method has been developed for labelling an oligonuclectide having a repeated sequence of (XY)n (where X and Y consists of a combination of adenine and thymine or uracil or guanine and cytosine, and n is an integer of 1 or more) at the 3'-terminal side in which the repeated sequence is added and extended using a labelled body of the nucleotide constituting the repeated sequence and a DNA polymerase lacked in 5' to 3' exonuclease activity. The method can be used for detecting a gene. The method can be used for detecting a gene. The prior art methods. The present sequence represents a primer used in an Gaps Primer; quantitation; genetic instability; tumour cell; detection; neoplastic transformation; carcinogenesis; ss. This invention describes a novel method for quantitating genetic ô Labelling of an oligonuclectide - useful for detecting genes Length 18; 1; Indels Sequence 18 BP; 9 A; 0 C; 0 G; 9 T; 0 U; 0 Other Match 1.6%; Score 16.4; DB 1; Local Similarity 94.4%; Pred. No. 1.40+02; es 17; Conservative 0; Mismatches 1; KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO prior art methods. The present seq example from the present invention Claim 4; Col 27-28; 27pp; English. Example 1; Page 7; 10pp; Japanese Quantitating genetic instability. 1813 TATATATATATGTA 1830 AAX77485 standard; DNA; 18 BP 96US-00734973 96US-00734973 98JP-00195719. 97JP-00205378. 18 rararararararara 05-AUG-1999 (first entry) Anderson G, Stoler D, (HEAL-) HEALTH RES INC WPI; 1999-357197/30. JS5912147 primer 29 22-OCT-1996; 22-OCT-1996; JP11075880-A JS5912147-A 15-JUN-1999 23-MAR-1999 Synthetic, Query Match Best Local S Matches 17 AAX77485; RESULT 213 AAX77485/c CXSXLXBXBXBXBXBXBXBXCXXXXXXXCXCC ઠે g

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instability independent of microsatellite alterations by treating a comparison pair comprising genomic DNA from tumour cells and genomic DNA from tumour cells and genomic DNA comparison pair comprising genomic DNA from tumour cells and genomic DNA comparison primers selected from (i) a nucleotide sequence (CG)×RG, where R is a mucleotide sequence (CG)×RM, where R is as in (i) and x = 3- CM (ii) a nucleotide sequence (CG)×RN, where R is as in (i) and x = 3-7, (ii) a nucleotide sequence (CG)×RN, where R is a pin (i) and x = 3-7, (ii) a nucleotide sequence (CG)×RN, where R is a purimidine selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence (CG)×RN, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence (CA)×RN, where R is a purime selected from cytosine, admine and Y is a pyrimidine selected from cytosine, admine and Y is a pyrimidine selected from companies and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)×RN, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, (viii) a nucleotide sequence (CA)×RN, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, (viii) a nucleotide sequence (CA)×RN, where Y is a pyrimidine selected from cytosine, thymine and uracil and x = 6-16, (viii) a nucleotide sequence (CA)×RN, where Y is a pyrimidine selected from cytosine, thymine and uracil and x = 6-16, (viii) a nucleotide sequence (CA)×RN, where Y is a pyrimidine selected from cytosine, thymine and uracil and x = 6-16, (viii) a nucleotide sequence (CA)×RN, where Y is a pyrimidine selected from cytosine, thymine and uracil and x = 6-16, (viii) a nucleotide sequence (CA)×RN, where Y is a pyrimidine selected from cytosine, thymine and uracil and uracil and x = 6-16, and thymine commonly associated view to various stages of neoplastic transformation and carcinogenesis. The method is rapid and simple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel method for quantitating genetic instability independent of microsatellite alterations by treating a comparison pair comprising genomic DNA from tumour cells and genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer; quantitation; genetic instability; tumour cell; detection;
neoplastic transformation; carcinogenesis; DNA/RNA hybrid; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18 BP; 9 A; 8 C; 1 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Col 31-32; 27pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quantitating genetic instability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1793 TGTGTGTGTGTGTGTG 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/note= "uracil"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-AUG-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HEAL-) HEALTH RES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-357197/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US5912147 primer 38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5912147-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 214
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from normal cells. The method involves the cells from the same individual with oligonucleotide primers selected from (1) a nucleotide sequence (CG)xXY, where R is as in (1) and Y is a pyrimidine selected from addenine and x = 3-7 (11) a nucleotide sequence (CG)xXY, where R is as in (1) and x = 3-7, (11) a nucleotide sequence (CG)xXY, where R is as in (1) and x = 3-7, (11) a nucleotide sequence (CG)xXY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence (CG)xXY, where Y is a pyrimidine selected from addenine and guanine and x = 6-16, (vi) a nucleotide sequence (CA)xXY, where R is a purine selected from adenine and guanine and x = 6-16, (vi) a nucleotide sequence (CA)xXY, where R is a purine selected from definine selected from cytosine, continuine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xYY, where Y is a pyrimidine selected from definine and guanine and x = 6-16, (viii) a nucleotide sequence (CA)xYY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination of from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination continuity associated with the various stages of neoplastic transformation and carcinogenesis. The method is rapid and simple Seguence 18 BP; 8 A; 8 C; 0 G; 0 T; 2 U; 0 Other;

Query Match 1.6%; Score 16.4; DB 1; Length 18; Best Local Similarity 94.4%; Pred. No. 1.4e+02; Matches 17; Conservative 0; Mismatches 1; Indels

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Gabe

; 0

1791 ATTGTGTGTGTGTGTG 1808 18 AATGTGTGTGTGTGTG

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RESULT 215

Primer, quantitation, genetic instability, tumour cell, detection, neoplastic transformation, carcinogenesis, DNA/RNA hybrid, ss.

Location/Qualifiers /*tag= a /note= "uracil"

Basik M;

Quantitating genetic instability.

Claim 4; Col 31-32; 27pp; English.

This invention describes a novel method for quantitating genetic instability independent of microsatellite alterations by treating a comparison pair comprising genomic DNA from tumour cells and genomic DNA from normal cells. The method involves the cells from the same individual with oligonucleotide primers selected from (i) a nucleotide sequence

CC (CG)xRG, where R is a purine selected from adenine and guanine and x = 37, (ii) a nucleotide sequence (CG)xRY, where R is as in (i) and Y is a
CC anucleotide sequence (CG)xRY, where R is as in (i) and x = 3-7, (iii)
CC anucleotide sequence (CG)xRY, where R is as in (i) and x = 3-7, (iv) a
cc cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence
CC (CA)xRY, where R is a purine selected from adenine and guanine and x = 6CC (CA)xRY, where R is a purine selected from adenine and guanine and x = 6CC (CA)xRY, where R is a purine selected from cytosine,
cc adenine and guanine and Y is a pyrimidine selected from cytosine,
cc trymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRR,
cc (viii) a nucleotide sequence (CA)xYY, where Y is a pyrimidine selected
cc (viii) a nucleotide sequence (CA)xYY, where Y is a pyrimidine selected
cc (viii) a nucleotide sequence (CA)xYY, where Y is a pyrimidine selected
cc (viii) a nucleotide sequence (CA)xYY, where Y is a pyrimidine selected
cc (viii) a nucleotide sequence (CA)xYY, where Y is a pyrimidine selected
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cc (viii) a nucleotide sequence (CA)xYY, where Y is a pyrimidine selected
cc (viii) a nucleotide sequence (CA)xYY, where Y is a pyrimidine selected
cc (viii) a nucleotide sequence (CA)xYY, where Y is a pyrimidine
cc ö Gaps ö Score 16.4; DB 1; Length 18; Pred. No. 1.4e+02; 0; Mismatches 1; Indels Sequence 18 BP; 8 A; 8 C; 0 G; 1 T; 1 U; 0 Other; 1791 ATTGTGTGTGTGTGTG 1808 н Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative 18 AATGTGTGTGTGTGTGTG ð

Primer; quantitation; genetic instability; tumour cell; detection; neoplastic transformation; carcinogenesis; DNA/RNA hybrid; ss.

Location/Qualifiers /*tag= a /note= "uracil"

Quantitating genetic instability.

Claim 4; Col 19-20; 27pp; English.

This invention describes a novel method for quantitating genetic instability independent of microsatellite alterations by treating a comparison pair comprising genomic DNA from tumour cells and genomic DNA from normal cells. The method involves the cells from the same individual with oligonucleotide primers selected from (i) a nucleotide sequence (CG)xRG, where R is a purine selected from adenine and guanine and x = 3-7, (ii) a nucleotide sequence (CG)xRY, where R is as in (i) and Y is a

pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii) a nucleotide sequence (CG)xRR, where R is as in (i) and x = 3-7, (iv) a nucleotide sequence (CG)xYY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence (CA)xRY, where R is a purine selected from adenine and guanine and x = 6-16, (vi) a nucleotide sequence (CA)xRY, where R is a purine selected from adenine and guanine and Y is a pyrimidine selected from cytosine, thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRR, where R is a purinine selected from cytosine, is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, (viii) a nucleotide sequence (CA)xXR, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination of the primers. The method is useful for detecting genomic instability which are commonly associated with the various stages of neoplastic transformation and carcinogenesis. The method is rapid and simple 9999999999999999989888

Sequence 18 BP; 8 A; 8 C; 1 G; 0 T; 1 U; 0 Other;

Query Match
1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels

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AAX77491 standard; DNA; 18 BP RESULT 21 AAX77491/

(first entry) 05-AUG-1999

USS912147 primer 35.

Primer, quantitation; genetic instability; tumour cell; detection; neoplastic transformation; carcinogenesis; DNA/RNA hybrid; ss.

Synthetic

Location/Qualifiers 18 /*tag= a /note= "uracil" misc_RNA

US5912147-A

22-OCT-1996;

96US-00734973 22-OCT-1996;

96US-00734973

RES INC. (HEAL-) HEALTH Stoler D, Basik M; Anderson G,

WPI; 1999-357197/30

Claim 4; Col 31-32; 27pp; English.

Quantitating genetic instability.

This invention describes a novel method for quantitating genetic instability independent of microsatellite alterations by treating a comparison pair comprising genomic DNA from tunour cells and genomic DNA from normal cells. The method involves the cells from the same individual with oligonuclectide primers selected from (i) a nucleotide sequence (CG)xRG, where R is a purine selected from adenine and guanine and x = 3-7, (ii) a nucleotide sequence (CG)xRY, where R is as in (i) and X is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii) a nucleotide sequence (CG)xRR, where R is as in (i) and X = 3-7, (iii)

nucleotide sequence (CG)xYY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence (CA)xRG, where R is a purine selected from adenine and guantine and x = 6-16, (vi) a nucleotide sequence (CA)xRY, where R is a purine selected from adenine and quantine and Y is a pyrimidine selected from cytosine, thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRX, where R is a purine selected from cytosine, where R is a purine selected from adenine and x = 6-16, (vii) a nucleotide sequence (CA)xYY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, and (xx) a combination of the primers. The method is useful for detecting genomic instability which are commonly associated with the various stages of neoplastic transformation and carcinogenesis. The method is rapid and simple %

Sequence 18 BP; 8 A; 8 C; 0 G; 1 T; 1 U; 0 Other;

.. 0 Gaps ö Query Match
1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels

.; 0

AAX77489 standard; DNA; 18 RESULT 218

Вр. .

05-AUG-1999 (first entry)

AAX77489;

Primer, quantitation, genetic instability, tumour cell, detection, neoplastic transformation, carcinogenesis, ss. JS5912147 primer 33

Synthetic.

JS5912147-A.

96US-00734973 22-OCT-1996;

96US-00734973 22-OCT-1996;

(HEAL-) HEALTH RES INC.

Anderson G, Stoler D, Basik M;

Quantitating genetic instability. WPI; 1999-357197/30.

Claim 4; Col 29-30; 27pp; English.

This invention describes a novel method for quantitating genetic instability independent of microsatellite alterations by treating comparison genomic DNA from tumour cells and genomic DNA from the same individual with oligonucleotide primers selected from adenine and guanine and x = 3-7 (5) xRG, where R is a purine selected from adenine and guanine and x = 3-7 (14) a nucleotide sequence (CG) xRY, where R is as in (i) and Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iv) a nucleotide sequence (CG) xRR, where R is a purine selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence (CA) xRG, where R is a purine selected from adenine and guanine and x = 6-6 (cA) xRG, (vi) a nucleotide sequence (CA) xRR, where R is a purine selected from cytosine, thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA) xRR, where R is a purine selected from cytosine, thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA) xRR, where R is a purine selected from cytosine,

mcgarry191-19.rng

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(viii) a nucleotide sequence (CA)xYY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6·16, and (ix) a combination of the primers. The method is useful for detecting genomic instability which are commonly associated with the various stages of neoplastic transformation and carcinogenesis. The method is rapid and simple
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Sequence 18 BP; 8 A; 8 C; 0 G; 2 T; 0 U; 0 Other;

ö Query Match . 1.6%; Score 16.4; DB 1; Length 18; Best Local Similarity 94.4%; Pred. No. 1.46+02; Matches 17; Conservative 0; Mismatches 1; Indels 1791 ATTGTGTGTGTGTGT 1808 ò 셤

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Gaps

18 AATGTGTGTGTGTGTG 1

AAX77463 standard; DNA; 18 BP. RESULT 219 AAX77463/c

(first entry) 05-AUG-1999 AAX77463;

antitation; genetic instability; tumour cell; detection; transformation; carcinogenesis; ss. quantitation; US5912147 primer 7. Primer; qua neoplastic

Synthetic.

US5912147-A

15-JUN-1999

96US-00734973. 22-OCT-1996; 96US-00734973. 22-OCT-1996;

(HEAL-) HEALTH RES INC

Basik M; Stoler D, Anderson G,

WPI; 1999-357197/30.

Quantitating genetic instability

Claim 4; Col 19-20; 27pp; English.

Claim 6; Page 51; 72pp; English.

This invention describes a novel method for quantitating genetic instability independent of microsatellite alterations by treating a comparison pair comparising genomic DNA from tumour cells and genomic DNA from the same individual with oligonucleotide primers selected from defenine and genomic DNA from the same individual (GO)xRG, where R is as in (i) and X = 3-7 (ii) a nucleotide sequence (CO)xRY, where R is as in (i) and X = 3-7, (iii) a nucleotide sequence (CO)xRY, where R is as in (i) and X = 3-7, (iii) a nucleotide sequence (CO)xRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence (CO)xRY, where R is a purine selected from defenine and guanine and X = 6-16, (vi) a nucleotide sequence (CA)xRY, where R is a purine selected from defenine and guanine and Y is a pyrimidine selected from cytosine, thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from defenine and guanine and Y is a pyrimidine selected from cytosine, (viii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, (viii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, (viii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, (viii) a nucleotide sequence (CA)xRY, where Y is a combination conduction and carcinogenesis. The method is rapid and simple

Sequence 18 BP; 8 A; 8 C; 1 G; 1 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                       New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species
                                                                                                                                                                            SSR; ryegrass; fescue; tandem repeat; seed batch purity testing.
                    Gaps
                    ô
  Length 18;
1.6%; Score 16.4; DB 1; Length 194.4%; Pred. No. 1.46+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                            STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R. UNIV SOUTHERN CROSS.
STATE VICTORIA DEPT NATURAL RES & ENVIRO.
                                                                                                                                                                                                                                                                                                                                          UNIV ADELAIDE.
INT MAIZE & WHEAT IMPROVEMENT CENT.
                                                                                                                                                                              Simple sequence repeat, plant, ds, cereal profiling,
                                                                                                                                                             Simple sequence repeat, SSR, #30.
                                       1808
                                                                                                      AAS13733 standard; DNA; 18 BP.
                                                                                                                                                                                                                                                                                   24-DEC-1999; 99AU-00004906.
04-MAY-2000; 2000AU-00007310.
                                                                                                                                                                                                                                                                 03-JAN-2001; 2001NZ-00509193
                                                   18 ACTGTGTGTGTGTGTGTGTG
                                        1791 ATTGTGTGTGTGTGTG
                                                                                                                                           (first entry)
   Query Match
Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                      Jones ES;
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-512563/56.
                                                                                                                                            08-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                       Forster JW,
                                                                                                                                                                                                                              NZ509193-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        varieties.
                                                                                                                          AAS13733;
                                                                                                                                                                                                                                                                                                                         (UYSC-)
                                                                                                                                                                                                                                                                                                                                                     (ITMA-)
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                                                                                                                                                                                                             Poeae.
                                                                                      220
                                                                                    RESULT 22
AAS13733/
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The invention relates to a substantially purified or isolated nucleic acid (1) from ryegrass or fescue species including a simple sequence repeat (SSR), having 2 or more tandemly repeated nucleotide core elements 2.6 nucleotides in length. Also included are a nucleic acid primer suitable for amplifying an SSR, included are a nucleic acid primer cautable for amplifying an SSR, included for SSR by preparing a library of ryegrass or fescue genomic DNA enriched for SSRs a library of ryegrass or fescue genomic DNA enriched for SSRs prepared by the MI, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely a second control of the son and the gene are preferentially co-inherited, and selecting for the SSR in the breeding, a method for DNA profiling grass or cereal species varieties by assessing variation between SSRs varieties and testing the purity of grass or cereal seed batches by assessing variation within seed batch of an SSR. The SSRs may be used in the selection of genes in grass or cereal breeding, for profiling grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, and for DNA profiling to establish the distinct identity, uniformity and/or stability of a cultivar. The present sequence is a ryegrass or fescue SSR

Seguence 18 BP; 9 A; 8 C; 0 G; 1 T; 0 U; 0 Other;

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Gaps

94.48;

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The invention relates to a substantially purified or isolated nucleic acid (I) from ryegrass or fescue species including a simple sequence repeat (SSR). having 2 or more tandemly respeated nucleotide core elements 2 conclections in length. Also included are a nucleic acid primer suitable for amplifying an SSR, identifying (M1) an SSR by preparing a library of ryegrass or fescue genomic DNA enriched for SSRs and identifying clones in the library containing SSRs, a library of ryegrass or fescue genomic containing SSRs, a library of ryegrass or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely associated with the gene such that the SSR and the gene are preferentially co-inherited, and selecting for the SSR in the breeding, a method for DNA profilling grass or cereal species varieties by assessing each batches by assessing variation between SSR varieties and testing the purity of grass or cereal seed batches by assessing variation within seed batch of an SSR. The SSRs may be used in the selection of genes in grass or cereal breeding, for profilling grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or dereal species varieties, for testing the purity of grass or dereal species varieties, for testing the purity of grass or dereal species varieties, for testing the purity of grass or dereal species varieties, for testing the purity of grass or dereal species varieties, for testing the purity of grass or dereal species varieties, for testing the purity of distinct identity, uniformity and/or stability of a cultivar. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species varieties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat; cereal profiling; grass profiling; seed batch purity testing.
                                                  Gapa
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     Length 18;
                                                1; Indels
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STATE VICTORIA DEPT NATURAL RES & ENVIRO.
UNIV ADELAIDE.
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Query Match
1.6%; Score 16.4; DB 1;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1;
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(ITMA-) INT MAIZE & WHEAT IMPROVEMENT CENT.
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                                                                                                                                                                                                                                                                                                                                                                                                          Simple sequence repeat, SSR, #36.
                                                                                                  1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Fig 6; 72pp; English.
                                                                                                                           18 rGrGrGrGrArGrGrG 1
                                                                                                                                                                                                                                                                 AAS13764 standard; DNA; 18 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-DEC-1999; 99AU-00004906.
04-MAY-2000; 2000AU-00007310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JAN-2001; 2001NZ-00509193.
                                                                                                  1793 TGTGTGTGTGTGTGTGTG
                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Forster JW, Jones ES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-512563/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lolium rigidum.
                                                                                                                                                                                                                                                                                                                                                            08-MAY-2002
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                                                                                                                                                                                                                         RESULT 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel simple sequence repeats in clover species useful for selection genes in legume breeding, for profiling legume species varieties and testing the purity of legume seed batches.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                              Simple Sequence Repeat, SSR, clover, microsatellite, genome mapping; trait mapping, marker-assisted selection, gene selection, legume; DNA profiling, breeding, ds.
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1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels
              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18 BP; 8 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
Pred. No. 1.4e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            was used in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1793 rerererererere 1810
                                            1811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; Page 35; 52pp; English
                                                                        18
                                                                                                                                                 ВР
                                                                                                                                                                                                                                                                                                                                                                                                                 03-JAN-2001; 2001NZ-00509194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-DEC-1999; 99AU-00004907.
28-MAR-2000; 2000AU-00006520.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABX79779 standard; cDNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 TGTGTGGGTGTGTGTGTG
                                             1794 GTGTGTGTGTGTGTGT
                                                            AAI64450 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Koelliker R, Forster JW;
   Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-431058/46.
                                                                                                                                                                                                                                       SSR motif #10
                                                                                                                                                                                                                                                                                                                              Unidentified.
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                                                                                                                                                                                                            23-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                        25-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                            NZ509194-A.
                                                                                                                                                                              AAI64450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 223
ABX79779
                                                                                                                      RESULT 222
AAI64450/c
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EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat; polymorphic marker prediction of ubiquitous simple sequences; POWPOUS; Rep-X; human; genetic disease; drug-treatment; Machado-Joseph; Haw River syndrome; Huntington's disease; fragile-X syndrome; Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia; spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
                                                                                                                                                                                                                                                                                                   Identifying a candidate polymorphic repeat within a coding sequence, funderstanding or treating genetic disease, comprises detecting tandem repeats in a target coding sequence and scoring the repeats for polymorphic probability.
          EST polymorphic DNA repeat polynucleotide #104.
                                                                                                                                                                                                                                                                                                                                                                    Example; Col 385; 588pp; English.
                                                                                                                                                                                                                                                           Garner HR, Wren JD, Minna JD,
                                                                                                                                                                                       99US-00475947.
                                                                                                                                                                                                             99US-00475947.
                                                                                                                                                                                                                                     (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                   WPI; 2003-208818/20
                                                                                                                                                                                        31-DEC-1999;
                                                                                                                    Homo sapiens
                                                                                                                                         US6472154-B1
                                                                                                                                                                                                             31-DEC-1999;
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Fondon JW;

The invention discloses a method for identifying a candidate polymorphic repeat within a coding sequence (expressed sequence tag, EST), which comprises detecting tandem repeats in a target coding sequence, scoring the repeats for polymorphic probability and generating a dataset correlating the repeats with polymorphic probability to identify a candidate polymorphic repeat. The computational methods (polymorphic repeat. The computational methods (polymorphic repeats) which can be useful for identifying and detecting candidate polymorphic repeats in human genes, which can be used to understand, treat or eliminate genetic diseases, predispositions or adverse drug-treatment reactions. Examples of diseases linked to nucleotide repeats are Machado-Joseph, Haw River syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis, myotionic dystrophy, hyperandrogenaemial spinoaratrophy and spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are the polymorphic repeats identified for a search of human ESTs . 0 Query Match
1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels Sequence 18 BP; 8 A; 0 C; 1 G; 9 T; 0 U; 0 Other;

8 셤

RESULT 224

BP

EST polymorphic DNA repeat polymucleotide #104.

EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat; polymorphic marker prediction of ubiquitcus simple sequences; POMPOUS; Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

The invention discloses a method for identifying a candidate polymorphic repeat within a coding sequence (expressed sequence tag, EST), which comprises detecting tandem repeats in a target coding sequence, scoring the repeats for polymorphic probability and generating a dataset correlating the repeats with polymorphic probability to identify a carcilating the repeats with polymorphic probability to identify a marker repeat. The computational methods (polymorphic repeat in custul for identifying and detecting candidate polymorphic repeat in custul for identifying and detecting candidate polymorphic repeats in custul for identifying and detecting candidate polymorphic repeats in custul for identifying and detecting candidate polymorphic repeats in custul for identifying and detecting candidate polymorphic repeats in custome, which can be used to understand, treat or aliminate genetic diseases linked to nucleotide repeats are Nachado-Joseph, Haw River of syndrome, Huntington's disease, fragile-K syndrome, Federach's ataxis, motionic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and spinocrebellar ataxia. The seguences presented in ABX79676-ABX80022 are the polymorphic repeats identified for a search of human ESTS Identifying a candidate polymorphic repeat within a coding sequence, funderstanding or treating genetic disease, comprises detecting tandem repeats in a target coding sequence and scoring the repeats for polymorphic probability. 0; Gaps Query Match
1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels Sequence 18 BP; 8 A; 0 C; 1 G; 9 T; 0 U; 0 Other; Fondon JW Example, Col 385; 588pp; English. 1814 ATATATATATATGTAC 1831 Garner HR, Wren JD, Minna JD, 18 ATATATATATATATAC 1 99US-00475947. 99US-00475947. (TEXA) UNIV TEXAS SYSTEM. WPI; 2003-208818/20 31-DEC-1999; Homo sapiens 29-OCT-2002 à

for

AAH91159 standard; DNA; 19 BP 09-OCT-2001 AAH91159;

RESULT 225

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Gaps

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Human inflammatory bowel disease associated polymorphic site #234

Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis; single nucleotide polymorphism; SNP; chromosome 19p13; paternity test; chromosome 5q31-33; forensic test; gene therapy; ds.

Homo sapiens

Location/Qualifiers misc_feature

Haw River syndrome; Huntington's disease; fragile-X syndrome; Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia; spinal atrophy; bulbar atrophy; spinocerebellar ataxia.

for

(first entry) AAH91159/ XX AC AAH9: XX DT 09-00 XX Huma XW Huma XW Sing XW Sing XX Homo XX Homo XX Homo

The present invention describes a method for detecting the presence of polymorphisms associated with inflammatory bowel diseases such as ulcerative collists and Crohn's disease. The methods can be used to detect the presence of genetic polymorphisms associated with inflammatory bowel disease and correlating their occurrence with disease states. They may be used in this way for phenotypic correlations, forensics, paternity testing, medicine and genetic analysis. The present sequence is a polymorphic site described in the exemplification of the invention Testing for the presence of polymorphisms associated with inflammatory bowel disease, using a hybridization assay. Human, ds, UGT1A1, promoter, Gilbert's syndrome, hyperbilirubinaemia, uridine diphosphate glucuronosyltransferase, Crigler-Najjar syndrome, UGT, polymorphism detection, TA repeat, glucuronidation, Irinotecan, TAS-103; xenoblotic. /note= "SNP, optional deletion at this position" duman UGTlal promoter polymorphism (TA)8 repeat region. Sequence 19 BP; 9 A; 4 C; 0 G; 5 T; 0 U; 1 Other; Lander ES, Rioux J, (WHED) WHITEHEAD INST BIOMEDICAL RES. (BLLI-) ELLIPSIS BIOTHERAPEUTICS CORP. 1802 GTGTGTGTGTATATA 1820 Ratain MJ, Claim 1; Page 48; 463pp; English 19 GTATGTGTGTNTATATATA 1 ABK90423 standard; DNA; 19 BP 99US-00251274 99US-00251274 Query Match
Best Local Similarity 89.5%;
Matches 17; Conservative 11-DEC-2000; 2000WO-US033632 99US-0170257P 10-APR-2000; 2000US-0196046P 05-NOV-2002 (first entry) Iyer L, (ARCH-) ARCH DEV CORP Daly M, Hudson TJ, WPI; 2001-367874/38 WO200142511-A2 Di Rienzo A, 16-FEB-1999; 16-FEB-1999; Homo sapiens US6395481-B1 28-MAY-2002. 10-DEC-1999; 14-JUN-2001 RESULT 226 ABK90423 #X4X6X#X##X##X#X#X#X##X%\$666666666 셤

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Gaps

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Score 16.4; DB 1; Length 19; Pred. No. 1.5e+02; 0; Mismatches 2; Indels

The invention relates to detecting (M1) polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter, the presence of five thymidine-adenine (TA) repeats in the promoter, where the presence of the five TA repeats correlates with increased expression of the gene. The method is used for detecting polymorphisms in a UGT gene promoter. The method is used for detecting polymorphisms in a UGT gene promoter. (M1) is costinially for optimising drug dosages for a patient, where the drugs activity, for optimising drug dosages for a patient, where the drugs (GTIAL) and the activity of the drug is effected by its level of corrainment or TAS-103 are glucurodianation. The method preferably involves obtaining DNA from an inthe promoter. Thus the DNA being amplified comprises all or part of inthe promoter. Thus the DNA being amplified comprises all or part of in the promoter. The DNA is amplified by a polymerase chain reaction and the number of five trapeats is determined by gel electrophoresis or by sequencing the amplified DNA. The polymorphism comprises an allele consisting of five five TA repeats (TA)5, (TA)5 Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, comprises determining the presence of five thymidine-adenine repeats in Sequence 19 BP; 10 A; 0 C; 0 G; 9 T; 0 U; 0 Other; 11; 13pp; English. Example 6; Col the promoter

Siminovitch

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. 1.6%; Score 16.4; DB 1; Length 19; 94.4%; Pred. No. 1.5e+02; ative 0; Mismatches 1; Indels Query Match Best Local Similarity 94.4 Matches 17; Conservative ò

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Gaps

1813 TATATATATATGTA 1830 TATATATATATATATA 18 g

Human UGT1a1 promoter polymorphism (TA)8 repeat region. 멾 ABK90423 standard; DNA; 19 (first entry) 05-NOV-2002 ABK90423; RESULT 227 ABK90423/c

Human, ds, UGT1A1, promoter, Gilbert's syndrome; hyperbilirubinaemia, uridine diphosphate glucuronosyltransferase, Crigler-Najjar syndrome, UGT, polymorphism detection, TA repeat; glucuronidation, Irinotecan; TAS-103; xenobiotic. Homo sapiens

99US-00251274. 16-FEB-1999; JS6395481-B1

WPI; 2002-588597/63.

US2002115097-A1

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The invention relates to detecting (M1) polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter by determining the presence of five thymidhae-adenine (TA) repeats in the promoter, where the presence of the five TA repeats correlates with increased expression of the gene. The method is used for detecting polymorphisms in a UGT gene promoter. For preferably a UGT I (UGTAL) gene promoter. (M1) is conseful for screening individuals for variation in glucuronidate. (M1) is useful for screening individuals for variation in glucuronidate. (M1) is conseful for screening individuals for variation in glucuronidate of UGTAL) and the activity of the drug is effected by its level of activity dial. Amplifying all or part of a UGT gene promoter (UGTAL) and the box is amplified by a polymerase obtaining DNA from an individual, amplifying all or part of a UGT gene promoter. Thus the DNA being amplified by a polymerase chain reaction and the promoter. Thus the DNA being amplified by a polymerase all or part of UGTALD promoter. The DNA is amplified by a polymerase chain reaction and the number of TA repeats is determined by gel electrophoresis or by sequencing the amplified DNA. The polymorphism comprises an allele constitution to amplified DNA. The polymorphism comprises an allele constitution to ATA repeats (TA)5, (TA)5/(TA)6, (TA)5/(TA)6, (TA)5/(TA)9, (TA)5/(TA)9,
                                                                                                                                                                                                                  Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, comprises determining the presence of five thymidine-adenine repeats in
                                                                                                                                                                                                                                                                                                                                                         Example 6; Col 11; 13pp; English.
                                                                                                                  Ratain MJ;
  99US-00251274
                                                    (ARCH-) ARCH DEV CORP.
                                                                                                            Iyer L,
                                                                                                                                                                 WPI; 2002-588597/63.
                                                                                                            Di Rienzo A,
  16-FEB-1999;
                                                                                                                                                                                                                                                                                                    the promoter
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Sequence 19 BP; 10 A; 0 C; 0 G; 9 T; 0 U; 0 Other;

0; Gaps Query Match 1.6%; Score 16.4; DB 1; Length 19; Best Local Similarity 94.4%; Pred. No. 1.5e+02; Matches 17; Conservative 0; Mismatches 1; Indels

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AAL50681 standard; DNA; 19 BP, AAL50681; RESULT 228

16-JAN-2003 (first entry)

Human uridine diphosphate glucuronosyltransferase gene polymorphism #15.

Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat; uridine diphosphate glucuronosyltransferase gene promoter; UGTA1; drug dosage optimisation; xenobiotic sensitivity.

Homo sapiens

Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, involves determining number of thymidine-adenine repeats in the promoter. The invention comprises a method for detecting polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter (preferably UGT1A1). The method involves determining the number of thymidine-adenine (TA) repeats in the promoter as the number of TA repeats correlates with expression of the UGT gene. The method of the invention is useful for detecting polymorphisms in a UGT gene promoter. The method of the invention is useful invention is also useful in optimising drug desages and predicting an individual s ensitivity to xenobiotics for drugs and xenobiotics that are glucuronidated by UGT. The present DNA sequence represents a UGT gene TA repeat polymorphism Gaps .. 0 Query Match 1.6%; Score 16.4; DB 1; Length 19; Best Local Similarity 94.4%; Pred. No. 1.5e+02; Matches 17; Conservative 0; Mismatches 1; Indels Sequence 19 BP, 10 A; 0 C; 0 G; 9 T; 0 U; 0 Other; Example 6; Page 3; 13pp; English. 1813 TATATATATATATGTA 1830 Rienzo AD, Iyer L, Ratain MJ; 1 TATATATATATATA 18 01-FEB-2002; 2002US-00061693 99US-00251274 (ARCH-) ARCH DEV CORP. WPI; 2002-740095/80. 16-FEB-1999; 22-AUG-2002 à g

Human uridine diphosphate glucuronosyltransferase gene polymorphism #15. Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat; uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1; drug dosage optimisation; xenobiotic sensitivity. AAL50681 standard; DNA; 19 BP. (first entry) 16-JAN-2003 AAL50681;

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Homo sapiens.

US2002115097-A1.

22-AUG-2002

99US-00251274. 01-FEB-2002; 2002US-00061693 16-FEB-1999;

(ARCH-) ARCH DEV CORP.

Rienzo AD, Iyer L, Ratain MJ;

WPI; 2002-740095/80.

Detecting polymorphisms in uridine diphosphate glucuronosyltransferase

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This invention describes a novel murine calpain protease 12 (capn12). The calpain procease of the invention, related proceins and nucleic acid that encodes it, are useful for treatment (including gene therapy) of diseases associated with insufficient expression of the calpain protease. The protein is also used to screen for calpain protein effectors and to raise specific immunoglobulins (Ig) useful for diagnosis. Also the polynucleotide encoding capn12 is useful, e.g. as primers and probes, for
                                                                                  The invention comprises a method for detecting polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter (preferably UGTA1A1). The method involves determining the number of thymidine-adenine (TA) repeats in the promoter — as the number of TA repeats correlates with expression of the UGT gene. The method of the invention is useful for detecting polymorphisms in a UGT gene promoter. The method of the invention is also useful in optimising drug dosages and predicting an individual's sensitivity to xenobiotics for drugs and xenobiotics that are glucuronidated by UGT. The present DNA sequence represents a UGT gene
gene promoter, useful for optimizing drug dosages for a patient, involves determining number of thymidine-adenine repeats in the promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calpain protease; murine; gene therapy; screening; diagnosis; capn12; ss.
                                                                                                                                                                                                                                                                                                                                                         Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New calpain protein 12 with cysteine protease activity, useful for treating specific deficiency disorders.
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                                                                                                                                                                                                                                                                                                                  1.6%; Score 16.4; DB 1; Length 19;
94.4%; Pred. No. 1.5e+02;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                  Sequence 19 BP; 10 A; 0 C; 0 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine capn12 exon 7 splice donor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 2c; 36pp; German.
                                                                                                                                                                                                                                                                                                                                                                                            1813 TATATATATATGTA 1830
                                                      Example 6; Page 3; 13pp; English
                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 94.4%; Pr
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                          TATATATATATATATA 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-2000; 2000DE-01031932
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/*tag= a
/number= 7
11. .20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= b
/number= 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABA99798 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                rA repeat polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-115441/16.
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                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 230
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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 by with an (ACJ15 and a (TC)15 oligomordeotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information of in the bovine part of estimated at >100, 000. The sequence information of specification and indexed herein (see below). The sequences upstream and commistream of the microsatellite sequence were used to generate the incrosatellite (using the program optification of the corresp. microsatellite (using the program optification of the corresp. microsatellite (using the program optification of the determinism of conomically important traits esp. in cattle, to allow selective of breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
diagnosis of diseases, or predisposition to them, and for recombinant production of capn12. This sequence represents the murine calpain 12, capn12 exon 7 splice donor site described in the disclosure of the invention
                                                                                                                                                                   Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
0
                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cattle; parentage;
                                                                                                                             Score 16.4; DB 1; Length 20;
Pred. No. 1.5e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 1.5%; Score 16; DB 1; Length 16; Local Similarity 100.0%; Pred. No. 1.5e+02; les 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16 BP; 0 A; 0 C; 8 G; 8 T; 0 U; 0 Other;
                                                                                            Sequence 20 BP; 5 A; 2 C; 10 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR; selection; primers; OPTIPRIM; breeding; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Microsatellite sequence from clone TGLA158.
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                                                                                                                                                                                                      1589 AGTGACAGCTAGGATGTG 1606
                                                                                                                                                                                                                          3 AGTGACAGCTAGGATGGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91US-00642342.
                                                                                                                                 Query Match 1.6%;
Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                           AAQ33743 standard; DNA; 16
                                                                                                                                                                                                                                                                                                                                                                                              (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENM-) GENMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9213102-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JAN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus.
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                                                                                                                                                                                                                                                                                                                                                             AAQ33743;
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Matches
                                                                                                                                                                                                                                                                                            RESULT 231
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RESULT 232

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AAQ33749

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 screening a library of bovine MboI DNA fragments of between 250 and 500 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100,000. The sequence information of co. ca. 230 such bovine microsatellites is summarised in the sequence information constrained properties in the sequence by the correspond of the microsatellite sequence were used to generate the comparised for in vitro amplification of the correspond crosatellite (using the program of the microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
                                                                                               Microsatellite sequence from clone TGLA311.
                                                                                                                                                          genetic mapping, traits; amplification; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Table 7; Page 291; 517pp; English.
                                                                                                                                                                                                                                                                                                                            92WO-US000340
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                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    маввеу ЛМ;
                                         (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1992-284684/34.
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                                                                                                                                                                                                                                                                                                                                                                                                               (GENM-) GENMARK.
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16-FEB-1995
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                                         25-MAR-2003
02-FEB-1993
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                                                                                                                                                                                                        Bos taurus.
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AAQ33903;
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AAQ68236/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 creening a library of bovine MboI DNA fragments of between 250 and 500 colones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information of in the bovine genome is estimated at >100, 000. The sequence information of specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence where used to generate the required PCR primers for in vitro amplification of the corresp. The microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                      PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
genetic mapping; traits; amplification; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16 BP; 0 A; 0 C; 8 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                 dicrosatellite sequence from clone TGLA160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rable 7; Page 229; 517pp; English
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                                1793 TGTGTGTGTGTGTGTG 1808
                                                                                                                                                                       AAQ33749 standard; DNA; 16 BP
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                                                        1 1GTGTGTGTGTGTG 16
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(first entry)
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02-FEB-1993
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AAQ33903
ID AAQ339
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                                                                                Gaps
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                                          Length 16;
                                                                                0; Indels
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Sequence 16 BP; 0 A; 0 C; 8 G; 8 T; 0 U; 0 Other;
                                        1.5%; Score 16; DB 1; Le
100.0%; Pred. No. 1.5e+02;
:ive 0; Mismatches 0;
                                                                                                                          1794 GTGTGTGTGTGTGT 1809
                                                                                                                                                                                                                                                                 AAQ68236 standard; RNA; 16 BP
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(first entry)
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AAQ33903 standard; DNA; 16 BP.

Matches

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Gaps

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Two sets of methylphosphonate oligonucleosides ("MP oligomers") and complementary ribooligonucleosides ("RNA oligomers") contg. alternating purines and pyrimiddines were examined for their ability to form triple helix complexes. (Set 1:d2019 and R138; Set 2:G2018 and R139 - see halix complexes twas shown that MP oligomers contg. alternating purines and pyrimidines are capable of forming triple stranded complexes with complementary RNA oligomers. (Updated on 25-MAR-2003 to correct PN
   stranded target nucleic acid sequences - by formation of a triple helix structure using 2 oligomers which block translation.
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oligonucleoside, ss.
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100.0%; Pred. No. 1.5e+02;
iive 0; Mismatches 0;
                                                  Example 2; Page 37; 67pp; English
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                                                                                                                                                                                                                                                                                                              1794 GTGTGTGTGTGTGT 1809
                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ68238 standard; RNA; 16 BP
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(first entry)
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Matches 16; Conservative
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16-PEB-1995
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100.0%; Pred. No. 1.5e+02;
vative 0; Mismatches 0;
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Best Local Similarity 100.(
Matches 16, Conservative
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16-FEB-1995
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RESULT 237 AAQ68237

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Repeat sequence found in ADP/ATP translocase gene
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                                                                                            Homo sapiens
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oligonucleoside; ss.
                   Gaps
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                   Indels
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      50.0%; Pred. No. 1.5e+02; ive 8; Mismatches 0;
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100.0%; Pred. No. 1.5e+02;
ative 0; Mismatches 0;
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ID AAT66090 standard; DNA; 16 BP.
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                    Conservative
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es 16; Conserv
    Best Local Similarity
Matches 8; Conserv
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18-JUN-1997
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16-FEB-1995
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Best Loca Matches

RESULT 238

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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dc-dA)n.(dg-dT)n which can be used to detect these markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. The sequences AAT66084-T66107 represent repeat sequences of low informativeness found in specific human genes. This repeat sequence is found in the ADP/ATP translocase gene. The sequence is amplified by primers AAT66091-2. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Satellite sequence; DNA fragmentation; microsatellite DNA; DNA marker;
Haliotis discus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels
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The invention provides a novel method for isolation of satellite sequences from genomic DNA that comprises fragmentation of the DNA by a method which is not dependent on base sequences, then selection of the satellite sequences from the obtained genomic library of high homogeneity. The method is useful for the isolation of microsatellite DNA sequences which can be used as DNA markers. The new method markedly improves the efficiency of isolation of satellite sequences in comparison to prior art methods which are reliant on base sequences. Sequences AAX39483-514 represent sequences from Haliotis discus, used in the method
                                                                                                                                                         Isolation of satellite sequences from genomic DNA for use as DNA markers comprises isolating a library with high homogeneity by DNA fragmentation.
                      (NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES.
                                                                                                                                                                                                                           Example 5; Page 14; 35pp; Japanese.
                                                                  Takahashi H, Sekino M;
                                                                                                               WPI; 2000-224692/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the invention
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1.5%; Score 16; DB 1; Length 16; 100.0%; Pred. No. 1.5e+02; tive 0; Mismatches 0; Indels Sequence 16 BP; 8 A; 8 C; 0 G; 0 T; 0 U; 0 Other; Query Match Best Local Similarity 100.0 Matches 16; Conservative

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0, Gaps

1793 TGTGTGTGTGTGTG 1808 16 TGTGTGTGTGTGTGTG 1 ઠે g

AAD17599 standard; DNA; 17 BP. AAD17599;

5' variation generator oligonucleotide PCR primer #14. (first entry)

Genomic DNA analysis; 5' variation generator; 3' fragment generator; endangered animal identification; PCR primer; ss.

Unidentified

EP1130114-A1

05-SEP-2001.

03-MAR-2000; 2000EP-00200757.

03-MAR-2000; 2000EP-00200757

(VHAE-) VAN HAERINGEN LAB BV.

Van Haringen H, Van Haringen WA;

WPI; 2001-572636/65.

Analyzing genomic DNA in a sample, useful for analyzing genes of organisms (e.g. a species or individual) or identifying endangered animals or plants, by using oligonucleotide primers comprising universal variable fragments.

The patent discloses a method and associated kit for analysing genomic DNA in a sample. The method comprises conducting a nucled caid amplification on the genomic DNA in the sample using both first and second oligonucleotide primer to produce DNA fragments based on repeat sequences on at least one end of the genomic DNA. The first primer is a 5' variation generator including a repeat sequence and at least one nonrepeat nucleotide. The second oligonucleotide primer is a 3' fragment generator starting within such a generic distance that amplification of the genomic DNA can be performed and preferably includes incoine. The method is useful for the genetic analysis of an individual organism, particularly of a species or individual. It is also useful for the rapid and straight forward identification of endangered animals or the rapid present DNA sequence is a 5' variation generator oligonucleotide PCR.

Analyzing genomic DNA in a sample, useful for analyzing genes of organisms (e.g. a species or individual) or identifying endangered animals or plants, by using oligonucleotide primers comprising universal variable fragments.

Example 1; Page 6; 23pp; English.

Van Haringen H, Van Haringen WA;

WPI; 2001-572636/65.

03-MAR-2000; 2000EP-00200757. 03-MAR-2000; 2000EP-00200757. (VHAE-) VAN HAERINGEN LAB BV

EP1130114-A1 Unidentified

05-SEP-2001.

Example 1; Page 6; 23pp; English.

The patent discloses a method and associated kit for analysing genomic DNA in a sample. The method comprises conducting a nucleic acid amplification on the genomic DNA in the sample using both first and

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second oligonucleotide primer to produce DNA fragments based on repeat sequences on a least one end of the genomic DNA. The first primer is a 5 variation generator including a repeat sequence and at least one non-repeat nucleotide. The second oligonucleotide primer is a 3 fragment generator starting within such a generator distance that amplification of the genomic DNA can be performed and preferably includes inceine. The method is useful for the genetic analysis of an individual organism. Particularly of a species or individual it is also useful for the rapid and straight forward identification of endangered animals or plants. The present DNA sequence is a 5 variation generator oligonucleotide PCR
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                                                                                                                                                                           1.5%; Score 16; DB 1; Length 17;
100.0%; Pred. No. 1.5e+02;
live 0; Mismatches 0; Indels
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                                                                                                                                                     Sequence 17 BP; 8 A; 8 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                               1793 TGTGTGTGTGTGTG 1808
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AAD17597/c
ID AAD17597 standard; DNA; 17 BP.
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                                                                                                                                                                                                                                              17 TGTGTGTGTGTGTG
                                                                                                                                                                                         Local Similarity 100.0
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AAD17595 standard; DNA; 17 BP AAD17595;

10-DEC-2001 (first entry)

5' variation generator oligonucleotide PCR primer #10.

Genomic DNA analysis; 5' variation generator; 3' fragment generator; endangered animal identification; PCR primer; ss.

Unidentified

EP1130114-A1.

05-SEP-2001.

03-MAR-2000; 2000EP-00200757.

03-MAR-2000; 2000EP-00200757.

(VHAE-) VAN HAERINGEN LAB BV.

Van Haringen H, Van Haringen WA;

WPI; 2001-572636/65.

Analyzing genomic DNA in a sample, useful for analyzing genes of organisms (e.g. a species or individual) or identifying endangered animals or plants, by using oligonucleotide primers comprising universal variable fragments.

Example 1; Page 6; 23pp; English.

The patent discloses a method and associated kit for analysing genomic DNA in a sample. The method comprises conducting a nucleic acid amplification on the genomic DNA in the sample using both first and second oligonucleotide primer to produce DNA fragments based on repeat sequences on at least one end of the genomic DNA. The first primer is a softwartion generator including a repeat sequence and at least one non-repeat nucleotide. The second oligonucleotide primer is a 3' fragment generator starting within such a genetic distance that amplification of the genomic DNA can be performed and preferably includes inosine. The method is useful for the genetic analysis of an individual organism, particularly of a species or individual. It is also useful for the rapid and straight forward identification of endangered animals or plants. The present DNA sequence is a 5' variation generator oligonucleotide PCR

Sequence 17 BP; 1 A; 0 C; 8 G; 8 T; 0 U; 0 Other;

0; Gaps 1.5%; Score 16; DB 1; Length 17; 100.0%; Pred. No. 1.5e+02; ative 0; Mismatches 0; Indels 0; Indels 16; Conservative Best Local Similarity Matches 16; Conserv Query Match

AAD17596 standard; DNA; 17 BP. AAD17596

RESULT 243

AAD17596;

10-DEC-2001 (first entry)

5' variation generator oligonucleotide PCR primer #11.

Genomic DNA analysis; 5' variation generator; 3' fragment generator; endangered animal identification; PCR primer; ss.

Unidentified

05-SEP-2001.

03-MAR-2000; 2000EP-00200757.

03-MAR-2000; 2000EP-00200757.

(VHAE-) VAN HAERINGEN LAB BV

Van Haringen H, Van Haringen WA;

WPI; 2001-572636/65.

Analyzing genomic DNA in a sample, useful for analyzing genes of organisms (e.g. a species or individual) or identifying endangered animals or plants, by using oligonucleotide primers comprising universal variable fragments.

Example 1; Page 6; 23pp; English.

The patent discloses a method and associated kit for analysing genomic DNA in a sample. The method comprises conducting a nucleic acid amplification on the genomic DNA in the sample using both first and second oligonucleotide primer to produce DNA fragments based on repeat sequences on at least one end of the genomic DNA. The first primer is a sequences on at least one end of the genomic DNA. The first primer is a feweral nucleotide. The second oligonucleotide primer is a 3' fragment the generator starting within such a generic distance that amplification of the genomic DNA can be performed and preferably includes incesine. The method is useful for the genetic analysis of an individual organism, particularly of a species or individual. It is also useful for the rapid and straight forward identification of endangered animals or plants. The present DNA sequence is a 5' variation generator oligonucleotide PCR. The

Seguence 17 BP; 0 A; 1 C; 8 G; 8 T; 0 U; 0 Other;

0; Gaps 1.5%; Score 16; DB 1; Length 17; 100.0%; Pred, No. 1.5e+02; tive 0; Mismatches 0; Indels Local Similarity 100.0 Matches

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1793 TGTGTGTGTGTGT 1808 Š 셤

2 TGTGTGTGTGTGTGTG 17

'598/c AAD17598 standard; DNA; 17 BP. AAD17598/

X B X B X B X B X

o;

10-DEC-2001 (first entry)

variation generator oligonucleotide PCR primer #13.

Page 115

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The patent discloses a method and associated kit for analysing genomic amplification to the method comprises conducting a nucleic acid second oligonuclectide primer to produce DNA in the sample using both first and second oligonuclectide primer to produce DNA fragments based on repeat sequences on at least one end of the genomic DNA. The first primer is a 5' variation generator including a repeat sequence and at least one nor repeat nucleotide. The second oligonucleotide primer is a 3' fragment the generator starting within such a genetic distance that amplification of the genomic DNA can be performed and preferably includes incosine. The method is useful for the genetic analysis of an individual organism, and straight forward identification of endangered animals or plants. The present DNA sequence is a 5' variation generator oligonucleotide PCR.
                                                                                                                                                                                                                                                                                                              Analyzing genomic DNA in a sample, useful for analyzing genes of organisms (e.g. a species or individual) or identifying endangered animals or plants, by using oligonucleotide primers comprising universal variable fragments.
Genomic DNA analysis; 5' variation generator; 3' fragment generator;
endangered animal identification; PCR primer; ss.
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                                                                                                                                                                                                                                                   Van Haringen WA;
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                                                                                  EP1130114-A1.
                                                  Unidentified.
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This invention describes a novel method for quantitating genetic instability independent of microsatellite alterations by treating comparison galar comparison genomic DNA from tumour cells and genomic DNA from tumour cells and genomic DNA from tumour cells and genomic DNA from tumour cells. The method involves the cells from the same individual with oligonucleotide primers selected from debanine and x = 3-7 (ii) a nucleotide sequence (CG)xRY, where R is as in (i) and Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii) a nucleotide sequence (CG)xRY, where R is as in (i) and x = 3-7, (iii) a nucleotide sequence (CG)xXY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence (CG)xRY, where R is a pyrimidine selected from cytosine, thymine and y is a pyrimidine selected from adenine and guanine and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where R is a pyrimidine selected from adenine and guanine and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, and uracil and x = 6-16, and uracil and x = 6-16, and its a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, and its a pyrimidine selected from cytosine, thymine, and uracil and is useful for detecting genomic instability which are commonly associated with the various stages of neoplastic transformation and carcinogenesis. The method is rapid and simple
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Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                         Claim 4; Col 17-18; 27pp; English.
                                                                                                                                                                             Quantitating genetic instability.
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                                                                                       Stoler D,
                                         (HEAL-) HEALTH RES INC
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22-OCT-1996;
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                                                                                       Anderson G,
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This invention describes a novel method for quantitating genetic instability independent of microsatellite alterations by treating comparison genomic DNA from tumour cells and genomic DNA candinal cells. The method involves the cells from the same individual colls. The method involves the cells from the same individual colls. The method involves the cells from the same individual colls. The object of sequence (CG)xRV, where R is as in (i) and x = 3-7, (ii) a nucleotide sequence (CG)xRY, where R is as in (i) and x = 3-7, (iii) a nucleotide sequence (CG)xXY, where R is a sin (i) and x = 3-7, (iv) a nucleotide sequence (CG)xXY, where R is a pyrimine selected from adenine and guanine and vacil, and x = 5-16, (vii) a nucleotide sequence (CA)xRY, where R is a purine selected from cytosine, (vii) a nucleotide sequence (CA)xRY, where R is a purine selected from adenine and guanine and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, (vii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, and Quanine and x = 6-16, (viii) a nucleotide sequence (CA)xRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, and Quanine and x = 6-16, which are commonly associated with the various stages of neoplastic transformation and carcinogenesis. The method is rapid and simple
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                                                     Claim 4; Col 17-18; 27pp; English.
                    Quantitating genetic instability.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX77492;
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This invention describes a novel method for quantitating genetic instability independent of microsatellite alterations by treating a comparison genomic DNA from tumour cells and genomic DNA (13) a nucleotide sequence (CG) XRY, where R is as in (i) and x = 3-7, (ii) a nucleotide sequence (CG) XRY, where R is as in (i) and x = 3-7, (iii) a nucleotide sequence (CG) XRY, where R is as in (i) and x = 3-7, (iii) a nucleotide sequence (CG) XRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iv) a nucleotide sequence (CG) XRY, where R is a pyrimidine selected from cytosine, thymine and guanine and Y is a pyrimidine selected from cytosine, (vi) a nucleotide sequence (CA) XRY, where R is a purine selected from cytosine, (vii) a nucleotide sequence (CA) XRY, where R is a purine selected from denine and guanine and x = 6-16, (vii) a nucleotide sequence (CA) XRY, where R is a pyrimidine selected from cytosine, (viii) a nucleotide sequence (CA) XRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination of the primers. The method is useful for detecting genomic instability which are commonly associated with the various stages of neoplastic transformation and carcinogenesis. The method is rapid and simple
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel method for quantitating genetic instablity independent of microsatellite alterations by treating a comparison pair comprising genomic DNA from tumour cells and genomic DNA from normal cells and genomic DNA from normal cells. The method involves the cells from the same individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primer; quantitation; genetic instability; tumour cell; detection; neoplastic transformation; carcinogenesis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.5%; Score 16; DB 1; Length 18; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18 BP; 8 A; 9 C; 0 G; 0 T; 1 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Col 29-30; 27pp; English.
                  Claim 4; Col 31-32; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quantitating genetic instability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Basik M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1793 TGTGTGTGTGTGTGTG 1808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX77490 standard; DNA; 18 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HEAL-) HEALTH RES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-357197/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US5912147 primer 34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US5912147-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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with oligonucleotide primers selected from (i) a nucleotide sequence (CG) xRG, where R is a purine selected from adenine and guanine and x = 3-7, (ii) a nucleotide sequence (CG) xRY, where R is as in (i) and Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii) a nucleotide sequence (CG) xRX, where R is as in (i) and x = 3-7, (iv) a nucleotide sequence (CG) xRY, where R is a pin did selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence (CG) xRY, where R is a purine and guanine and contine and guanine and cytosine, where R is a purine selected from adenine and guanine and x = 6-16, (vii) a nucleotide sequence (CA) xRY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination of the primers. The method is useful for detecting genomic instability which are commonly associated with the various stages of neoplastic transformation and carcinogenesis. The method is rapid and simple \$

Seguence 18 BP; 8 A; 9 C; 0 G; 1 T; 0 U; 0 Other;

Gape ; 1.5%; Score 16; DB 1; Length 18; 100.0%; Pred. No. 1.6e+02; tive 0; Mismatches 0; Indels 1793 TGTGTGTGTGTGTG 1808 Conservative Local Similarity les 16; Conserv Query Match Matches ઠે

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16 rererererererei 1 a

ABZ89513 standard; DNA; 20 BP ABZ89513; RESULT 249

17-OCT-2003 (first entry)

Human oligonucleotide sequence.

Human, antisense, lung dysfunction; nasal airway dysfunction, antinflammatory; antiallergic; antiaflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy, antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens.

WO200285308-A2.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P

(EPIG-) EPIGENESIS PHARM INC.

Katz E, Pabalan J, Aguilar D; i Y, Sandrasagra A, Ka Tang L, Shahabuddin S; Li Y, Nyce JW, L Miller S,

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid ubiquinone

Disclosure; SEQ ID NO 4755; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions,

1.5%; Score 15.8; DB 1; Length 19;

Sequence 19 BP; 2 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

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junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunctions, or regions within 2-10 nucleotides of nasal airway dysfunction and a second active agent comprising an antinflammatory steroid and ubiquinone. A composition of the invention has antinflammatory steroid and ubiquinone. A composition of the invention antinflammatory antialergic, antiasthmatic, hypotensive.

In antinflammatory and cytostatic activity. The composition may have a use in antiaense gene therapy. The composition is useful for treating preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung aurfactant in a subject s tissue, or treating bronchconneriction, lung allergies, or a respiratory disease or condition. Note: The sequence date for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNNs by using an aggregate of mRNAs and a plural type of abelied reverse transcription primers (GENESED files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of CDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                                                                                                                                                                                                                                                               1.5%; Score 16; DB 1; Length 20; 100.0%; Pred. No. 1.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 3 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 5; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1865 TTTTTTTTTTTT 1880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93JP-00112515.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ75552 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-AUG-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-018287/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JP06303997-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ75552;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 250
           88888888888888888888888888888888
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Detection; polymorphism; perfect compound simple sequence repeat; adaptor directed primer; genome; genetic; fingerprinting; amplified fragment length polymorphism assay; microsatellite regigenetic trait marking; germplasm comparisons; 5'-anchored; ss.

5'-anchored simple sequence repeat primer HVH(TG)7.5.

(first entry)

28-JAN-1997

AAT27914;

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Gaps

AAT27914 standard; DNA; 18 BP.

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 screening a library of bovine Mbol DNA fragments of between 250 and 500 clones that an (RC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100,000. The sequence information construction and indexed herein (see below). The sequence information constructed pcz primers for in vitro amplification of the corresp. microsatellite (using the program OPTTRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait lost, or genes involved the determinism of economic trait craits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                  PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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Sequence 40 BP; 7 A; 1 C; 13 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                   Sequence of a microsatellite from clone TGLA53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Table 7; Page 369; 517pp; English.
                                                             1865 TITITATITITA 1883
                                                                                                1 rrrrrrrrrrrrrrrrrrrr 19
                                                                                                                                                                                   AAQ34094 standard; DNA; 40 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92WO-US000340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91US-00642342
                                                                                                                                                                                                                                                    (revised)
(first entry)
                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1992-284684/34.
              Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .5-JAN-1992;
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                                                                                                                                                                                                                                                    25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-AUG-1992.
                                                                                                                                                                                                                                                                                                                                                                                            30s taurus
                                                                                                                                                                                                                     AAQ34094;
                                                                                                                                                                    AAQ34094/C
                                                                                                                                                    RESULT 251
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Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme; target; substrate; catalyst; modulation; expression; Raf gene; delivery; screening; identification; synthesis; deprotection; purification; cancer; inflammation; psoriasis; non-hepatic ascites; infection; genetic drift; restenosis; rheumatoid arthritis; ss.
                                                                                                                                                                                                                                                                             Human C-raf target site nucleotide position 2899.
                                                                        1790 TATTGTGTGTGTGTGT 1807
                                                                                                       1 HVHTGTGTGTGTGTGT 18
                                                                                                                                                                                     BP
                                                                                                                                                                                   AAV91399 standard; RNA; 17
                                                                                                                                                                                                                                                     (first entry)
Query Match
Best Local Similarity 83.5.
Local Similarity 83.5.
Local Similarity
                                                                                                                                                                                                                                                     18-FEB-1999
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                                                                                                                                                                           AAV91399
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Gaps

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1814 ATATATATATATATGTACA 1832

39 ATATATATATATACACA 21

RESULT 252 AAT27914

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Gaps

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1.5%; Score 15.6; DB 1; Length 18; 83.3%; Pred. No. 1.8e+02; tive 3; Mismatches 0; Indels

Sequence 18 BP; 0 A; 0 C; 7 G; 8 T; 0 U; 3 Other;

germplasm comparisons

Detecting polymorphisms between 2 nucleic acid samples, esp. in microsatellite regions, comprises digesting the nucleic acid to generate fragments, ligating adaptor segments to their ends, amplifying them using primer directed amplification and comparing the prods. to detect differences. The primers used in the amplification comprise a primer directed primer, comprising of a perfect cpd. simple sequence repeat (SSR), and an adaptor directed primer, comprising a sequence complementary to an adaptor segment. The present sequence is an example of a SSR primer, which is segment. The gramming degenerate nucleotides. The method represents a modified amplified fragment length polymorphism assay, which is particuseful for general fingerprinting, i.e. for genetic trait marking and

Modified amplified fragment length polymorphism assay – for detection of polymorphism esp. in micro:satellite regions.

Example 1; Page 77; 173pp; English.

(DUPO) DU PONT DE NEMOURS & CO B I.

Vogel JM;

Morgante M,

WPI; 1996-277795/28.

95WO-US015150

21-NOV-1995; 28-NOV-1994;

WO9617082-A2.

Synthetic.

06-JUN-1996

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capable of modulating a process in a biological system. The method capable of modulating a process in a biological system. The method comparises: (a) introducing into the system a random library of nucleic acid catalysts (NAC) having a substrate binding domain (SBD), comprising a random sequence, and a catalytic domain (CD); and (b) identifying NAC in systems where modulation has occurred and/or determining the sequence of a least part of the SBDs in such systems. Nucleic acid molecules with endomuclease activity and catalylic activity, from the present invention, are used to modulate gene expression in plant and mammalian cells and to cleave target nucleic acid, particularly for treating systemic diseases caused by specific RNA, eg. cancer, inflammation, psoriasis, non-hepatic ascites and infection. They may also be used to detect genetic drift and ascites and infection, they may also be used to detect genetic drift and catally and condition ascociated with the level of c-raf. Introduction genetized to generally any condition associated with the level of c-raf. Introduction of such systems and activity. AAV90922 to AAV93877 represent NACs that can be used in the method, specifically for modulating the expression of a Raf gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying new catalytic nucleic acid that modulates selected processes - especially ribozymes that cleave Raf RNA for treating cancer, restenosis, and also new ribozymes and modified nucleoside triphosphates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17 BP; 3 A; 0 C; 1 G; 0 T; 13 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used as antiviral agents and synthons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 177; Page 154; 259pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1866 TITIATITITIA 1882
                                                                                                                                                                                                                                                                                                                                                  Jarvis T, Matulic-Adamic J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV21967 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                 (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 17.6
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-009494/01.
                    Homo sapiens
                                                    WO9850530-A2
                                                                                                                       05-MAY-1998;
                                                                                                                                                                                                                           02-OCT-1997;
02-OCT-1997;
05-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                     rhompson J,
                                                                                       12-NOV-1998
                                                                                                                                                        09-MAY-1997
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AAV21967
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DE Nucl
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ic J. Reynolds M. Kisich K, Bellon L Mcswiggen JA, Karpeisky A, Burgin A; Beaudry A, Sweedler D;

Beigelman L, Md J, Workman CT,

97US-0046059P. 97US-0051718P. 97US-0051718P. 97US-0061321P. 97US-0061324P. 97US-006324P. 97US-0063224P.

98WO-US009249

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This antisense oligonucleotide is nuclease resistant and can be used in the treatment of animals, including humans, having a bacterial infection. The treatment comprises administration of such nuclease resistant oligonucleotides, targeted to a nucleic acid or protein of the bacterium, and formulated with a carrier. A compound comprising this nuclease central targets or resistant oligonucleotide can be covalently linked to an antibitotic. The method is used to treat infections by a wide variety of Gram-positive and Gram-negative, or acid-fast, bacteria, in human and veterinary medicine. The methods are particularly used in immuno-compromised individuals (e.g. patients with acquired immunodeficiency syndrome or those receiving chemotherapy or radiation therapy), optionally in combination with, or fused to, antiviral or other antimicrobial oligonucleotides. Apart from therapt codes, beverages and indistrial processes. The oligonucleotides are specific for bacteria, without affecting metabolism of numanian cells. They may also activate Rhase H and have a general, one specific immune-stimulating effect. The oligonucleotides can be administered orally, intranasally, rectally, topically or by injection, or parameter or polyamine) that
                                                                                                                                                                                                                                                                                                                                                                                   Treating bacterial infections in humans or animals with oligo:nucleotide(s) - resistant to nuclease and targetted to bacterial nucleic acid or proteins, also conjugates of these oligo:nucleotide(s) with antibiotics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nuclease resistant antisense oligo NBT 140 targeted against (AT)9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nuclease resistant; bacterial infection; antibiotic; target; veterinary medicine; treatment; human; industrial process; bacterial control; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.5%; Score 15.4; DB 1; Length 18; 94.1%; Pred. No. 1.9e+02; vative 0; Mismatches 1; Indels
            Nuclease resistant; bacterial infection; antibiotic; targe
veterinary medicine; treatment; human; industrial process;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18 BP; 9 A; 0 C; 0 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                             OLIG-) OLIGOS ETC & OLIGOS THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 49; Page 87; 163pp; English.
                                                                                                                                                                                                                                                                                                                   Thompson TL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1814 ATATATATATATGTA 1830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17
                                                                                                                                                                                                    97WO-US012961
                                                                                                                                                                                                                                         96US-00685575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV21967 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 94.1
es 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enhances cellular uptake
                                    veterinary medicine; t
bacterial control; ss.
                                                                                                                                                                                                                                                                                                                   Arrow A, Dale RMK,
                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-120687/11.
                                                                                                                                                                                                      23-JUL-1997;
                                                                                                                                                                                                                                           24-JUL-1996;
                                                                                                                                409803533-A1
                                                                                                                                                                  29-JAN-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV21967;
                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
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ID AAV2
XX AAV2
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KW Veck
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à
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1.5%; Score 15.4; DB 1; Length 17; 17.6%; Pred. No. 1.8e+02; stive 13; Mismatches 1; Indels

unumanunugunun 17

Nuclease resistant antisense oligo NBT 140 targeted against (AT)9.

(first entry)

14-JUL-1998

AAV21967;

WO200129262-A2.

26-APR-2001

Thompson TL;

96US-00685575 97WO-US012961

Homo sapiens

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This antisense oligonucleotide is nuclease resistant and can be used in the treatment of animals, including humans, having a bacterial infection. The treatment comprises administration of such nuclease resistant of coligonucleotides, targeted to a nucleic acid or protein of the bacterium, and formulated with a carrier. A compound comprising this nuclease resistant oligonucleotide can be covalently linked to an antibiotic. The method is used to treat infections by a wide variety of Gram-positive and Gram-negative, or acid-fast, bacteria, in human and veterinary medicine. The methods are particularly used in immuno-compromised individuals (e.g. patients with acquired immunodeficiency syndrome or those receiving chemotherapy or radiation therapy), optionally in combination with, or fused to, antiviral or other antimicrobial oligonucleotides. Apart from therapy or oligonucleotides can be used to control bacteria in laboratory cultures, foods, beverages and industrial processes. The oligonucleotides are specific for bacteria, without affecting metabolism on mammanian cells. They may also activate Rhase H and have a general, one specific immune stimulating effect. The oligonucleotides can be administered orally, intranasally, rectally, topically or by injection, enhances celling a magent (e.g. carbohydrate or polyamine) that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; lesch.Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis imperfecta; autoimmune disease; acute intermittent porphyria; rheumancid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                           Treating bacterial infections in humans or animals with oligo:nucleotide(s) - resistant to nuclease and targetted to bacterial nucleic acid or proteins, also conjugates of these oligo:nucleotide(s) with antiblotics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.5%; Score 15.4; DB 1; Length 18; Best Local Similarity 94.1%; Pred. No. 1.9e+02; Matches 16; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 BP; 9 A; 0 C; 0 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                          (OLIG-) OLIGOS ETC & OLIGOS THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP specific lower PCR primer SEQ ID 310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 49; Page 87; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1814 ATATATATATATGTA 1830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH37514 standard; DNA; 18 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enhances cellular uptake
                                                                                                                                                                                                                                                                                    Dale RMK,
                                                                                                                                                                                                                                                                                                                               WPI; 1998-120687/11
                                                                 WO9803533-A1
                                                                                                                                                      3-JUL-1997;
                                                                                                                                                                                                24-JUL-1996;
                                                                                                           29-JAN-1998
                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH37514;
                                                                                                                                                                                                                                                                                       Arrow A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 256
AAH37514
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Sequences AAH17205 - AAH40944 represent PCR primers, single nucleotide continues of single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the includes kits for determining the presence or absence of a SNP, using the cligonucleotides of the invention. The PCR primers are used to amplify a coligonucleotides of the invention. The PCR primers are used to amplify a coligonucleotides are useful for genotyping a nucleic acid sample by performing a single-nucleotide primer extension reaction. The cligonucleotides are useful for determining the presence, absence or cligonucleotides are useful for determining the presence, absence or identity of a SNP and for genotyping nucleic acid samples, for e.g. to assess by association analysis the genotype of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include diseases e.g. agammaglobulinaemia, diabetes insipidus, lesch-Nyhan syndrome, muscular dystrophy, familial hypercholesterolaemia, polycystic kidney disease, osteogenesis imperfecta and acute intermittent porphyria. Phenotypic traits also include symptoms of or susceptibility to multifactorial cates and infection and cute intermittent porphyria. Phenotypic cinflammation, cancer, nervous system diseases and infection and microorganism. The method is also useful in forensic investigations and microorganism. The method is also useful in forensic investigations and containing DNA sequence
                                                                                                                                                                                                                                                                                                             New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody-induced cell lysis; cancer; immunostimulatory; CD20; angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 BP; 0 A; 2 C; 9 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunostimulatory nucleic acid SEQ ID NO: 85.
                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 51; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1794 GIGIGIGIGIGIGIGI 1810
                                                                                                                                                                                       (ORCH-) ORCHID BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grererererererece 17
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                                                                                                               .3-OCT-2000; 2000WO-US028436
                                                                                                                                                                                                                                Pohl M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 94.1
Matches 16, Conservative
                                                                                                                                                                                                                                                                      WPI; 2001-290930/30.
                                                                                                                                                                                                                                  Picoult-Newburg L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-APR-2002
                                                                                                                                                   15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                     acid sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL38718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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ABL38718
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Gaps ô Location/Qualifiers

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The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal call carcinoma, bladder cancer, bone cancer, brain and central nervous system (CNS) cancer, pression cancer, colon and rectum cancer, connective tissue cancer, oesophageal cancer, colon and rectum cancer, larynx cancer, leukaemia, liver cancer, lung cancer, kidney cancer, larynx cancer, pancreatic cancer, lung cancer, rad cavityr cancer, ovarian cancer, stomach cancer, testicular cancer, rad cavityr cancer, ovarian cancer, stomach cancer, testicular cancer, and uterine cancer. The
                                                                                                                                                                                                                                                                                               Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detection; polymorphism; perfect compound simple sequence repeat; adaptor directed primer; genome; genetic; fingerprinting; amplified fragment length polymorphism assay; microsatellite region; genetic trait marking; germplasm comparisons; 5'-anchored; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.5%; Score 15.4; DB 1; Length 18; 94.1%; Pred. No. 1.9e+02; ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5'-anchored simple sequence repeat primer DBD(AC)7.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18 BP; 9 A; 0 C; 0 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 116; 312pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1814 ATATATATATATGTA 1830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT27912 standard; DNA; 18 BP.
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                                                                                   22-JUN-2001; 2001WO-US020154.
                                                                                                                           22-JUN-2000; 2000US-0213346P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.5%;
Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                                                                                                                        (IOWA ) UNIV IOWA RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JAN-1997 (first entry)
                                                                                                                                                                                                                     Hartmann
                                                                                                                                                                                                                                                              WPI; 2002-154611/20.
                                                                                                                                                                                                                                                                                                                                                                             developing cancer,
WO200197843-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        409617082-A2
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                                        27-DEC-2001
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                                                                                                                                                                                                                     Weiner G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT27912;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to methods for treating or preventing cancer involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce axpression of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal cell carcinoma, bladder ancer, bore cancer, baren and central nervous system (CNS) cancer, breast cancer, cervical cancer, colon and rectum cancer, connective tissue cancer, cervical cancer, colon and rectum cancer, connective tissue cancer, leukacimia, liver cancer, lung cancer, Hodgkin's lymphoma, non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian cancer, pancreatic cancer, prostate cancer, rhaddomyosarcoma, skin cancer, esticular cancer, inhaddomyosarcoma, skin present sequence is an immunostimular cancer, and uterine cancer. The exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                          Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibody-induced cell lysis; cancer; immunostimulatory; CD20; angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.5%; Score 15.4; DB 1; Length 18; 94.1%; Pred. No. 1.9e+02; rative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mod_base= OTHER
/note= "phosphorothioate backbone"
                                                                    /note= "phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18 BP; 9 A; 0 C; 0 G; 9 T; 0 U; 0 Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunostimulatory nucleic acid SEQ ID NO: 85.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 116; 312pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
    1. .18
/*tag= a
/mod_base= OTHER
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                                                                                                                                                                                                       22-JUN-2001; 2001WO-US020154.
                                                                                                                                                                                                                                                  22-JUN-2000; 2000US-0213346P.
                                                                                                                                                                                                                                                                                               (IOWA ) UNIV IOWA RES FOUND
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                              Weiner G, Hartmann G;
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-154611/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    developing cancer.
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                                                                                                               WO200197843-A2
         modified base
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Query Match

Best Loca Matches

RESULT 258

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Gaps

Sequence 41 BP; 9 A; 0 C; 11 G; 21 T; 0 U; 0 Other;

the invention

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Detecting polymorphisms between 2 nucleic acid samples, esp. in microsatellite regions, comprises digesting the nucleic acid to generate fragments, ligating adaptor segments to their ends, amplifying them using primer directed amplification and comparing the prods. to detect differences. The primers used in the amplification comprise a primer observable of a perfect cpd. simple sequence repeat (SSR), and an adaptor directed primer, comprising a sequence complementary to an adaptor segment. The present sequence is an example of a SSR primer, which is a flanked ant its 5°-end by degenerate nucleotides. The method represents a modified amplified fragment length polymorphism assay, which is particuuseful for genome fingerprinting, i.e. for genetic trait marking and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides the protein and coding sequences of human zinc finger protein 14. The sequences can be used in the treatment of cancer, haemopathy, HIV infection, immunological diseases and inflammation. The present sequence is a probe for the coding sequence of
                                                                             Modified amplified fragment length polymorphism assay - for detection of polymorphism esp. in micro:satellite regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human zinc finger protein 14 for diagnosing and treating malignant neoplasm, hemopathy, human immunodeficiency virus infection, immunological diseases and various inflammations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, zinc finger protein 14; cancer; haemopathy, HIV infection; immunological disease; inflammation; gene therapy; probe; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 1.4%; Score 15.2; DB 1; Length 18; 1. Similarity 93.8%; Pred. No. 2e+02; 15; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human zinc finger protein 14 coding sequence probe #1.
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18 BP; 8 A; 7 C; 0 G; 0 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
                                                                                                                                        Example 1; Page 76; 173pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 6; Page 20; 37pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1799 IGIGIGIGIGIGIA 1814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH77495 standard; DNA; 41 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-MAR-2000; 2000CN-00111978
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             Vogel JM;
                                                                                                                                                                                                                                                                                                                                                                             germplasm comparisons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-565570/63.
                                                WPI; 1996-277795/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-SEP-2001
               Morgante M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH77495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local
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Gaps

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The sequence is that of a bovine microsatellite sequence obtd. by

screening a library of bovine Mbol DNA fragments of between 250 and 500

by with an (AC)15 and a (TC)15 oligomucleotide probe. One out of 50

clones cross-hybridised. Assuming independent distribution of

microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites

in the bovine genome is estimated at >100,000. The sequence information

for a. 230 such bovine microsatellites is summarised in the

specification and indexed herein (see below). The sequences upstream and

specification and indexed herein (see below). The sequences upstream and

commerces of the microsatellite sequence were used to generate the

required PCR primers for in vitro amplification of the corresp.

crequired PCR primers for in vitro amplification of the corresp.

microsatellite (using the program OPTIPRIM). The microsatellites may be

microsatellity individuals, for parentage testing, and in the genetic

mapping of economic trait loci, or genes involved the determinism of

economically important traits esp. in cattle, to allow selective

breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                         PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                           ö
/ Match 1.4%; Score 15.2; DB 1; Length 41; Local Similarity 85.0%; Pred. No. 2.8e+02; les 17; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.4%; Score 15; DB 1; Length 15;
100.0%; Pred. No. 1.8e+02;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15 BP; 0 A; 0 C; 8 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                          Microsatellite sequence from clone TGLA171.
                                                                              1813 TATATATATATATACA 1832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rable 7; Page 235; 517pp; English.
                                                                                                          40 TATAAATTTATATATACA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1794 GIGTGTGTGTGTG 1808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92WO-US000340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91US-00642342
                                                                                                                                                                                                            AAQ33764 standard; DNA; 15
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Best Local Similarity 100.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                        (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Georges M, Massey JM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JAN-1991;
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02-FEB-1993
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                                                                                                                                                                                                                                                       AAQ33764;
               Query Match
                                     Best Loca
Matches
                                                                                                                                                                                RESULT 261
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GTGTGTGTGTGTGTG

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Use of isolated gene transcripts - useful for developing products for the diagnosis, prognosis and treatment of cancers, particularly colon and pancreatic cancer. Tag sequence; colorectal cancer; pancreatic cancer; colon cancer; diagnosis; prognosis; treatment; ss. rag sequence of a transcript increased in pancreatic cancer. Claim 13; Page 69; 120pp; English AAX31678 standard; DNA; 15 BP (UYJO) UNIV JOHNS HOPKINS. Vogelstein B, Kinzler KW WPI; 1999-070161/06. Homo sapiens. 20-MAY-1998; 21-MAY-1997; WO9853319-A2 21-MAY-1999 26-NOV-1998 AAX31678;

98WO-US010277 97US-0047352P

(first entry)

; 0 differentially expresent tag sequences of transcripts that are differentially expressed in colorectal cancer, in pancreatic cancer, or in both. The tag sequences can be used to identify genes by matching the tag to a gen data base member, or by using the tag sequences as probes to isolate unidentified genes from cDNA libraries. The tag sequences can also be used in a method for diagnoshing colon or pancreatic cancer in a sample suspected of being neoplastic. The method comparises comparing the level of at least one transcript in a first sample of a tissue to a being neoplastic and the second sample is a colonic tissue suspected of being neoplastic and the second sample is a normal human colonic tissue. The transcript is identified by a tag selected from AAX30947-31815. The methods of the invention can be used in the diagnosis, prognosis and Gaps Length 15; Sequence 15 BP; 2 A; 4 C; 2 G; 7 T; 0 U; 0 Other; treatment of cancer Query Match

. 0 0; Indels 1.4%; Score 15; DB 1; Le 100.0%; Pred. No. 1.8e+02; ive 0; Mismatches 0; Best Local Similarity 100. Matches 15, Conservative

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AAH46010 standard; DNA; 15 BP RESULT 263 AAH46010

12-SEP-2001

AAH46010;

Synthetic oligonucleotide 10 SEXUXEX

Composition comprising synthetic oligonucleotides which comprise multiple repeats of dinucleotides such as GT, TG useful for treating cancer by inducing cell cycle arrest, inhibiting proliferation, activating Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis; cell cycle arrest; cell proliferation; caspase; cytokine; interleukin; tumour necrosis factor; INF; cancer; carcinoma; sarcoma; leukemia; lymphoma; se. Claim 5; Page 17; 77pp; English (BION-) BIONICHE LIFE SCI INC. 13-DEC-1999; 99US-0170325P. 29-AUG-2000; 2000US-0228925P. 12-DEC-2000; 2000WO-CA001467 Phillips NC, Filion MC; WPI; 2001-398150/42 WO200144465-A2 21-JUN-2001 Synthetic.

. ö Query Match

1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels

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ABK32632 standard; DNA; 15 BP. 23-APR-2002 (first entry)

Human pancreatic cancer SAGE tag #184.

colon cancer; colorectal cancer; pancreatic cancer; SAGE tag; analysis of gene expression; diagnostic; prognostic; probe; cancer marker; ss. serial

Homo sapiens

US6333152-B1

The present sequence is that of a synthetic oligonucleotide useful to the invention. The invention relates to a composition, comprising a 2 to 20 invention. The invention relates to a composition, comprises multiple base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple crepeats of dinucleotides such as GTT, TG, etc., according to specific formula and having cytostatic activity. The oligonucleotide compositions are useful for inducing cell cycle arrest, inhibition of proliferation, are useful for inducing cell cycle arrest, inhibition of proliferation, activation of caspases and induction of apoptosis or production of cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumnour necrosis factor (INF)-alpha by immune system cells, in an animal having and secondary sarcoma such as, leukemia, lymphoma, breast, prostate, colorectal, ovarian or bone cancer. The compositions induce apoptosis induce apoptosis is induce apoptosis.

Independent of Fas, p53/p21, p21/waf-1/CIP, p15iink4B), p16(ink4), drug resistance, caspase 3, transforming growth factor (IGF)-beta 1 receptor

Sequence 15 BP; 0 A; 0 C; 8 G; 7 T; 0 U; 0 Other;

Claim 7; Col 17; 13pp; English.

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that has the same sequence as a mRNA found in humans and is a SAGE (sexial analysis of gene expression) ag comprisiting a single stranded probe containing at least 10 consecutive mucleotides. SAGE tags, are diagnostic and prognostic markers of cancer, especially of the colon and pancreas. ARX1100-ARX12770 represent human colon and pancreatic cancer SAGE tags of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, comprises determining the presence of five thymidine-adenine repeats in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; ds; UGT1A1; promoter; Gilbert's syndrome; hyperbilirubinaemia; uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome; UGT; polymorphism detection; TA repeat; glucuronidation; Irinotecan; TAS-103; xenobioci
                                                                                                                                                                                                                                                                             The invention relates to an isolated, purified human nucleic acid (I)
                                                                                                                                                                                                New human nucleic acid containing specific SAGE tags, useful as diagnostic markers for cancer, also derived probes.
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15 BP; 2 A; 4 C; 2 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human UGTlal promoter polymorphism (TA)8 repeat.
                                                                                                                                    Vogelstein B, Kinzler KW, Zhang L,
                                                                                                                                                                                                                                               Disclosure; Col 83; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Di Rienzo A, Iyer L, Ratain MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2231 CATGITIGCACCITY 2245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABK90419 standard; DNA; 16 BP
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                                             98US-00081646.
                                                                         98US-00081646.
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                                                                                                     (UYJO ) UNIV JOHNS HOPKINS
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                                                                                                                                                                   WPI; 2002-153821/20.
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                                         20-MAY-1998;
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                                                                         20-MAY-1998;
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The invention relates to detecting (M1) polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter by determining the presence of five thymidine-adenine (TA) respeats in the promoter, where the presence of the gene. The method is used for detecting polymorphisms in a UGT gene promoter, preferably a UGT I (UGTIA1) gene promoter. (M1) is useful for screening individuals for variation in glucuronidation at UGT gene promoter. (M1) is a UGT gene promoter or TAS-103) are glucuronidated by UGT (Preferably UGT (e.g. Irinotecan or TAS-103) are glucuronidated by UGT (Preferably UGT (e.g. Irinotecan or TAS-103) are glucuronidated by UGT (Preferably UGT (e.g. Irinotecan or TAS-103) are glucuronidated by UGT (Preferably UGT (e.g. Irinotecan or TAS-103) are glucuronidated by UGT (Preferably UGT (e.g. Irinotecan or TAS-103) are glucuronidated by UGT (Preferably UGT (INT)) and the activity of the drug is effected by its level of glucurodination. The method operation of a UGT gene promoter. Thus the DNA and determining the number of TA repeats of in the promoter. The DNA is amplified by a polymerase chain reaction and undividual promoter. The DNA is amplified by a polymerase chain reaction and the number of TA repeats is determined by gel electrophoreals or by a CGT (TA) 5, (TA) 5, (TA) 5, (TA) 5, (TA) 5, (TA) 8, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, dŝ, UGTIA1, promoter, Gilbert's syndrome, hyperbilirubinaemia, uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome, UGT, polymorphism detection; TA repeat, glucuronidation; Irinotecan, TAS-103; xenobiotic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.4%; Score.15; DB 1; Length 16; Best Local Similarity 100.0%; Pred. No. 1.9e+02; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16 BP; 8 A; 0 C; 0 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human UGT1al promoter polymorphism (TA)8 repeat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1813 TATATATATATAT 1827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABK90419 standard; DNA; 16 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 266
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The invention relates to detecting (M1) polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter by determining the presence of five thymidine-adenine (TA) respeats in the promoter, where the presence of the five TA repeats correlates with increased expression of the gene. The method is used for detecting polymorphisms in a UGT gene promoter. The method is used for detecting polymorphisms in useful for screening individuals for variation in glucuronidate. (M1) is useful for screening individuals for variation in glucuronidate (TA) and the activity for optimising drug desages for a patient, where the drugs activity, for optimising drug desages for a patient, where the drugs activity (UGTIA) and the activity of the drug is effected by its level of glucurodination. The method preferably involves obtaining DNA from an individual, amplifying all or part of a UGT gene promoter. Thus the DNA and determining the number of TA repeats in the DNA and determining the number of TA repeats of details or by consisting of five TA repeats is determined by gel electrophoresis or by sequencing the amplified DNA. The polymorphism comprises an allele consisting of five TA repeats (TA)5, (TA)6, (TA)5, (TA)6, (TA)5, (TA)7, (TA)5, (TA)8, (TA)6, (TA)6, (TA)7, (TA)6, (TA)6, (TA)6, (TA)7, (TA)6, (TA)6, (TA)6, (TA)7, (TA)6, (TA)6, (TA)6, (TA)7, (TA)6, (TA)6, (TA)6, (TA)6, (TA)6, (TA)7, (TA)6, (TA)6, (TA)6, (TA)7, (TA)6, (T
                                                       Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, comprises determining the presence of five thymidine-adenine repeats in
                                                                                                                                                                                                         Claim 7; Col 17; 13pp; English.
WPI; 2002-588597/63.
                                                                                                                                                  the promoter.
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0; Gaps Query Match 1.4%; Score 15; DB 1; Length 16; Best Local Similarity 100.0%; Pred. No. 1.9e+02; Matches 15; Conservative 0; Mismatches 0; Indels 0; Indels Sequence 16 BP; 8 A; 0 C; 0 G; 8 T; 0 U; 0 Other;

1813 TATATATATATAT 1827 16 TATATATATATAT 2 g ઠે

AAL50677 standard; DNA; 16 BP. 16-JAN-2003 (first entry) AAL50677;

Human uridine diphosphate glucuronosyltransferase gene polymorphism #11.

Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat; uridine diphosphate glucuronosyltransferase gene promoter; UGTLA1; drug dosage optimisation; xenobictic sensitivity.

US2002115097-A1

22-AUG-2002.

01-FEB-2002; 2002US-00061693.

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Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing druq desages for a patient, involves determining number of thymidine-adenine repeats in the promoter.
                                                                                                                                                                                                                                                                                                                        The invention comprises a method for detecting polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter (preferably UGT1A1). The method involves determining the number of thymidine-adenine (TA) repeats in the promoter - as the number of TA repeats correlates with expression of the UGT gene. The method of the invention is useful for detecting polymorphisms in a UGT gene promoter. The method of the invention is useful invention is also useful in optimising drug dosages and predicting an intelvidual s semislivity to xenobiotics for drugs and xenobiotics that are glucuronidated by UGT. The present DNA sequence represents a UGT gene TA repeat polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16 BP; 8 A; 0 C; 0 G; 8 T; 0 U; 0 Other;
                                                                                             Rienzo AD, Iyer L, Ratain MJ;
                                                                                                                                                                                                                                                                                  Claim 7; Page 9; 13pp; English.
  99US-00251274.
                                                  (ARCH-) ARCH DEV CORP.
                                                                                                                                           WPI; 2002-740095/80.
16-FEB-1999;
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1813 TATATATATATAT 1827 1 TATATATATATAT 15 ઠે В

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0; Gaps

Query Match
1.4%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels

AALS0677 standard; DNA; 16 BP. RESULT 268 AAL50677

AAL50677; CXSXLLLLXBXBXBXBXBXBXXXXXXXXXXXXCCX

Human uridine diphosphate glucuronosyltransferase gene polymorphism #11.

(first entry)

16-JAN-2003

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Human, polymorphism; TA repeat, ds; UGT; thymidine-adenine repeat; uridine diphosphate glucuronosyltransferase gene promoter; UGTIA1; drug dosage optimisation; xenobiotic sensitivity.

Homo sapiens.

US2002115097-A1.

01-FEB-2002; 2002US-00061693. 99US-00251274. 16-FEB-1999;

(ARCH-) ARCH DEV CORP.

Rienzo AD, Iyer L, Ratain MJ;

WPI; 2002-740095/80.

Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, involves determining number of thymidine-adenine repeats in the promoter.

Claim 7; Page 9; 13pp; English.

The invention comprises a method for detecting polymorphisms in a uridine

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diphosphate glucuronosyltransferase (UGT) gene promoter (preferably UGTIA1). The method involves determining the number of thymidine-adenine (TA) repeats in the promoter - as the number of TA repeats correlates with expression of the UGT gene. The method of the invention is useful for detecting polymorphisms in a UGT gene promoter. The method of the invention is also useful in optimising drug desages and predicting an individual's sensitivity to xenobiotics for drugs and xenobiotics that are glucuronidated by UGT. The present DNA sequence represents a UGT gene TA repeat polymorphism
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Sequence 16 BP; 8 A; 0 C; 0 G; 8 T; 0 U; 0 Other;

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1.4%; Score 15; DB 1; Length 16; 100.0%; Pred. No. 1.9e+02; Ative 0; Mismatches 0; Indels
                                                            1813 TATATATATAT 1827
                                                                                        16 rarararararar 2
                              15; Conservative
                Local Similarity
 Query Match
                              Matches
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0; Gaps

RESULT

ABK90422 standard; DNA; 17 BP. 05-NOV-2002 (first entry) ABK90422;

Human UGTlal promoter polymorphism (TA)7 repeat region.

Human, ds, UGT1A1, promoter, Gilbert's syndrome, hyperbilirubinaemia, uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome; UGT; polymorphism detection; TA repeat, glucuronidation; Irinotecan; TAS-103; xenobiotic.

Homo sapiens.

US6395481-B1.

28-MAY-2002.

99US-00251274. 16-FEB-1999;

99US-00251274. 16-FEB-1999;

(ARCH-) ARCH DEV CORP.

Iyer L, Ratain MJ; WPI; 2002-588597/63. Di Rienzo A,

Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, comprises determining the presence of five thymidine-adenine repeats in the promoter.

Example 6; Col 11; 13pp; English.

The invention relates to detecting (M1) polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter by determining the presence of five thymidine adenine (TA) repeats in the promoter, where the presence of the five TA repeats correlates with increased a UGT gene promoter, preferably a UGT IG (UGTA1) gene promoter. (M1) is useful for screening individuals for variation in glucuronidation activity, for optimising drug desages for a patient, where the drugs (e.g. Irinotecan or TAS-103) are glucuronidated by UGT (preferably UGTIA1) and the activity of the drug is effected by UGT (preferably UGTIA1) and the activity of the drug is effected by its level of glucurodination. The method preferably involves obtaining DNA from an individual, amplifying all or part of a UGT gene promoter (UGTIA1) gene promoter (UGTIA1) gene promoter. Thus the DNA and determining the number of TA repeats in the promoter. Thus the DNA being amplified comprises all or part of

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the number of TA repeats is determined by gel electrophoresis or by dequencing the amplified DNA. The polymorphism comprises an allele consisting of fave TA repeats (TA) is any one of the genotypes (TA) is any one of the determining the number of TA repeats or genetation of the operation of the UT gene, and the individuals sensitivity to the order of the UT gene, and the individuals sensitivity to the order of the UT genetation of the UT genetation of the presence of five, six or seven TA repeats in the promoter. Defects in glucurodination is associated with dibbert's syndrome (TA) repeat region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.4%; Score 15; DB 1; Length 17; 100.0%; Pred. No. 2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17 BP; 9 A; 0 C; 0 G; 8 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.0
Matches 15; Conservative
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ABK90422 standard; DNA; 17 BP 05-NOV-2002 (first entry) ABK90422; RESULT 270

Human; ds; UGT1A1; promoter; Gilbert's syndrome; hyperbilirubinaemia; uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome; UGT; polymorphism detection; TA repeat; glucuronidation; Irinotecan; Human UGT1a1 promoter polymorphism (TA)7 repeat region. TAS-103; xenobiotic.

Homo sapiens.

US6395481-B1.

28-MAY-2002.

99US-00251274. 16-FEB-1999;

16-FEB-1999;

99US-00251274.

(ARCH-) ARCH DEV CORP.

Ratain MJ Di Rienzo A, Iyer L,

WPI; 2002-588597/63.

Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, comprises determining the presence of five thymidine-adenine repeats in

Example 6; Col 11; 13pp; English.

The invention relates to detecting (M1) polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter by determining the presence of five thymidine-adenine (TA) repeats in the promoter, where the presence of the five TA repeats correlates with increased where the presence of the five TA repeats correlates with increased a verpression of the gene. The method is used for detecting polymorphisms in a UGT gene promoter, preferably a UGT I (UGTAAL) gene promoter. (M1) is useful for screening individuals for variation in glucuronidation

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cc activity, for optimising drug dosages for a patient, where the drugs (e.g. Irinotecan or TAS-103) are glucuronidated by UGT (preferably CC UGTLAI) and the activity of the drug is effected by its level of glucurodination. The method preferably involves obtaining DNA from an individual, amplifying all or part of a UGT gene promoter (UGTLAI gene promoter) contained in the DNA and determining the number of TA repeats in the promoter. Thus the DNA being amplified comprises all or part of UGTLAI promoter. The DNA is amplified by a polymerase chain reaction and the promoter. The DNA is amplified by a polymerase chain reaction and consisting of five TA repeats is determined by gel electrophoresis or by sequencing the amplified DNA. The polymorphism comprises an allele consisting of five TA repeats (TA) 5, six TA repeats (TA) 5, (TA) 5, (TA) 5, (TA) 8, (TA) 6, (TA) 8, (TA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17 BP; 9 A; 0 C; 0 G; 8 T; 0 U; 0 Other;
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Gaps ö 1.4%; Score 15; DB 1; Length 17; 100.0%; Pred. No. 2e+02; tive 0; Mismatches 0; Indels Query Match Best Local Similarity 100. Matches 15; Conservative

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1813 TATATATATATAT 1827

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AALS0679 standard; DNA; 17 BP AAL50679; RESULT 271

16-JAN-2003 (first entry)

Human uridine diphosphate glucuronosyltransferase gene polymorphism #13.

Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat; uridine diphosphate glucuronosyltransferase gene promoter; UGTLA1; drug dosage optimisation; xenobiotic sensitivity. Human; polymorphism; uridine diphosphate c

sapiens Ношо

US2002115097-A1

22-AUG-2002

01-FEB-2002; 2002US-00061693

99US-00251274. 16-FEB-1999;

(ARCH-) ARCH DEV CORP.

Rienzo AD, Iyer L,

WPI; 2002-740095/80.

Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, involves determining number of thymidine-adenine repeats in the promoter.

Example 6; Page 2; 13pp; English.

The invention comprises a method for detecting polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter (preferably

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Gaps

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Query Match 1.4%; Score 15; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 2e+02; Matches 15; Conservative 0; Mismatches 0; Indels

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UGTIA1). The method involves determining the number of thymidine-adenine (TA) repeats in the promoter - as the number of TA repeats correlates with expression of the UGT gene. The method of the invention is useful for detecting polymorphisms in a UGT gene promoter. The method of the invention is also useful in optimising drug dosages and predicting an individual's sensitivity to xenobiotics for drugs and xenobiotics that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, involves determining number of thymidine-adenine repeats in the promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human uridine diphosphate glucuronosyltransferase gene polymorphism #13.
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat; uridine diphosphate glucuronosyltransferase gene promoter; UGTLA1; drug dosage optimisation; xenobiotic sensitivity.
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100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                             Sequence 17 BP; 9 A; 0 C; 0 G; 8 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                      1 TATATATATAT 15
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                                                                                                                                                                                                                   Local Similarity 100.
                                                                                                                                   IA repeat polymorphism
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                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                              RESULT 272
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simple sequence repeat primer BDB(CA)7.5.

(first entry)

95WO-US015150. 94US-00346456.

Vogel JM;

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Modified amplified fragment length polymorphism assay - for detection of polymorphism esp. in micro:satellite regions.
                                                                                 Detection; polymorphism; perfect compound simple sequence repeat; adaptor directed primer; genome; genetic; fingerprinting; amplified fragment length polymorphism assay; microsatellite region; genetic trait marking; germplasm comparisons; 5'-anchored; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                               (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 76; 173pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-277795/28
                                                                                                                                                                                                                                                                                                                                         21-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                       28-NOV-1994;
                                                                                                                                                                                                                                                WO9617082-A2
28-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Morgante M,
                                                5' -anchored
                                                                                                                                                                                                                                                                                              96-JUN-1996
                                                                                                                                                                                                       Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel short interfering RNA and enzymatic nucleic acid useful for treating cancer, modulates the expression of a nucleic acid encoding HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
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                                                                                                                                                                                                                                                                                                                                      Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
anti-rheumatic; cancer; AIDS; ss.
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1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 10; Conservative 5; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                     Human K-Ras DNAzyme substrate #878.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 58; Page 101; 185pp; English.
                                                                                                                                                              ABZ60766 standard; RNA; 17 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAY-2001; 2001US-0294140P.
06-JUN-2001; 2001US-0296249P.
10-SEP-2001; 2001US-0318471P.
         1813 TATATATATATAT 1827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAY-2002; 2002WO-US016840.
                                 . 16 TATATATATATAT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (RIBO-) RIBOZYME PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the invention
                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                          21-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mcswiggen J;
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                                                                                                                                                                                                              ABZ60766;
                                                                                                                        RESULT 273
                                                                                                                                                ABZ60766
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Detecting polymorphisms between 2 nucleic acid samples, esp. in microsatellite regions, comprises digesting the nucleic acid to generate fragments, ligating adaptor segments to their ends, amplifying them using primer directed amplification and comparing the prode. to detect differences. The primers used in the amplification comprise a primer directed primer, compressing a sequence repeat (SSN) and an adaptor segment. The present sequence complementary to an adaptor segment. The present sequence is an example of a SSR primer, which is modified amplified fragment nucleotides. The method represents a modified amplified fragment in polymorphism assay, which is particuseful for genome fingerprinting, i.e. for genetic trait marking and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detection; polymorphism; perfect compound simple sequence repeat; adaptor directed primer; genome; genetic; fingerprinting; amplified fragment length polymorphism assay; microsatellite region; genetic trait marking; germplasm comparisons; 5'-anchored; 88.
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                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5'-anchored simple sequence repeat primer VHV(GT)7.5.
                                                                                                                                                                                                                                                                                                                                                              Sequence 18 BP; 7 A; 8 C; 0 G; 0 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1794 GIGIGIGIGIGIG 1808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT27915 standard; DNA; 18 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT27915;
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AAT27913 standard; DNA; 18 BP

RESULT 274 AAT27913/C

AAT27913

SXXX

1391 TGTTAAGACTTGACA 1405

ugunaagacuugaca 16

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06-JUN-1996

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Detecting polymorphisms between 2 nucleic acid samples, esp. in microsatellite regions, comprises digesting the nucleic acid to generate fragments, ligating adaptor segments to their ends, amplifying them using primer directed amplification and comparing the prods. to detect differences. The primers used in the amplification comprise a primer consisting of a perfect cpd. simple sequence repeat (SSR), and an adaptor segment. The present sequence is an example of a SSR primer, which is flanked at its 5'-end by degenerate nucleotides. The microsense modified implified framer modified amplified framer in the presents a modified amplified framer polymorphism assay, which is particuseful for genome fingerprinting, i.e. for genetic trait marking and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haematopoietic cell proliferation disorder related oligonucleotide #1242.
                                                                                                                                                                                           Modified amplified fragment length polymorphism assay - for detection of polymorphism esp. in micro:satellite regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; probe; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Howe A, Mueller J;
G, Lesche R, Leu E;
Mueller V, Otto T, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.4%; Score 15; DB 1; Length 18; Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18 BP; 0 A; 0 C; 8 G; 7 T; 0 U; 3 Other;
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                                                                                                  (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                  Example 1; Page 77; 173pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1794 GTGTGTGTGTGTG 1808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAR-2001; 2001US-0278333P.
                                   95WO-US015150.
                                                                 94US-00346456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 crererererere 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABZ11102 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EPIG-) EPIGENOMICS AG.
                                                                                                                                  Vogel JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         germplasm comparisons
                                                                                                                                                                  WPI; 1996-277795/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40200277272-A2.
                                                                   28-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens
                                 21-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33-OCT-2002,
                                                                                                                                  Morgante M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABZ11102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Нощо
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2:
ABZ11102
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The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. AEZ03861 to ABZ1118 crepresent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative disorder haematopoietic cells, for differentiating between acute of invention. Oligonucleotides from the present invention acute of secretaring the cytosine methylation state and/or single nucleotide determining the cytosine methylation state and/or single nucleotide cell proliferation disorder related sequences and their complements; and as primers for the sequences and their complements; and as primers for the cytosine methylation state and/or minion can also be used for detecting a predisposition to, differentiation between the subclasses, diagnosis, prognosis, treatment and/or minioring of haematopoietic cell proliferation of haematopoietic cell proliferative disorders changed the subclasses diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders. The present method enables chighly specific classification of haematopoietic cell proliferative disorders. The present method enables con disorders allowing for improved and informed treatment of patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haematopoietic cell proliferation disorder related oligonucleotide #650.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Howe A, Mueller J;
G, Lesche R, Leu E;
Mueller V, Otto T, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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I P, Grabs
Model F,
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Olek A, Piepenbrock C, Adorjan
Lewin A, Lipscher E, Maier S,
Schwope I, Ziebarth H;
                                                                                                                                                                                                                                 Claim 15; Page 69; 117pp; English.
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Best Local Similarity 100.0
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EPIG-) EPIGENOMICS AG
WPI; 2003-018942/01
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ABZ10510
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Pelet C;

10-DEC-2002; 2002WO-EP014026 #O2003052135-A2 18-DEC-2003 ADC70018

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ADC7

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ADC7

THIP

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carcinoma
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                                                                                                                                                                                                                                                                                          The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distingishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118 crepresent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative clicanter haematopoietic cells; for differentiating between acute disorder haematopoietic cells; for differentiating between acute contact and acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nucleotide coll proliferation disorder related sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation disorder related sequences from the present invention can also be used for detecting a predisposition to, differentiation between contacting and acute method enables a highly specific classification of haematopoietic cell proliferative chighly specific classification of haematopoietic cell proliferative chigh patients
                                                                                                Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.
                                                                                                                                                                                                                                             Claim 15; Page 47; 117pp; English
                                 WPI; 2003-018942/01
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RESULT 279 ADE84378 g ô Gaps ö 1.4%; Score 15; DB 1; Length 18; 100.0%; Pred. No. 2.1e+02; Pative 0; Mismatches 0; Indels Sequence 18 BP; 1 A; 0 C; 4 G; 13 T; 0 U; 0 Other; Query Match Best Local Similarity 100. Matches 15; Conservative

1867 TTTTTTTTTTT 1881 rrrarrrrrrrrr 15

ADC70018 standard; DNA; 18 BP ADC70018; RESULT 278

Primer oligo used for analysing CpG islands in genomic DNA (SeqID 507). (first entry)

PCR; primer; ss; lung cell proliferative disorder; CpG dinucleotide; adenocarcinoma; squamous cell carcinoma; cytostatic; probe; PNA-oligomer; adenocarcinoma; squamous ce cytosine methylation state.

Unidentified

26-JUN-2003

14-DEC-2001; 2001DE-01061625

(EPIG-) EPIGENOMICS AG

Maier S: Lipscher E, Liloglou T, Genc B, Burger M, Field JK, Nimmrich I;

Detecting and differentiating between lymphoid cell proliferative disorders comprises contacting a target nucleic acid with at least one reagent that distinguishes between methylated and non-methylated CpG dinucleotides.

Maier S, Nimmrich I;

Becker E,

Genc B,

Burger M, Caldwell C, (EPIG-) EPIGENOMICS AG

WPI; 2003-457621/43.

23-NOV-2001; 2001DE-01057491. 28-DEC-2001; 2001DE-01064501.

WPI; 2003-533029/50.

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This invention relates to a novel method for detecting and differentiating between lung cell proliferative disorders associated with refers to one gene and/or their regulatory regions. Specifically, it refers to a method comprising contacting a target nucleic acid in a biological sample with at least one reagent, wherein the reagent is able present in the target DNA. As such, it is possible to further differentiate and diagnose medical conditions including adenocarcinoma differentiate and diagnose medical conditions including adenocarcinoma differentiate und diagnose sytostatic oligomers and squamous cell carcinoma, and their respective adjacent lung tissue. The present invention describes cytostatic oligomers and pNA-oligomers that are useful as probes for determining the cytosine methylation state or single nucleotide polymorphisms (SNPe) of the target sequence. This oligomucleotide sequence is a primer oligomer used for the analysis of the contaction within genomic DNA, used in an exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human lymphoid cell proliferative disorder gene CpG analysis oligo #84.
                              lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gapa
Detecting and differentiating cytosine methylation state of genomic useful for diagnosing, treating prognosticating and/or monitoring lucell proliferative disorders e.g. adenocarcinoma and squamous cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lymphoid cell proliferative disorder, methylation; methylated CpG dinucleotide; single nucleotide polymorphism; SNP; diffuse large B-cell lymphoms; mantle cell lymphoms; chronic lymphocytic leukenta; small lymphocytic leukenta; fellicular lymphoma; diagnosis; prognosis; primer; s8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 18; 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18 BP; 1 A; 0 C; 4 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.4%; Score 15; DB
100.0%; Pred. No. 2.1
ative 0; Mismatches
                                                                                                                        Claim 15; SEQ ID NO 507; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1867 TITATITITITI 1881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADE84378 standard; DNA; 18 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-NOV-2002; 2002WO-EP013265.
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Best Local Similarity 100.
Matches 15, Conservative
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The invention relates to a method of detecting and differentiating

Co between lymphoid cell proliferative disorders associated with at least

cone gene and/or their regulatory regions in a subject by contacting a

target nucleic acid in a biological sample obtained from the subject with

at least one reagent or series of reagents that distinguish between

contacting an lond-methylated CDG dinuclectides within the target nucleic

acid. The genes and/or thair regulatory regions are preferably selected

from MDRI, CSNYEB, EGA, AR, CDK4, RB2, CDC25A, GPID beta, MYDD1, CDR3,

CF C From MDRI, CSNYEB, EGA, BAX, DAY, CDKA1B, CDKA1B, CDKA1B, THC-1, MGMT, MLH1, MOS, MYC, PTEN, RB12, TGFBR2, TP73, CDKA1E,

CG SKIDPLA, ARPRI, BAXI, BAX or HOXAS, Oligomers, peptide nucleic

acid (PNA)-oligomers and/or isolated nucleic acids based on the sequence

cof the genes are useful for detecting the methylation state of all the

CC for dinuclectides within one or more the sequences, or their complements,

CC for dinuclectides within one or more the sequences, or their complements

CC for determining the cytosine methylation state and or single nuclectide

CC polymorphisms (SNPS) and for differentiating at least two of the medical

CC conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma,

CC conditions between subclasses, disposition to,

differentiation between subclasses, disposition proper conditional cell proliferative disposition to,

monitoring of lymphoid cell proliferative disorder. This sequence Claim 30; SEQ ID NO 374; 448pp; English. above mentioned genes.

Seguence 18 BP; 1 A; 0 C; 4 G; 13 T; 0 U; 0 Other;

0 Gaps ő 1.4%; Score 15; DB 1; Length 18; 100.0%; Pred. No. 2.1e+02; iive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 15; Conservative

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RESULT 280 ABK66312

ABK66312 standard; DNA; 32 BP.

(first entry) 02-JUL-2002 ABK66312;

Human gene specific PCR primer #400.

Primer; ss; DNA microarray; differential expression analysis; human.

Homo sapiens

US6352829-B1

35-MAR-2002

99US-00225928 05-JAN-1999; 97US-00859998. 21-MAY-1997; Chenchik A, Jokhadze G, Bibilashvilli R;

(CLON-) CLONTECH LAB INC

analyzing Producing sub-population of labeled nucleic acids, useful for analy differences in RNA profiles between several different physiological sources, using set of distinct gene specific primers. WPI; 2002-314699/35.

Example 3; SEQ ID NO 400; 11pp; English

The invention relates to producing a sub-population of labeled nucleic acids (NAs) comprising contacting a NA sample from a physiological

conditions to enzymatically generate sub-population of NAs, where each conditions to enzymatically generate sub-population of NAs, where each gene specific primer has a sequence complementary to a distinct mRNA, and each labeled NA is generated using a single gene apecific primer. The cach labeled NA is generated using a single gene specific primer. The complementary state of the complementary of labeled NAs which is different physiological sources, where the method comprises producing subpopulation of labeled NAs for the RNA profiles between several comprising the populations for each physiological sources, differences in the population, where the comparison is preferably differences in the population, where the comparison is preferably confidences in the population, where the comparison is preferably confidences in the population, where the comparison is preferably confidences in the population, where the comparison is preferably confidences to an array of probe NAs stably associated with the sources, and comparing the patterns for each of the distinct sources, and comparing the patterns for each of the sources, where confidence of a substrate to produce a hybridiatation pattern for each of the sources, and comparing the patterns for each of the sources, where confidence is a substrate to reason of the sources, where confidence is a substrate of diseased a normal lissue of neoplastic a normal comparing of diseased a normal lissue e.g. neoplastic a normal comparing the sequence data for this patent did not form part of the printed confidence, but was obtained in electronic format directly from USPTO specification, but was obtained in electronic format directly from USPTO confidence in the printed confide

% KGGGGGGGGGGGGGGGGGGGGGGGGGGG

Sequence 32 BP; 9 A; 8 C; 7 G; 8 T; 0 U; 0 Other;

Gaps ö 1.4%; Score 15; DB 1; Length 32; 67.7%; Pred. No. 2.8e+02; rative 0; Mismatches 10; Indels Ouery Match Best Local Similarity 67,79 Matches 21; Conservative

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1731 GCTTGTGGCAAGTGAATTTGCCTGTAACAAG 1761 GCTTGTTACAGGCAAATTCACTTGCCACAAG 32

ਨੇ g RESULT 281 AAT94667

AAT94667 standard; DNA; 18

AAT94667;

27-MAR-1998 (first entry

Anchored poly(T) oligonucleotide polyT-AnchA.

Plavonoid 3' hydroxylase; pigmentation; flower colour; transgenic plant; snapdragon; primer; ss.

Synthetic.

WO9732023-A1

97WO-AU000124. 28-FEB-1997; 04-SEP-1997.

96AU-00008386. 01-MAR-1996;

(FLOR-) FLORIGENE LTD.

Michael MZ; Holton TA, Brugliera F,

WPI; 1997-448691/41.

Novel flavonoid 3'-hydroxylase(s) from flowering plants - and corresponding DNA, used in the manipulation of pigmentation in plants.

Example 15; Page 59; 234pp; English,

Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream region of a polyadenylation sequence. They were used to prime cDNA synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and were also utilised in the PCR amplification of plant cytochrome. P450 sequences (see also AAT94670-73). A CDNA clone (see AAT94657) encoding

Integrin beta 3; human endothelial glycoprotein; GP3A; GPIIIa; ITGB3; CD61; platelet glycoprotein 3a; cellular adhesion; vitronectin receptor; fibronectin receptor; expression inhibition; antisense; tumour formation; cancer invasion; bleeding disorder; inflammation; ss.

Human integrin beta 3 antisense oligonucleotide, SEQ ID NO:40.

(first entry)

03-JUL-2000

AAA07067;

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This sequence represents a primer of the invention. The invention relates to gequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta-N3; or (X)m5'-(gamma)N-(delta-N3; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = th/whine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or thymine; gamma = th/mine; A = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1;3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene
                                                                                                                                       ö
flavonoid 3' hydroxylase (see AAW35704) was isolated using a differential display approach. This can be used to manipulate the pigmentation of transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptides having at least two new nucleotides - useful as primers in RT-PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                 RT-PCR primer; DNA sequence determination; gene sequence analysis; ss
                                                                                                                                     Gaps
                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.4%; Score 14.8; DB 1; Length 18; 88.9%; Pred. No. 2.2e+02; ative 0; Mismatches 2; Indels
                                                                                              Score 14.8; DB 1; Length 18; Pred. No. 2.2e+02; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18 BP; 2 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
                                                                     Sequence 18 BP; 1 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                             RT-PCR primer of the invention SEQ ID 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 11; 19pp; Japanese.
                                                                                                                                                                         1865 TITITATITITATITA 1882
                                                                                                                                                                                                          1 rrrrrrrrrrrrrrr 18
                                                                                                                                                                                                                                                                                          AAX18372 standard; DNA; 18 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TAKI ) TAKARA SHUZO CO LTD.
                                                                                                        1.4%;
                                                                                                                 Local Similarity 88.9%; tes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                 11-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4PI; 1999-183822/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP11032765-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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                                                                                                                                                                                                                                                                                                                                 AAX18372;
                                                                                                        Query Match
                                                                                                                                                                                                                                                               RESULT 282
                                                                                                                                                                                                                                                                                 AAX1837
                                                                                                                                                                                                                                                                                                             88888
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New antisense compound that inhibits human integrin beta3, useful e.g. for treating or preventing infection, inflammation and tumors.

Monia BP;

Sennett CF, Cowsert LM, (ISIS-) ISIS PHARM INC

WPI; 2000-246189/21

99US-00344520. 99US-00344520

25-JUN-1999;

25-JUN-1999;

Homo sapiens

US6037176-A. 14-MAR-2000.

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Sequences AAA07035-A07074 represent antisense oligonucleotides targetted to the human integrin beta 3 gene, which inhibit its expression. The antisense oligonucleotides were designed to target different regions of the human integrin beta 3 RNA, and were analysed for their effect on integrin beta 3 RNA, and were analysed for their effect on (glyceraldehyden-3-phosphate) mRNA levels were measured as a control. Integrins constitute one of four classes of cellular adhesion molecules, and play an important role in cell migration, cell anchorage to substrates and cytoahdesion signalling pathways. They are netrodimeric cation-dependent membrane glycoproteins composed of an alpha and beta subunit. Integrin beta 3 (also known as human endothellal glycoprotein.) GP3A, GPIIIa TrGB3, CD61 and platelet glycoprotein 33 is the common of the membrane of the membrane of the beta-3 subfamily of integrins. This family consists of the vitronectin receptor (alpha-T-beta-3) and the cytoahdesion-driven cellular restenosis, excessing this class of integrin can adhere to various matrix proteins and participate in various conditions such as vascular restenosis, excessive bone resorption and anglogenesis (in melanoma), tumour invasion, platelet aggregation and canderen the thrombasthenia. The oligonucleotides of the invention are useful for diseases mentioned above infermation, inflammation, inflammation, inflammation, inflammation, conditions and the diseases mentioned above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.4%; Score 14.8; DB 1; Length 18; 88.9%; Pred. No. 2.2e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18 BP; 10 A; 7 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 15; Col 40; 33pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1794 GIGIGIGIGIGIGIGI 1811
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD69515;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Gaps

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1866 TITIATITITITAA 1883

16; Conservative

Best Local Similarity

Matches

ð g AAA07067 standard; DNA; 18 BP

AAA07067/c ID AAA070 RESULT 283

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New set of inter-simple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes, useful for genotyping diverse genomes of plant and
                                                                                                                                                       The invention relates to a novel set of inter-simple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes. The primers of the invention may be useful for genotyping diverse genomes of plant and animal systems, in particular for distinguishing Basmati rice varieties from non-Basmati rice varieties and traditional Basmati rice varieties from evolved Basmati rice varieties. The current sequence is that of the ISSR-related PCR primer of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Therapy and diagnosis of conditions involving telomerase using inhibitor - partic. for neoplasia, infection with pathogenic parasites and age-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= b
/note= "May be truncated by multiples of 2 bp"
                                                                                                                                                                                                                                                                                                Query Match 1.4%; Score 14.6; DB 1; Length 15; Best Local Similarity 93.3%; Pred. No. 2e+02; Matches 14; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Telomere, budding yeast, eukaryotic, conserved region, phylogenetic relationship, ss.
                                                                                                                                                                                                                                                                       Sequence 15 BP; 0 A; 0 C; 7 G; 7 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shay J, Wright W, Blackburn EH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYCA-) UNIV CALIFORNIA SAN FRANCISCO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                              Disclosure, Page 19, 60pp; English.

    cerevisae telomeric sequence.

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/note= "May be
                                                                                                                                                                                                                                                                                                                                                           1794 GTGTGTGTGTGTG 1808
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93US-00038766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ51146 standard; DNA; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
                                            WPI; 2003-804317/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1993-386602/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GERO-) GERON CORP
                                                                                                  animal systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-MAY-1993;
                Nagaraju JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-AUG-2003
25-MAR-2003
02-JUN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ51146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                West MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 286
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                                                                                                                                                                                                                                                                                                                                       New set of inter-simple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes, useful for genotyping diverse genomes of plant and animal systems.
                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel set of inter-simple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes. The primers of the invention may be useful for genotyping diverse genomes of plant and animal systems, in particular for distinguishing Basmati rice varieties from non-Basmati rice varieties and traditional Basmati rice varieties from evolved Basmati rice varieties. The current sequence is that of the ISSR-related PCR primer of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inter-simple sequence repeat; ISSR; SSR; PCR; primer; genotyping; plant; animal; Basmati rice; ss.
                                                                      inter-simple sequence repeat; ISSR; SSR; PCR; primer; genotyping; plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
1.4%; Score 14.6; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 15 BP; 0 A; 0 C; 7 G; 7 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                     (DNAF-) CENT DNA FINGERPRINTING & DIAGNOSTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DNAF-) CENT DNA FINGERPRINTING & DIAGNOSTICS.
                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 19; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADD69514 standard; DNA; 15 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1792 TIGIGIGIGIGIGI 1806
                                                                                                                                                                                               09-JAN-2003; 2003WO-IB000041.
                                                                                                                                                                                                                           08-APR-2002; 2002IN-CH000260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JAN-2003; 2003WO-IB000041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-APR-2002; 2002IN-CH000260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ricrerererere 15
            15-JAN-2004 (first entry)
                                         ISSR-related PCR primer 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISSR-related PCR primer 1
                                                                                   animal; Basmati rice; ss.
                                                                                                                                                                                                                                                                                                            WPI; 2003-804317/75
                                                                                                                                         WO2003085133-A2.
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                                                                                                               Unidentified.
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                                                                                                                                                                   16-OCT-2003,
                                                                                                                                                                                                                                                                                 Nagaraju JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2003
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The present sequence can be used in a novel method for detecting a subtaryotic pathogen in a patient. The method comprises obtaining a sample of somatic tissue or calls from the patient, determining it telomerase activity is present and correlating this with the presence of the abthogen. The method is useful for diagnosis of fungal infections, especially a fungus of the genus Candida, Kluyveromyces, Saccharomyces, Sporothrix, Coccidioides, Histoplasma, Blastomyces, Paracoccidioides, especially a beservallus, Mucor or Rhizopus, or malarial infections, especially plasmodium vivax, P. ovale, P. malariae or P. falciparum. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                 The sequences given in AAOS113B-46 represent telomeric sequences derived from various budding yeast species. There is a great variety in the length and sequence complexity of these sequences compared to those of other eukaryotes, yet they all have a 6 base conserved region at the 3' end. The telomeric relationships between these yeasts is fairly consistent with the phylogenetic relationship and it has been shown that C. tropicalis contains at least two forms of telomeric sequences. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-WAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detection of eukaryotic pathogens, especially fungal or Plasmodium spp. by detecting telomerase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detection, eukaryotic pathogen; telomeric nucleic acid sequence; telomerase activity; diagnosis; fungal infection; fungus; fungi; malaria; es.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 1.4%; Score 14.4; DB 1; Length 16; Local Similarity 93.8%; Pred. No. 2.2e+02; es 15; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16 BP; 0 A; 0 C; 9 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fungal telomeric nucleic acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYCA-) UNIV CALIFORNIA SAN FRANCISCO.
(TEXA ) UNIV TEXAS SYSTEM.
                                                                            Disclosure, Fig 30, 186pp, English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1793 TGTGTGTGTGTGTG 1808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT96310 standard; DNA; 16 BP
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93US-00038766.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae.
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   related diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .3-MAY-1992;
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08-APR-1998
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AAT96310

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AAT96310

DT 25-MAR,
DY 25-MA
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#X8X0000000000X8
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The invention relates to a substantially purified or isolated nucleic acid [1] from rygrass or fescue species including a simple sequence repeat (SSR), having 2 or more tandemly respeated nucleotide core elements of nucleotides in length. Also included are a nucleic acid primer suitable for amplifying an SSR, identifying (MI) an SSR by preparing a library of rygrass or fescue genomic DNA enriched for SSRs and identifying clones in the library containing SSRs, a library of rygrass. Or fescue genomic DNA enriched for SSRs prepared by the MI, selecting for a sectiated with the gene such that the SSR and the gene are preferritably co-inherited, and selecting for the SSR in the breeding, a method for DNA profiling grass or cereal species varieties by assessing variation between SSR variaties and testing the purity of grass or cereal species variation breeding, the second patches by assessing variation within seed barches in the selection of genes in grass or cereal species variation breeding, for profiling grass or cereal species variation breeding, for profiling grass or cereal species variation breeding to establish the distinct identity, uniformity and for DNA profiling to establish the distinct identity, uniformity and for DNA profiling to establish the sequence is a ryegrass or fescue SSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species
                                                                                                                                                                                                                                                                                                                                                                                                                   Simple sequence repeat; plant, ds; SSR; ryegrass; fescue; tandem repeat; cereal profiling; grass profiling; seed batch purity testing.
                                                                              Gapa
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                                  1.4%; Score 14.4; DB 1; Length 16; 93.8%; Pred. No. 2.2e+02; tive 0; Mismatches 1; Indels
Sequence 16 BP; 0 A; 0 C; 9 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNIV SOUTHERN CROSS.
STATE VICTORIA DEPT NATURAL RES & ENVIRO.
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                                                                                                                                                                                                                                                                                                                                                                                Simple sequence repeat, SSR, #42
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                                                                                                                   1793 TGTGTGTGTGTGTG 1808
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04-MAY-2000; 2000AU-00007310.
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                                                                                                                                                                                                                                                          AAS13770 standard; DNA; 16
                                                                                                                                                                                                                                                                                                                                         08-MAY-2002 (first entry)
                       Query Match
Best Local Similarity 93.8%
Marches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phalaris aquatica.
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The invention describes a method use for treating increased rate of proliferation of a cell or extending the ability of a cell to replicate, or treating a disease associated with cell sensecence. The method comprises administering an agent to reduce loss of telomers length within the cell during proliferation or replication, or to derepress telomerase to the sensecing cells. The method is useful for treating a condition associated with an increased rate of proliferation of a cell extending the ability of a cell to replicate, or for treating a disease or condition associated with cell sensecence e.g. neoplasia. A second method disclosed in the invention is useful for treating a condition associated with an elevated level of telomerase activity within a cell e.g. cancer. Also disclosed is a method useful for diagnosis of a condition associated with an increased rate of proliferation in a cell in an individual e.g. age-related manular degeneration, astrocytes associated with his called matular degeneration, astrocytes associated with his sequence represents a polynucleotide used in the study of telomere length sequence represents a polynucleotide used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating condition associated with cell senescence or increased rate of cell proliferation, by administering to cell an agent that derepresses telomerase in the senescing cells or that reduces loss of telomere
                                                                                                                                                                                                                                                                                                                                                                                 Cell proliferation; cell senescence; telomere length; telomerase activity; cel replication; neoplasia; cancer; age-related macular degeneration; Alzheimer's disease; atherosclerosis; telomerase; telomerase inhibitor; immortalised cell; ss.
                                                                                                                                                                                                                                                                                                                                                Telomere length and/or telomerase activity related polynucleotide #57.
                                   Length 16;
                                                                         1; Indels
Sequence 16 BP; 0 A; 1 C; 7 G; 8 T; 0 U; 0 Other;
                                    1.4%; Score 14.4; DB 1;
93.8%; Pred. No. 2.2e+02;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blackburn EH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 51; 86pp; English.
                                                                                                                1794 GTGTGTGTGTGTGT 1809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92US-00882438.
93US-00038766.
93US-00060952.
                                                                                                                                                                                                                                             ABX50034 standard; DNA; 16 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-00463404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shay J, Wright W,
                                                                                                                                      1 GTCTGTGTGTGTGT 16
                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                           15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHAY J.
WRIGHT W.
BLACKBURN E H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-066896/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (WEST/) WEST M D.
(SHAY/) SHAY J.
(WRIG/) WRIGHT W.
(BLAC/) BLACKBURN F
                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2002127634-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-MAR-1993;
13-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAY-1992;
                                                                                                                                                                                                                                                                                                                   12-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  West MD,
                                                                                                                                                                                                                                                                                  ABX50034;
                                          Query Match
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                                                              Best Loca
Matches
                                                                                                                                                                                                            RESULT 289
                                                                                                                                                                                                                             ABX50034
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Sequence 16 BP; 0 A; 0 C; 9 G; 7 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel nucleic acid nanocircle comprising at least two repeats of a telomere repeat sequence. The nanocircle of the invention demonstrates cytostatic and ophical activities and may be useful during the diagnosis and treatment of cancer, liver degeneration, macular degeneration and skin aging, as well as during gene literapy procedures. Purthermore, the nanocircle may be used to extend the lifespan of non-cancercus cell populations in culture, providing enhanced materials for biomedical research, tissue enginering and contract sequence is that of the Gaccharomyces cerevisiae telomere repeat sequence is that of the Gaccharomyces sequence is not displayed within the specification per se but was created
                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acid nanccircle comprising at least 2 repeats of a telomere repeat sequence, useful for extending length of telomere in vitro or in vivo, and for treating macular degeneration, and cancer in mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                             Gaps
                                                                                                                                                                                                                                                                                                     nanocircle; telomere repeat sequence; cytostatic; ophthalmological; cancer; liver degeneration; macular; skin aging; gene therapy; biomedical research; tissue engineering; transplantation; de; yeast.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Optionally absent"
7. .16
7. .16 /rag= b
/note= "Each TG unit may be optionally absent"
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1.4%; Score 14.4; DB 1; Length.16;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
Length 16;
                               1; Indels
                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae telomere repeat sequence DNA
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1.4%; Score 14.4; DB 1;
93.8%; Pred. No. 2.2e+02;
iive 0; Mismatches 1;
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"Optionally absent"
                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page; 81pp; English.
                                                                 1808
                                                                                                                                                                                BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JAN-2003; 2003WO-US000109
                                                                                                                                                                                ADC06894 standard; DNA; 16
                                                                                                                                                                                                                                              (first entry)
                                                                                                1 recerererererere
                                                                 1793 TGTGTGTGTGTGTG
                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae.
 Query Match
Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (STRD ) UNIV STANFORD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-697275/66
                                                                                                                                                                                                                                                                                                                                                                                                                          misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc difference
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                                                                                                                                                                                                                                               18-DEC-2003
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                                                                                                                                                                                                                ADC06894;
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                                                                                                                                                  RESULT 290
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Human c-myb hammerhead ribozyme target sequence (nt. position 2896)

AAT81558 standard; RNA; 17 BP.

AAT81558/

14-DEC-1997 (first entry)

AAT81558;

smooth muscle cell; hyperproliferation; restenosis; cancer; c-myb; coronary angioplasty; ss.

Homo sapiens.

WO9531541-A2 23-NOV-1995.

Enzymatic nucleic acid; hammerhead; ribozyme; cleavage; human;

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The sequences given in AAQ35675-90 were used in the construction of NYVAC based recombinants expressing the EHV-1 gB, gC and gD glycoprotein chomologs. Expression of the EHV-1 gB glycoprotein was accomplished by putting the EHV-1 gB bomolog gene under the control of the vaccinia virus 13L promoter. The EHV-1 gC gene was expressed by placing the homolog gene under the control of the vaccinia virus H6 promoter and the EHV-90 conder the control of the vaccinia virus H6 promoter and the EHV-90 conder the control of the entomopox virus 42 kD gene promoter. The homolog genes were derived by polymerase chain reaction (PCR) and were inserted into the ATI and HA delection loci of NYVAC. NYVAC is a Copenhagen vaccine strain of vaccinia virus which has been modified by deletion of six non-essential regions of the genome encoding known or potential virulence factors. The foreign genes. See also AAQ35501-864. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccine comprises recombinant, attenuated pox-virus - use for vaccinating against viral infections such as rabies, hepatitis B, HIV, HSV, EBV, CMV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Taylor J, Tartaglia J, Norton EK;
Limbach KJ, Johnson GP, Pincus SE, Cox WI;
                                                                                                                                                                                                                                                                                 NYVAC; EHV-1; gB; gC; gD; glycoprotein; homolog; vaccinia virus; AII; 13b promoter; H6 promoter; A2 kD gene promoter; H3; deletion loci; Copenhagen vaccine; virulence factors; deletion loci; copenhagen vaccine; virulence factors; deletion loci; recipient loci; polymerase chain reaction; PCR; amplify; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.4%; Score 14.4; DB 1; Length 17; 93.8%; Pred. No. 2.3e+02; ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 6 A; 0 C; 1 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 182; 456pp; English.
                                                                                                                                                                                                                                                42kD promoter element primer RG286.
1793 TGTGTGTGTGTGTG 1808
                                                                                                                         AAQ35687 standard; DNA; 17 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91US-00713967.
92US-00847951.
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                                    1 recererererere 16
                                                                                                                                                                                            25-MAR-2003 (revised)
24-FEB-1993 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perkus ME,
De Taisne C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gettig RR;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                            WO9215672-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JUN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Riviere M,
Francis J,
                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mumps etc.
                                                                                                                                                             AAQ35687;
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New enzymatic nucleic acid molecules - cleave RNA produced by e.g. $c-\pi y b$, for treating restenosis or cancer.

Claim 1; Page 78; 128pp; English.

Stinchcomb DT, Draper K, Mcswiggen J, Jarvis T;

WPI; 1996-010927/01.

(RIBO-) RIBOZYME PHARM INC.

94US-00245466. 95US-00373124. 95WO-US006368.

18-MAY-1994; 13-JAN-1995;

18-MAY-1995;

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The present sequence represents the preferred target sequence for an enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves the human c-myb sequence at the base position indicated in the descriptor line. The c-myb sequence was screened for optimal ribozyme target sites using a computer folding algorithm, and regions of the mRNA which did not corn secondary folding structures and contained potential ribozyme cleavage sites were identified. Ribozymes were synthesised and their activities optimised by either varying the length of the binding arms or by modification to prevent degradation by nucleases. The ribozymes cleave the c-myb sequence and can be used to prevent smooth muscle cell hyperproliferation in restenosis, especially after coronary angioplasty,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 1.4%; Score 14.4; DB 1; Length 17; Local Similarity 93.8%; Pred. No. 2.3e+02; es 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human KDR VEGF receptor hammerhead ribozyme substrate #421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17 BP; 7 A; 1 C; 0 G; 0 T; 9 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1811 TGTATATATATATA 1826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX71409 standard; RNA; 17 BP.
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1777 TITATATIGIAAATAT 1792

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15, Conservative

Matches

1 TTTATATTGTAATTAT 16

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The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (VBGP). A patient (preferably human) having a condition associated with the level of the free-like tyrosinh kinase 1 (fil-1), kinase insert domain containing receptor (XDR) and/or foceal liver kinase 1 (fik-1) (e.g. tumour angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAX67575 to AAX7572 represent specific examples of nucleic acid molecules from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Feline herpes virus type 1; FHV-1; vaccine; poxvirus; ALVAC; vCP243; canarypox virus; antigen; vector; primer; PCR; polymerase chain reaction; pJCA109; pJCA080; ss.
   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
fms-like tyrosine kinase 1; kinase insert domain containing receptor;
foetal liver kinase 1; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 2.3e+02;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17 BP; 4 A; 6 C; 4 G; 0 T; 3 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 109; 218pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1749 TGCCTGTAACAAGCCA 1764
                                                                                                                                                                                                                                                                                                                                                                                                      95US-0005974P.
96US-00584040.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (RIBO-) RIBOZYME PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-259017/23.
                                                                                                                                                                                                   WO9715662-A2
                                                                                                                                                                                                                                                                                                                                     25-OCT-1996;
                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                      26-OCT-1995;
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AAT47177
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AAT4717
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27-MAR-
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Primer
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Peline
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Canaryp
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PCR primers (AAT47159-78) were used in the construction of plasmid intermediates used in the generation of donor plasmid pJCA109. This plasmid is required for the insertion of genes encoding the felline herpes virus (FHV-1) homologues of gB, gC and gD under control of the 111, H6 and 42K promoters, respectively, into the C6 site of an ALVAC vector. Recombinant vCP243 is generated. Primers RG286 (AAT47175) and M13F (AAT47176) were used to synthesise by PCR a 130 bp EcoRI-blunt fragment contg, the 42K promoter using pJCA038 as template. The amplified fragment was used in the construction of intermediate plasmid pJCA088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, c-raf, A-raf, B-raf, hammerhead ribozyme, hairpin ribozyme, target, substrate; catalyst; modulation; expression; Raf gene; delivery; screening; identification; synthesis, deprotection; purification; cancer; inflammation; psoriasis; non-hepatic ascites; infection; genetic drift; restenosis; rheumatoid arthritis; ss.
                                                                                                                   Compsn. for inducing immunological response, esp. in dogs - comprises recombinant virus or expression prod., and additional antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bellon L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L,
Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;
Thompson J, Workman CT, Beaudry A, Sweedler D;
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                              Sequence 17 BP; 6 A; 0 C; 1 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human C-raf target site nucleotide position 2898.
                                                                                                                                                                       Example 18; Page 168; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1777 TTTATATTGTAAATAT 1792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV91398 standard; RNA; 17 BP.
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97US-0051718P.
97US-0056808P.
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97US-0061324P.
97US-0064866P.
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                (VIRO-) VIROGENETICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                  Paoletti E, Maki J;
                                                                                 WPI; 1997-051904/05.
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05-NOV-1997;
19-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV91398
ID AAV9
XX
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Bellon

Human, c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme; target; substrate; catalyst; modulation; expression; Raf gene; delivery; screening; identification; synthesis; deprotection; purification; cancer; inflammation; psoriasis; non-hepatic ascites; infection; genetic drift; restenosis; rheumatoid arthritis; ss. Seguence 17 BP; 2 A; 0 C; 2 G; 0 T; 13 U; 0 Other; Human C-raf target site nucleotide position 2900. Claim 177; Page 154; 259pp; English 1866 TITITATITITGITIT 1881 970S-0049002F 970S-0051718P 970S-0056808P 970S-0061321P 970S-0061324P AAV91400 standard; RNA; 17 BP 2 UUUUAAUUUUGUUUUU 17 98WO-US009249 97US-0046059P 18-FEB-1999 (first entry) Query Match
Best Local Similarity 12.54
Matches 2; Conservative Homo sapiens. WO9850530-A2 05-MAY-1998; 09-MAY-1997 12-NOV-1998 22-AUG-1997 03-JUL-1997 02-0CT-1997 AAV91400; RESULT 296 AAV91400 ద

capable of modulating a process in a biological system. The method capable of modulating a process in a biological system. The method comprises: (a) introducing into the system a random library of nucleic comprises: (a) introducing into the system a random library of nucleic acid catalytes (NAC) having a substrate binding domain (SD), comprising a random sequence, and a catalytic domain (CD); and (D) identifying NAC in systems where modulation has occurred and/or determining the sequence of at least part of the SBDs in such systems. Nucleic acid molecules with an endeath of a catalytic activity, from the present invention, are used to modulate gene expression in plant and mammalian cells and to cleave target nucleic acid, particularly for treating systemic diseases caused by specific NNA, e.g. cancer, inflammantion, specific NNA, e.g. cancer, inflammantion, proceed by specific NNA, e.g. cancer, inflammantion, considered by specific NNA, e.g. cancer, inflammantion, or the RAT gene, are used to treat cancer, restences, specials or rheumatoid arthritis, or generally any condition associated with the level of craf. Introduction of fray systems, and and inclease and cativity. AAV90022 to AAV93877 represent NACS that can be used in the method, specifically for modulating the expression of a Raf gene Identifying new catalytic nucleic acid that modulates selected processes - especially viboxymes that cleave Raf RNA for treating cancer, restenosis, and also new riboxymes and modified nucleoside triphosphates used as antiviral agents and synthons. Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Thompson J, Workman CT, Beaudry A, Sweedler D; Sequence 17 BP; 3 A; 0 C; 1 G; 0 T; 13 U; 0 Other; Claim 177; Page 154; 259pp; English. WPI; 1999-009494/01 ઠ capable of modulating a process in a biological system. The method capable of modulating a process in a biological system. The method capable of modulating a process in a biological system. The method comprises: (a) introducing into the system a random library of nucleic confidences: (a) introducing substrate binding domain (SBD), comprising a random sequence, and a catalytic domain (CD); and (D) identifying NAC in systems where modulation has occurred and/or determining the sequence of at least part of the SBDs in such systems. Nucleic acid molecules with condoulate gene expression in plant and mammalian cells and to cleave target nucleic acid, particularly for treating systemic diseases care used to modulate gene expression in plant and mammalian cells and to cleave target nucleic acid, particularly for treating systemic diseases causer to modulate apposite and and to detect genetic drift and mutations in diseased cells and to determine c-raf RNA. Specifically NACs with RNA-cleaving activity that modulate expression of the RM gragner, restences to statistic, or used to treat cancer, restences to statistic and activity. Adv90022 to Adv93877 represent NACs that can be used in the activity. Adv90022 to Adv93877 represent NACs that can be used in the method, specifically for modulating the expression of a Raf gene Identifying new catalytic nucleic acid that modulates selected processes - especially ribozymes that cleave Raf RNA for treating cancer, restenceis, and also new ribozymes and modified nucleoside triphosphates used as antiviral agents and synthons. Gaps ö 1.4%; Score 14.4; DB 1; Length 17; 12.5%; Pred. No. 2.3e+02; vative 13; Mismatches 1; Indels

Gaps ô Primer; mass-spectrometry; genetic mutation; amplification; ss. Query Match 1.4%; Score 14.4; DB 1; Length 17; Best Local Similarity 18.8%; Pred. No. 2.3e+02; Matches 3; Conservative 12; Mismatches 1; Indels Mass spectrometric mutation analysis primer 24. 1867 TITATITITITIA 1882 98DE-01024280. 98DE-01024280. 1 UUUAAUUUUGUUUUUA 16 (BRUK-) BRUKER DALTONIK GMBH AAZ43714 standard; DNA; 17 23-FEB-2000 (first entry) WPI; 2000-073581/07. DE19824280-A1 29-MAY-1998; 29-MAY-1998; 02-DEC-1999 Synthetic. AAZ43714; RESULT 297 셤

Mass-spectrometric analysis of known gene mutations.

97US-0068212P,

02-OCT-1997 05-NOV-1997

19-DEC-1997

(RIBO-) RIBOZYME PHARM INC

Example; Page 9; 16pp; German.

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This invention describes a method for mass-spectrometric analysis of known genetic mutations, using modified nucleoside triphosphates to improve the performance. The method compises: (1) amplifying a DNA sequence by polymerase chain reaction (PCR) using primers selected to sequence by polymerase chain reaction (PCR) using primers selected to amplify a sequence containing the mutation; (2) adding a particular set of modified nucleoside triphosphates (NTPS) to effect infited extension of already present or newly added primers, where: (a) the extension of already present or newly added primers, where: (a) the extension of already present or newly added primers, where: (a) the extension of the mutation site, so that wild-type amplification products will have a different molecular weight from mutant amplification products; and (c) the mutation of the NTPS results in stabilization of the DNA chains; (3) during ionization, a reduction in ion adduct formation, an increase in ionization yields and/or a change in the mass of the DNA chains; (3) erforming the limited primer extension using an enzyme that generates the complement of the DNA strand being copied; (4) performing at least partial primer degradation and optionally further modification of the mutation amplification products by mass spectrometry and assigning the masses to wild type or mutant. AAZ43691-Z43717 represent primers used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 BP; 6 A; 2 C; 4 G; 5 T; 0 U; 0 Other;
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%$6666666666666666666666666666888
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ó 1.4%; Score 14.4; DB 1; Length 17; ilarity 93.8%; Pred. No. 2.38+02; Conservative 0; Mismatches 1; Indels 1891 ATATITCAATGITAGC 1906 Query Match Best Local Similarity Matches 15; Conserv

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Gaps

16 ATATTTCAATGTCAGC

AAZ47021 standard; DNA; 17 AAZ47021; RESULT 298

BB

(first entry) 29-FEB-2000 Primer RG286 for PCR of promoter entomopoxvirus AmBPV 42K.

Antibacterial; antiviral; primer; RT-PCR; amplification; haemagglutinin; recombinant; vaccine; viral vector; pathogen; adjuvant; methacrylic acid; maleic anhydride; alkenyl derivative; animal; herpes virus; tetanus; influenza virus; feline leukemia; canine distemper; promoter; ss.

Synthetic

WO9944633-A1

10-SEP-1999

01-MAR-1999;

98FR-00002800 03-MAR-1998;

99WO-FR000453

(MERI-) MERIAL

WPI; 2000-022918/02.

Audonnet JF, Minke JM;

Live recombinant vaccine comprising viral vector and polymeric adjuvant, particularly directed against animal herpes and influenza viruses.

Example 7; Page 14; 41pp; French

Primers AAZ47021-Z47022 were used to PCR amplify the entomopoxvirus AmEPV 42K promoter for generating a plasmid construct in which the feline

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The present invention describes nucleic acids (A) that interact stably with a target sequence and contain at least one phosphoro(di)thioate nucleic acid (A') that modulates expression of the oestrogen receptor oncleic acid (A') that modulates expression of the oestrogen receptor gene, are used to treat cancer (particularly of breast or endometrium), in vivo or by transforming cells ex vivo and implanting treated cells, or for other conditions associated with levels of oestrogen receptor. Because of the high selectivity for targeted RNA, (A) can also be used to correlate inhibition of gene expression with alterations in phenotype, particularly for identification of therapeutic targets, and as research reagents (for RNA, in the same way that restriction endomucleases are used with DNA). The combination of modifications in (A) improves resistance to nucleases, binding affinity and/or activity. AAA23503 to AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
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herpes virus glycoprotein D (gD) gene is expressed under control of the 42K promoter. The gD gene is used to generate a live recombinant vaccine which comprises: (1) a viral vector including, and expressing in vivo, a heterologous nucleotide sequence particularly a gene from a pathogen; and (2) at least one adjuvant, i.e. a (methhacrylic acid polymer or a copolymer of maleic anhydride and alkenyl derivatives. The vaccines are used particularly to protect against animal herpes or influenza viruses, but also feline leukemia, tetanus and canine distemper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acids that interact, and optionally cleave, target sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Destrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide; gene expression modification; cancer; phosphorothioate; endonuclease; anticancer; breast cancer; endometrium cancer; ss.
                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                   Score 14.4; DB 1; Length 17; Pred. No. 2.38+02; 0; Mismatches 1; Indels
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Haeberli P;
                                                                                                                                                                                     Sequence 17 BP; 6 A; 0 C; 1 G; 10 T; 0 U; 0 Other;
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s T, Woolf T,
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Reynolds M, Zwick M, Jarvis T,
Matulic-Adamic J;
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98US-00103636.
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                                                                                                                                                                                                                           Query Match
Best Local Similarity 93.8%;
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 299
AAA25184
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target

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Gaps

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The present invention describes nucleic acids (A) that interact stably with a target sequence and contain at least one phosphoro(di)thioate link, having endonuclease activity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the oestrogen receptor gene, are used to treat cancer (particularly of breast or endometrium), in vivo or by transforming cells ex vivo and implanting treated cells, or for other conditions associated with levels of estrogen receptor. Because of the high selectivity for targeted RNA, (A) can also be used to correlate inhibition of gene expression with alterations in phenotype, correlate inhibition of gene expression with alterations in phenotype, correlate inhibition of gene expression with alterations in phenotype, caregents (for RNA, in the same way that restriction endomucleases are used with DNA). The combination of modifications in (A) improves resistance to nucleases, binding affinity and/or activity. AAA23503 to AAA24747 represent oestrogen receptor hammerhead ribozyme sequences.

AAA24748 to AAAA2592 represent their corresponding target sequences. AAA225931 to AAA24748
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AAA24748 to AAA25992 represent their corresponding target sequences. AAA25993 to AAA36105 represent oestrogen receptor hairpin ribozyme sequences, and AAA36107 to AAA326218 represent their corresponding targe sequences. AAA326219 to AAA32271 represent other ribozyme sequences and antisense oligonucleotides used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide; gene expression modification; cancer; phosphorothioate; endonuclease; anticancer; breast cancer; endometrium cancer; ss.
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                                                                                                                                                                           / Match 1.4%; Score 14.4; DB 1; Length 17; Local Similarity 93.8%; Pred. No. 2.3e+02; les 15; Conservative 0; Mismatches 1; Indels
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Haeberli P;
                                                                                                                                         Sequence 17 BP; 1 A; 0 C; 3 G; 13 T; 0 U; 0 Other;
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is I, Woolf I,
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Reynolds M, Zwick M, Jarvis T,
                                                                                                                                                                                                                                                                 1865 TITITATITITI 1880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used to treat cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-013248/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matulic-Adamic J;
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23-JUN-1998;
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                                                                                                         invention
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Matches
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The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL has two isoforms, with a few single base pair differences between the cool on the single base pair canges introduces a premature stop codon in HTPL.8 (8 for short) compared to HTPL-1 (L for long). HTPL shares an overall structure organisation with the Patched protein. The shares an overall features strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was mapped to human chromosome 10pl2.1. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of such disorder associated with decreased expression or activity of human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL.
sequences, and AAA26107 to AAA26218 represent their corresponding target sequences. AAA26219 to AAA26271 represent other ribozyme sequences and antisense oligonucleotides used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, gene therapy, tumour suppressor; HTPL; chromosome 10p12.1; human testis expressed Patched like protein; testis; adrenal; liver; male germ cell development; bone marrow; brain; kidney; lung; placenta; prostate; skeletal muscle; colon; male infertility; cancer; 88.
                                                                                                                                                            Gaps
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0
                                                                                                                     / Match 1-4%; Score 14.4; DB 1; Length 17; Local Similarity 93.8%; Pred. No. 2.3e+02; hes 15; Conservative 0; Mismatches 1; Indels
                                                                                     Sequence 17 BP; 2 A; 0 C; 2 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                            Human HTPL scanning oligonucleotide SEQ ID 4088.
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2001WO-US000665.
2001WO-US000669.
2001WO-US000669.
2001WG-US000669.
2001US-00864761.
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                                                                                                                                                                                                    1865 TTTTATTTTGTTTT
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23-MAY-2001;
09-OCT-2001;
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30-JAN-2001;
30-JAN-2001;
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                                                               invention
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                                                                                                                                Query Match
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The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV79762 and ABB98559 to ABB98520). HTPL has two isoforms, with a few single base pair differences between the two. One of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL shares an overall structure organisation with the Patched protein. The shared structural features strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was mapped to human chromosome lopl2.1. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL.
HTPL. Such disorders include disorders of testis, or adrenal, adult and foetal liver, bone marrow, brain, kidney, lung, placenta, prostate, skeletal muscle or colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potential therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1; human testis expressed Patched like protein; testis; adrenal; liver; male germ cell development; bone marrow; brain; kidney; lung; placenta; prostate; skeletal muscle; colon; male infertility; cancer; ss.
                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                          1.4%; Score 14.4; DB 1; Length 17; 93.8%; Pred. No. 2.3e+02; ive 0; Mismatches 1; Indels
                                                                                                                                        Sequence 17 BP; 2 A; 2 C; 3 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human HTPL scanning oligonucleotide SEQ ID 4089.
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                                                                                                                                                                                                                                                       2162 GCATTTGTTTCTACTT 2177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US000667.
30-JAN-2001; 2001WO-US000668.
30-JAN-2001; 2001US-US006669.
23-MAY-2001; 2001US-00864761.
09-OCT-2001; 2001US-0327898P.
                                                                                                                                                                                                                                                                                                                                                                                       ABV82843 standard; DNA; 17 BP
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2001WO-US000665.
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                                                                                                                                                                                                                                                                                             2 GCATTTGTTTCTAGTT 17
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                                                                                                                                                                                                  Local Similarity 93.8
hes 15; Conservative
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30-JAN-2001;
30-JAN-2001;
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The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma, numbur angiogenesis, diabetic retinopathy, macular degeneration, neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge wheber syndrome, rippel-Trenaunay-Weber syndrome, oster-Weber-rendu for syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for
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therapy and manufacture of a medicament for treatment or prevention of such disorder associated with decreased expression or activity of human PTPL. Such disorders include disorders of testis, or adrenal, adult and foetal liver, bone marrow, brain, kidney, lung, placenta, prostate, skeletal muscle or colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potenial therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic; ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic; vulnerary; cancer; lymphoma; Bwing's sarcoma; melanoma; psoriasis; tumour angiogenesis; diabetic retinopathy; macular degeneration; neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris; angiofibroma of tuberous sclerosis; port-wine stain; wound healing; studye Weber syndrome; Kippel-Trenaunay weber syndrome; leuksemia; si Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNAzyme; inozyme;
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useful for treating cancer, diabetic retinopathy, macular degeneration,
arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                  1.4%; Score 14.4; DB 1; Length 17; 93.8%; Pred. No. 2.3e+02; tive 0; Mismatches 1; Indels
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                                                                                                                                                                                            Sequence 17 BP; 2 A; 3 C; 3 G; 9 T; 0 U; 0 Other;
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Best Local Similarity 93.8
Matches 15; Conservative
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ABK18059/c
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the treatment. The method comprises the use of one or more therapies under conditions suitable for the treatment. Leukaemia or tumour angiogenesis is treated by administering (1) to the patient in conjunction with one or more of other therapies such as radiation or chemotherapy treatment. (I) is useful for reducing ERG activity in a call, by contacting the cell with (I). (I) is useful for neaving RNA of ERG gene, by contacting (I) with RNA, in the presence of a divalent cation such as Mg2+. (I) is useful for diagnosis of conditions and diseases related to the expression of ERG, and as diagnostic tool to the presence of ERG RNA in a cell. (I) is useful for specifically targeting genes that share homology with ERG gene or ERG fusion genes. ARK17354-ABK22719 represent nucleic acids, including antisense and enzymatic nucleic acid molecules which regulate expression of ERG, and carzymatic nucleic acid molecules which regulate expression of ERG, and carzymatic nucleic acid molecules which regulate expression of ERG, and carzymatic enzymention

Sequence 17 BP; 8 A; 3 C; 2 G; 0 T; 4 U; 0 Other;

ô Gapa ö 1.4%; Score 14.4; DB 1; Length 17; 93.8%; Pred. No. 2.3e+02; ive 0; Mismatches 1; Indels Local Similarity 93.8%; nes 15; Conservative Query Match Best Loca Matches

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RESULT 304

ACC51306 standard; DNA; 17 ACC51306/

BP.

(first entry) 27-JUN-2003 ACC51306;

Human tumour suppressor sequence #73

ss; tumour suppressor; antitumour; cytostatic; tumour suppression; tumour regression; apoptosis; virus resistance; diagnosis; cellular degeneration.

Homo sapiens

FR2826373-A1

27-DEC-2002

Disclosure, Page 482; 720pp; French.

20-JUN-2001; 2001FR-00008139

20-JUN-2001; 2001FR-00008139.

(MOLE-) MOLECULAR ENGINES LAB SA

Tuijnder M, Telerman A, Amson R;

WPI; 2003-250498/25.

New nucleic acid sequences associated with tumor suppression, regression, apoptosis or virus resistance are useful to diagnose and treat viral disease, development of tumor cells and cell degeneration.

Claim 1; Page 57; 798pp; French

The with tunnour suppression or regression, apoptosis or virus resistance. invention relates to these sequences or sequences having at least 80% identity to them, and polypeptides encoded by the sequences or polypeptides having 80% identities to the polypeptide sequences. The invention is used to diagnose or treat viral disease or disease characterized by development of tumour cells or cellular degeneration sequence represents an isolated nucleic acid sequence associated

Sequence 17 BP; 10 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

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                                                                                                                                                                       Cytostatic, virucide, neuroprotective, nootropic, neuroleptic, gene chip; antisense; sense; tumour, cell degeneration; cancer; Alzheimer's disease; schizophrenia; protein chip; gene therapy; tumour suppression; human fukutin; ds.
                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.
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                                                                                                                                                         Tumour suppression related human fukutin oligo SEQ ID No 3832.
Length 17;
                  1; Indels
1.4%; Score 14.4; DB 1;
93.8%; Pred. No. 2.3e+02;
iive 0; Mismatches 1;
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                                      2166 TIGITICIACTITGAT 2181
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                                                                                                      ABT38195 standard; DNA; 17 BP.
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  Query Match
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Matches 15; Conservative
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                                                                                                                          ABT38195;
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The invention relates to a novel isolated 17 mer nucleic acid sequence, cgiven in the specification, a sequence containing at least 15 consecutive given in the specification, a sequence a sequence with, after optimal and incleotides from the 17 mer sequence with, after optimal anyone in the least 80 % identity to the 17 mer sequence, a sequence that hybridizes to them under highly stringent conditions, or the complement of hybridizes to them under highly stringent conditions, or the complement of acids of the invention are useful as probes and primers for detecting, identifying and/or amplifying a mucleic acid, e.g. as one component of a gene chip, in vitro as (anti) sense reagents, and for component of a gene chip, in vitro as (anti) sense reagents, and for component of a recombinant polypeptides. Any of the nucleic acids, colypeptides, vectors containing the nucleic acids, cells containing the vector or antibodies directed against the polypeptides are useful for vector or antibodies directed against the polypeptides are useful for greatent of tumours or cell diseases that are characterised by development of tumours or cell containing the expression of the 17 mer nucleic acids in containing the expression of the 17 mer nucleic acids in containing the polypeptides can also be used to generate antibodies, and chipser the nucleic acid sequence represents a tumour suppression cheared human fukutin oligonucleotide of the invention

Sequence 17 BP; 8 A; 2 C; 2 G; 5 T; 0 U; 0 Other;

Score 14.4; DB 1; Pred. No. 2.3e+02; 1.4%; 93.8%; Best Local Similarity Query Match

Matches

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The invention relates to the isolation of 6327 nucleotide sequences, fragments of at least 15 consecutive nucleotides of these nucleotides, a fragments of at least 80% identity, after optimal alignment, with the nucleotides, or the complement, or corresponding RNA, of the nucleotides. The nucleotides are used as probes or primers for detecting, controllying, quantifying and/or amplifying nucleic acids, as in vitro sense and antisense sequences, of nucleotides involved in tumour suppression or reversion, apoptosis and or viral resistance, to produce recombnant polypeptides, and to prepare transgenic animals, as experimental models. The nucleotides (also vectors containing them and cells containing the vectors), the encoded polypeptides and antibodies (by viral infections or diseases characterized by development of tumours or viral infections or diseases characterized by development of tumours or viral infections or diseases. The nucleotides can be used for diagnosis and/or prognosis of these diseases. The nucleotides can be used for diagnosis and be used to screen for their specific interactive molecules.
                                                                      cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
primer; probe; tumour suppression; tumour reversion; apoptosis;
virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies.
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                                 Tumour suppression/reversion associated nucleotide #4252.
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04-DEC-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies
                                                                                                                                                                                                                                                                                                                                                              Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
                                                                                                                                                                                                                                                                                                                                                                                    tumour suppression; tumour reversion; apoptosis; virus resistance; viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                 Murine oligonucleotide associated with tumour supression, SEQ ID 1343.
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                                                                                                                                                                                              ACC64096 standard; DNA; 17
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                                                                                 17 TIGATATITICAATGAT
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             15, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       relerman A, Amson R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-333167/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                  schizophrenia; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003025176-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-DEC-2003
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ADB43929/c ID ADB439 XX AC ADB439 XX DC ADB439 DT 18-DEC

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Synthetic

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fragments of at least 15 consecutive nucleotides of these nucleotides, a sequence having at least 89 identity, after optimal alignment, with the nucleotides, or the complement, or corresponding the nucleotides, or the complement, or corresponding RNA, of the nucleotides are used as probes or primers for detecting, identifying and/or amplifying nucleic acids, as in vitro sense and antisense sequences, of nucleotides involved in tumour suppression or reversion, apoptosis and or viral resistance, to produce recombrant polypeptides, and to prepare transgenic animals, as experimental models. The nucleotides (also vectors containing them and cells containing the vectors), the encoded polypeptides and antibodies or viral infections or diseases characterized by development of tumours or viral infections or diseases characterized by development of tumours or viral infections or diseases characterized by development of tumours or cell degeneration (e.g. Alzheimer's disease or schizophrenia).

Analysis of the expression of the nucleotides and polypeptides can be used to screen for their specific interactive molecules, and also be used to screen for their specific interactive molecules.
cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss; primer; probe; tumour suppression; tumour reversion; apoptosis; virus resistance; transgenic animals; Alzheimer's disease; schizophrenia; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.4%; Score 14.4; DB 1; Length 17; 93.8%; Pred. No. 2.3e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17 BP; 10 A; 2 C; 4 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 654; 771pp; French
                                                                                                                                                                                                                                                                                                                     Ξ
                                                                                                                                                                                                                                                                                                                   Tuijnder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ20109 standard; DNA; 18 BP.
                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR ENGINES LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression of the nucleotides
                                                                                                                                                                                                             17-SEP-2002; 2002WO-IB004219
                                                                                                                                                                                                                                               17-SEP-2001; 2001FR-00011981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                       Amson R,
                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-441574/41.
                                                                                                                                          WO2003040369-A2.
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                                                                                                          Homo sapiens.
                                                                                                                                                                            5-MAY-2003
                                                                                                                                                                                                                                                                                                                       relerman A,
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The oligomer was designed to target human INF receptor mRNA beginning at nucleotide 2354 and to covalently cross-link to the target via the N4N4-ethanocytosine group. See also AAQ20108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New sequence-specific non-photo-activated crosslinking agents - bind to the major groove of duplex DNA and are esp. useful for treating latent infections e.g. HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human tumour necrosis factor receptor mRNA; AIDS; modified; HIV; RSV; HPV; malignancy; hepatitis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligomer TNFR943 for forming triplex with HUMNFR target duplex.
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/mod_base= OTHER
/note= "N6 methyl-8-oxo-2' deoxyadenine"
                                                                                                                                  /mod_base= OTHER
/note= "N-methyl-8-0x0-2"-deoxyadenine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= b
/mod_base= OTHER
/note= "OTHER= N4 N4 ethanocytosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                         /*tag= b
/mod_base= OTHER
/note= "N4N4-ethanocytosine"
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                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; Page 27; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1866 TTTTTTTTTTTT 1881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ30448 standard; DNA; 18 BP.
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mod base=
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matteucci MD, Krawczyk S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GILE-) GILEAD SCIE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1992-007480/01
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                                                     Key
modified_base
                                                                                                                                                                                  modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-JAN-1991;
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07-DEC-1992
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                                                                                                                                                                                                                                                                                                                     WO9118997-A
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Gaps

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deoxyribonucleic acid; major groove; ethanoamino group; tumour necrosis factor; receptor; messenger RNA; aziridinylcytosine; cross-linking group; ss.

Cross-linking oligomer 943 to target human TNF Receptor mRNA

WO9209705-A1

11-JUN-1992

25-NOV-1991;

23-NOV-1990 08-APR-1991 8-JAN-1991 .7-APR-1991 17-APR-1991; 27-SEP-1991;

7-APR-1991

Froehler B,

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Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of individuals e.g. by determining immunogenetic differences when transplanting between them.
                                                                                                                                                                                                                                                                        The specification describes a process for circularizing an oligomorlectide around a double-stranded nucleic acid that contains a target sequence. The method is used to detect or label nucleic acids, particularly plasmids, to detect target sequences in the nucleic acid, particularly plasmids between two sequences that differ in only 1 or 2 muctations. It can be used to select, e.g. from degenerate single-stranded nucleic acids, sequences that can bind to the nucleic acid, particularly sequences that promote entry of the nucleic acid into cells or can target the nucleic acid into cells or can target the nucleic acid in specific callular compartments. The method can also be used to purify nucleic acids, particularly plasmids, and in gene therapy for specific inhibition of a gene contained in the nucleic acid. The present sequence represents an oligomorlectide used in the course of the invention, during construction of a triple helix
                                                                                                                                             Circularizing oligonucleotide around double-stranded nucleic acid, usefule.g. for detecting mutations, using target-binding oligonucleotide with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, human leukocyte antigen; HLA; genotype; polymorphism;
immunogenetic; transplantation; genetic disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 14.4; DB 1; Length 18;
Pred. No. 2.4e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moriya S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human HLA genotyping oligonucleotide SEQ ID NO 1015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 BP; 0 A; 0 C; 10 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matsumura Y,
          (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
(CNRS ) CNRS CENT NAT RECH SCI.
                                                                     Roulon T;
                                                                        Helene C,
                                                                                                                                                                                                                                       Example 10; Page 41; 91pp; French
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1792 TTGTGTGTGTGTGT 1807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2000; 2000JP-00164798
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    e.g. for detecting mutations
complementary end sequences.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.8%;
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Best Local Similarity 93.0.
Best Local Similarity
Local Similarity
                                                                        Garestier T,
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                                                                                                               WPI; 2001-080698/09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2002
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                                                                          Escude C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL31526;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The synthetic oligomer is capable of forming a triplex at physiological pH with a purine rich target sequence by coupling into the major groove of the duplex. The specific target sequence of this oligomer is the human tumour necrosis factor receptor mRNA beginning at nucleotide 2354 contg. a purine rich sequence coned. on one strand of the duplex. The oligomer, and others like it are useful in diagnosis and therapy of diseases characterised by specific DNA duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant tumours and inflammation. The triple helices form under mild conditions thus assays may be carried out without and AA030226-447. (Updated on 25-MAR-2003 to correct PD field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          New oligomers contg. modified bases - which form a triplex with G-C doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis, herpes malignancy and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence of an oligonucleotide used for triple helix constrution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 14.4; DB 1; Length 18;
Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                  Milligan J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                  Matteucci MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; Page 72; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1866 TITITITITITITI 1881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL56770 standard; DNA; 18 BP.
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91US-00643382.
91US-00683420.
91US-00686544.
91US-00686546.
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                                                                                                      91WO-US008811
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Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                    Krawczyk S,
                                                                                                                                                                                                                                                                                                             (GILE-) GILEAD SCI INC
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1992-217083/26.
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nucleic acid
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Gaps

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Nishida

20-AUG-2002

RESULT 311 ABL56770

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21-DEC-2000

Synthetic.

cytokinesis or the

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The invention relates to antisense oligonuclectides targeted to a nucleic acid molecule encoding human Survivin, where the antisense oligonuclectide inhibits the expression of human Survivin. These antisense oligonuclectides are used in the treatment of an animal suffering from a disease or condition associated with Survivin, e.g. a hyperproliferative condition such as cancer, and comprises administering a therapeutically or prophylactically effective amount of the antisense oligonuclectide so that expression of Survivin is inhibited. The oligonuclectides can also be used to treat a human suffering from a disease or condition characterised by a reduction in apoptosis comprising administering the antisense oligonuclectide to a human. In addition, the antisense oligonuclectide and a cytotoxic chemotherapeutic agent e.g.
                              The invention relates to a typing kit for judging human leukocyte antigen (HLA) genotype of a sample by hybridising a substrate on which 10-24 base oligonucleotides (ABISO12-ABIS1809) originating in the sequences of genes e.g. belonging to HLA class I antigens on human genome and containing gene polymorphisms as alloantigens have been immobilised as primers for amplification of cleaved nucleic acids relating to gene polymorphisms. The method is useful for judging HLA genotypes of individuals by determining immunogenetic differences before transplanting between them, providing genetic information to decide compatibility of organ and tissue for transplantation e.g. of bone marrow, kidney, liver, pancreas, Langerhans islart in pancreas and cornea, susceptibility diagnosis of genetic diseases and identifying individuals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel antisense compounds for modulating the expression of Survivin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Survivin, human, mouse, cytostatic, antisense oligonucleotide, hyperproliferative condition, cancer, apoptosis, cytokinesis, ss.
                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                           1.4%; Score 14.4; DB 1; Length 18; 93.8%; Pred. No. 2.4e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cowsert LM;
                                                                                                                                                                                                                                                                                                      Sequence 18 BP; 5 A; 6 C; 6 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse Survivin antisense oligonucleotide #57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Swayze EE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 18; Page 62; 120pp; English.
Claim 10, Page 285; 345pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                              1470 GGGTACCAGCAGAAG 1485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS21755 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US002939.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-FEB-2000; 2000US-00496694.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GGGTACCAGCAGAACG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ackermann EJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                         Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-488863/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treatment of cancer
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200157059-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bennett CF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS21755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 313
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taxol or cisplatin, can be used to modulate apoptosis, cytokinesis or the cell cycle, or inhibit the proliferation in a cancer cell by contacting the cell with the antisense oligonucleotide. AAS1521-AAS21768 represent Survivin nucleic acids, and antisense oligonucleotides targeted to Survivin, used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                  Gaps
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                                                                                                                                         1.4%; Score 14.2; DB 1; Length 20;
84.2%; Pred. No. 2.7e+02;
ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat sequence found in epsilon haemoglobin gene.
                                                                                                           Sequence 20 BP; 11 A; 2 C; 0 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14 BP; 7 A; 7 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 9; Col 59-60; 186pp; English.
                                                                                                                                                                                                                      1814 ATATATATATATATGTACA 1832
                                                                                                                                                                                                                                                        1 ACATATATATATATAACA 19
                                                                                                                                                                                                                                                                                                                                                AAT66087 standard; DNA; 14 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89US-00341562.
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                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MARS-) MARSHFIELD CLINIC.
                                                                                                                                             Query Match
Best Local Similarity 84.2'
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-042299/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
18-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Weber JL;
                                                                                                                                                                                                                                                                                                                                                                                       AAT66087;
                                                                                                                                                                                                                                                                                                                  RESULT 314
AAT66087/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolation of satellite sequences from genomic DNA for use as DNA markers comprises isolating a library with high homogeneity by DNA fragmentation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Simple sequence repeat; plant; ds, SSR, ryegrass; fescue; tandem repeat; cereal profiling; grass profiling; seed batch purity testing.
                                                                                                                                                                                                                             Satellite sequence; DNA fragmentation; microsatellite DNA; DNA marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.3%; Score 14; DB 1; Length 14;
100.0%; Pred. No. 2.2e+02;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14 BP; 7 A; 7 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                    (NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 5; Page 14; 35pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Simple sequence repeat, SSR, #13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS13716 standard; DNA; 14 BP
                                                                                                                                                                                                   H. discus derived sequence #4.
                                                                                                        AAZ98486 standard; DNA; 14 BP.
                                                                                                                                                                                                                                                                                                                                                                        99WO-JP003551.
                                                                                                                                                                                                                                                                                                                                                                                                      98JP-00232153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1793 TGTGTGTGTGTG 1806
1794 GTGTGTGTGTGT 1807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAY-2002 (first entry)
                                                                                                                                                                     19-JUN-2000 (first entry)
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Best Local Similarity 100.0
Matches 14; Conservative
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                             14 Grererererer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sekino M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-224692/19.
                                                                                                                                                                                                                                               Haliotis discus; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the invention
                                                                                                                                                                                                                                                                             Haliotis discus.
                                                                                                                                                                                                                                                                                                           WO200011156-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rakahashi H,
                                                                                                                                                                                                                                                                                                                                                                                                      18-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1999;
                                                                                                                                                                                                                                                                                                                                          02-MAR-2000.
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                                                                                                                                       AAZ98486;
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AAZ98486/c
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The invention relates to a substantially purified or isolated nucleic acid (I) from ryegrass or fescue species including a simple sequence repeat (SSR), having 2 or more tandemly repeated nucleotide core elements or repeat (SSR), having 2 or more tandemly repeated nucleotide core elements cuttable for amplifying an SSR, identifying (M1) an SSR by preparing a library of ryegrass or fescue genomic DNA enriched for SRRs and core identifying clones in the library containing SSRs, a library of ryegrass or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely core associated with the gene such that the SSR and the gene are section between SSR varieties and electing for the SSR in the breeding, a preferentially co-inherited, and selecting for the SSR in the breeding, and cereal species varieties by assessing variation within seed batch of an SSR. The SSRs core and be used in the selection of genes in grass or cereal breeding, for profiling grass or cereal seed batches, and for DNA profiling to establish the constance is a ryegrass or fescue SSR
                                                                                                                                                                                                                                                                                                                                                                                              New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Syntheric oligonucleotide, dinucleotide repeat; cytostatic; apoptosis; cell cycle arrest; cell proliferation; caspase; cytokine; interleukin; tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                y Match 1.3%; Score 14; DB 1; Length 14; Local Similarity 100.0%; Pred. No. 2.2e+02; hes 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14 BP; 7 A; 7 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                             STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R. UNIV SOUTHERN CROSS.
STATE VICTORIA DEPT NATURAL RES & ENVIRO. UNIV ADELAIDE.
                                                                                                                                                                                                                                                                                         INT MAIZE & WHEAT IMPROVEMENT CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; Page 51; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH46009 standard; DNA; 14 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1793 TGTGTGTGTGTG 1806
                                                                                                                                                            24-DEC-1999; 99AU-00004906.
04-MAY-2000; 2000AU-00007310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic oligonucleotide 9.
                                                                                                                         03-JAN-2001; 2001NZ-00509193
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                                                                                                                                                                                                                                                                                                                              Jones ES;
                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-512563/56.
                                                                                                                                                                                                                                                                                                                              Forster JW,
                                                                                         25-MAY-2001
                                                    NZ509193-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                           varieties.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                       (UYAD-)
                                                                                                                                                                                                                   (SAUS-)
(UYSC-)
(VICT-)
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Matches
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The present sequence is that of a synthetic oligonucleotide useful to the invention. The invention relates to a composition, comprising a 2 to 20 base 3 'OH, 5 'OH synthetic oligonucleotide which comprises multiple repeats of dinucleotides such as GT, TG, etc., according to specific formula and having cytostatic activity. The oligonucleotide compositions are useful for inducing call cycle arrest, inhibition of proliferation, cutivation of caspases and induction of apoptosis or production of cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour necrosis factor (TMF)-alpha by immune system cells, in an animal having cancer such as primary carcinoma, secondary carcinoma, secondary sarcoma such as, leukemia, lymphoma, breast, prostate, colorectal, ovarian or bone cancer. The compositions induce apoptosis independent of Fas, p53/p21, p21/waf-1/CIP, p15(ink4B), p16(ink4), drug resistance, caspase 3, transforming growth factor (TGP)-beta 1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composition comprising synthetic oligonucleotides which comprise multiple repeats of dinucleotides such as GT, TG useful for treating cancer by inducing cell cycle arrest, inhibiting proliferation, activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping; trait mapping; marker-assisted selection; gene selection; legume; DNA profiling; breeding; ds.
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1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14 BP; 0 A; 0 C; 7 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 17; 77pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAI64441 standard; DNA; 14 BP
                                                                                                                                                                                                                                                                                                                                            (BION-) BIONICHE LIFE SCI INC.
                                                                                                                                                                                                                                                      13-DEC-1999; 99US-0170325P.
29-AUG-2000; 2000US-0228925P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1793 TGTGTGTGTGTG 1806
                                                                                                                                                                                                            12-DEC-2000; 2000WO-CA001467.
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                                                                                                                                                                                                                                                                                                                                                                                            Phillips NC, Filion MC;
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-398150/42.
                                                                                                      WO200144465-A2.
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lymphoma; ss
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                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          caspases
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The present invention relates to Simple Sequence Repeats (SSRs) from clover species. SSRs, also called microsatellites, are based on a 1-7 mucleotide core element which is tandemly repeated. The SSR array is embedded in complex flanking DNR. SSRs are ideal markers for genome mapping, trait mapping and marker-assisted selection. The SSRs may be used in methods for selecting genes in clover/legume breeding. The SSRs are also useful for DNA profiling of clover varieties and for testing the purity of legume seed barches. The present sequence is a SSR motif, which
                                                                                                                                                                             Novel simple sequence repeats in clover species useful for selection of genes in legume breeding, for profiling legume species varieties and for testing the purity of legume seed batches.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, comprises determining the presence of five thymidine-adenine repeats in the promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, ds, UG71A1, promoter, Gilbert's syndrome, hyperbilirubinaemia, uridine diphosphate glucuronosyltransferase, Crigler-Najjar syndrome, UG7; polymorphism detection; TA repeat; glucuronidation; Irinotecan;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14 BP; 0 A; 0 C; 7 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human UGT1a1 promoter polymorphism (TA)7 repeat.
                                                                               (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                            was used in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratain MJ;
                                                                                                                                                                                                                                                     Claim 6; Page 35; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-00251274.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK90418 standard; DNA; 14 BP
                                  24-DEC-1999; 99AU-00004907.
28-MAR-2000; 2000AU-00006520.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1794 GTGTGTGTGTGT 1807
03-JAN-2001; 2001NZ-00509194
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                                                                                                                     Koelliker R, Forster JW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-588597/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAS-103; xenobiotic
                                                                                                                                                   WPI; 2001-431058/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6395481-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABK90418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK90418
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Claim 7; Col 17; 13pp; English JS6395481-B1 28-MAY-2002. ABK90418; RESULT 320 ð

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where the presence of the five TA repeats correlates with intreased expression of the gene. The method is used for detecting polymorphisms in a UGT gene promoter. (M1) is useful for screening individuals for variation in glucuronidation activity, for optimising drug dosages for a patient, where the drugs (e.g. Irinotecan or TAS-103) are glucuronidated by UGT (preferably COT GUTLA1) and the activity of the drug is effected by its level of individual, amplifying all or part of a UGT gene promoter (GUTLA1 gene promoter) contained in the DNA and determining the number of TA repeats COT in the promoter. Thus the DNA being amplified comprises all or part of UGTLA1 promoter. The DNA is amplified by g polymerase chain reaction and the promoter. The DNA is amplified by glocymerase chain reaction and the number of TA repeats is determined by gel electrophoresis or by sequencing the amplified DNA. The polymorphism comprises an allele consisting of five TA repeats (TA) 5, six TA repeats (TA) 5, (TA) 8, (TA) 8, (TA) 8, (TA) 8, (TA) 8, (TA) 9, (TA) 8, (TA) 8, (TA) 8, (TA) 8, (TA) 8, (TA) 9, 
The invention relates to detecting (MI) polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter by determining the presence of five thymidine-adenine (TA) repeats in the promoter, where the presence of the five TA repeats correlates with increased.
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Sequence 14 BP; 7 A; 0 C; 0 G; 7 T; 0 U; 0 Other;

0; Gaps 1.3%; Score 14; DB 1; Length 14; 100.0%; Pred. No. 2.2e+02; 0; Indels 100.0%; Pred. No. 2.2 ative 0; Mismatches Best Local Similarity 100. Matches 14; Conservative

ABK90418 standard; DNA; 14 BP.

(first entry) 05-NOV-2002

Human UGT1al promoter polymorphism (TA)7 repeat.

Human; ds; UGT1A1; promoter; Gilbert's syndrome; hyperbilirubinaemia; uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome; UGT; polymorphism detection; TA repeat; glucuronidation; Irinotecan; TAS-103; xenobiotic.

Homo sapiens

99US-00251274 16-FEB-1999;

99US-00251274 16-FEB-1999;

(ARCH-) ARCH DEV CORP.

Di Rienzo A, Iyer L, Ratain MJ;

WPI; 2002-588597/63.

gene promoter, useful for optimizing drug dosages for a patient, comprises determining the presence of five thymidine-adenine repeats in polymorphisms in uridine diphosphate glucuronosyltransferase Detecting

Claim 7; Col 17; 13pp; English.

The invention relates to detecting (M1) polymorphisms in a uridine diphosphate glucuronsyltransferase (UGT) gene promoter by determining the presence of five thymidine-adenine (TA) repeats in the promoter, where the presence of the five TA repeats correlates with increased expression of the gene. The method is used for detecting polymorphisms in a UGT gene promoter. (M1) is conscreening individuals for variation in glucuronidation activity, for optimising drug dosages for a patient, where the drugs (G. irinotecan or TAS-103) are glucuronidated by UGT (preferably UGTIA) and the activity of the drug is effected by its level of contrained in the method preferably involves obtaining DNA from an individual, amplifying all or part of a UGT gene promoter (UGTIA) gene contained in the DNA baing amplified comprises all or part of in the promoter. Thus the DNA baing amplified comprises all or part of the number of TA repeats is determined by a polymerase chain reaction and the number of TA repeats is determined by gel electrophoresis or by capeats (TA) 7. The promoter has any one of the genotypes (TA) 5. (TA) 6. (TA) 7. (TA) 8. (M1) is also useful for predicting an individuals sensitivity to xenobiotics that are glucuronidated by a UGT (preferably contexts in a UGT gene, promoter, where the number of TA repeats CTA) 5. (TA) 5. (TA) 5. (TA) 6. (TA) 7. (TA) 8. (M1) is also useful for predicting an individuals sensitivity to xenobiotics that are glucuronidated by a UGT (Preferably to xenobiotics that are glucuronidated by a UGT (Preferably to xenobiotics that are glucuronidated by a UGT (Preferably involve determining the promoter. Where the number of TA repeats in a UGT gene promoter, where the number of a preferably involve determining the promoter. Defects in glucurodination is associated with repeats in the promoter. Defects in glucurodination is essentiated with the promoter. Defects in glucurodination is essentiated by the UGT gene, and the indivi

Sequence 14 BP; 7 A; 0 C; 0 G; 7 T; 0 U; 0 Other;

Gaps ô Query Match
1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels

1813 TATATATATATA 1826 14 TATATATATATA 1 d

RESULT 321

AAL50676 standard; DNA; 14 BP

AAL50676;

16-JAN-2003 (first entry)

Human uridine diphosphate glucuronosyltransferase gene polymorphism #10.

Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat; uridine diphosphate glucuronosyltransferase gene promoter; UGTLA1; drug dosage optimisation; xenobiotic sensitivity.

Homo sapiens.

US2002115097-A1.

22-AUG-2002.

01-FEB-2002; 2002US-00061693.

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(ARCH-) ARCH DEV CORP
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                                                                                                                                                         Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the promoter
                                                                                                                                                                                                                                                                                                                     05-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-MAY-2002.
                                                                                                                                                                                                                                                                                               ABK90421;
                                                                                                                                               Query Match
                                                                                                                                                                                                                                                   RESULT 323
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                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                   The invention comprises a method for detecting polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter (preferably UGTIA1). The method involves determining the number of thymidiane-adenine (TA) repeats in the promoter - as the number of TA repeats correlates with expression of the UGT gene. The method of the invention is useful for detecting polymorphisms in a UGT gene promoter. The method of the invention is also useful in optimising drug dosages and predicting an individual's sensitivity to xenobiotics for drugs and xenobiotics that are glucuronidated by UGT. The present DNA sequence represents a UGT gene TA repeat polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, involves determining number of thymidine-adenine repeats in the promoter.
                                                                                                   Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, involves determining number of thymidine-adenine repeats in the promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human uridine diphosphate glucuronosyltransferase gene polymorphism #10.
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, polymorphism, TA repeat, ds, UGT; thymidine-adenine repeat, uridine diphosphate glucuronosyltransferase gene promoter; UGTLA1; drug dosage optimisation; xenobiotic sensitivity.
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                                                                                                                                                                                                                                                                                                                   1.3%; Score 14; DB 1; Length 14;
100.0%; Pred. No. 2.2e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                Sequence 14 BP; 7 A; 0 C; 0 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Iyer L, Ratain MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Page 9; 13pp; English.
                                                                                                                                                  Claim 7; Page 9; 13pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAL50676 standard; DNA; 14 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-00251274
             99US-00251274.
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                                                                                                                                                                                                                                                                                                                                                                                         1 TATATATATATA 14
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 14; Conservative
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                                                         Rienzo AD, Iyer L,
                                                                               WPI; 2002-740095/80
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             16-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 322
AAL50676/c
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The invention relates to detecting (M1) polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter by determining the presence of five thymidine-ademine (TA) repeats in the promoter, where the presence of the five TA repeats correlates with increased expression of the gene. The method is used for detecting polymorphisms in a UGT gene promoter, preferably a UGT I (UGTIAI) agene promoter. (M1) is activity, for optimising drug dosages for a patient, where the drugs (e.g. Irinotecan or TAS-103) are glucuronidated by UGT (preferably UGTIAI) and the activity of the drug is effected by its level of glucurodination. The method preferably involves obtaining DNA from an individual, amplifying all or part of a UGT gene promoter (UGTIAI) gene promoter (UGTIAI) gene
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The invention comprises a method for detecting polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter (preferably QUITAL). The method involves determining the number of thymidine-adenine (TA) repeats in the promoter — as the number of TA repeats correlates with expression of the UGT gene. The method of the invention is useful for detecting polymorphisms in a UGT gene promoter. The method of the invention is also useful in optimising drug desages and predicting an individual's sensitivity to xenobiotics for drugs and xenobiotics that are glucuronidated by UGT. The present DNA sequence represents a UGT gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene promoter, useful for optimizing drug dosages for a patient, comprises determining the presence of five thymidine-adenine repeats in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, ds, UGT1A1, promoter, Gilbert's syndrome, hyperbilirubinaemia, uridine diphosphate glucuronosyltransferase, Crigler-Najjar syndrome, UGT, polymorphism detection, TA repeat, glucuronidation, Irinotecan, TAS-103, xenobiotic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.3%; Score 14; DB 1; Length 14; 100.0%; Pred. No. 2.2e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human UGTlal promoter polymorphism (TA)6 repeat region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14 BP; 7 A; 0 C; 0 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratain MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 6; Col 11; 13pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               IA repeat polymorphism
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in the promoter. Thus the DNA being amplified comprises all or part of UGTIA1 promoter. The DNA is amplified by a polymerase chain reaction and the mumber of TA repeats is determined by gel electrophoresis or by sequencing the amplified DNA. The polymorphism comprises an allele consisting of five TA repeats (TA)5, or seven TA repeats (TA)7. The promoter has any one of the genotypes (TA)5, or seven TA (TA)5 (TA)6, (TA)5/(TA)7, (TA)8, (TA)6/(TA)8, (TA)7/(TA)8, (TA)6/(TA)8, (TA)7/(TA)8, (TA)6/(TA)8, (TA)7/(TA)8, (TA)7/(TA)8, (TA)6/(TA)8, (TA)7/(TA)8, (TA)6/(TA)8, (TA)7/(TA)8, (TA)6/(TA)8, (TA)7/(TA)8, (TA)6/(TA)8, (TA)6/(TA)6/(TA)6/(TA)6/(TA)8, (TA)6/(TA)6/(TA)6/(TA)6/(TA)6/(TA)9, (TA)6/(TA)9, (TA)6/(TA)6/(TA)9, (TA)6/(TA)6/(TA)9, (TA)6/(TA)6/(TA)9, (TA)6/(TA)6/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)9/(TA)
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Sequence 15 BP; 8 A; 0 C; 0 G; 7 T; 0 U; 0 Other;

Gaps ; 0 1.3%; Score 14; DB 1; Length 15; 100.0%; Pred. No. 2.3e+02; tive 0; Mismatches 0; Indels 14; Conservative Local Similarity Query Match Matches

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ઠ g RESULT 324

ABK90421 standard; DNA; 15 BP ABK90421; ABK90421/

(first entry) 05-NOV-2002

Human UGT1al promoter polymorphism (TA)6 repeat region.

Human; ds; UGT1A1; promoter; Gilbert's syndrome; hyperbilirubinaemia; uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome; UGT; polymorphism detection; TA repeat; glucuronidation; Irinotecan; TAS-103; xenobiotic.

Homo

US6395481-B1.

28-MAY-2002

16-FEB-1999;

99US-00251274. 16-FEB-1999;

(ARCH-) ARCH DEV CORP.

Ratain MJ; Di Rienzo A, Iyer L,

WPI; 2002-588597/63.

gene promoter, useful for optimizing drug dosages for a patient, comprises determining the presence of five thymidine-adenine repeats in polymorphisms in uridine diphosphate glucuronosyltransferase the promoter. Detecting

Example 6; Col 11; 13pp; English.

The invention relates to detecting (M1) polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter by determining the presence of five thymidine-adenine (TA) repeats in the promoter, where the presence of the five TA repeats correlates with increased expression of the gene. The method is used for detecting polymorphisms in a UGT gene promoter, preferably a UGT I (UGTIAL) gene promoter. (M1) is

The invention comprises a method for detecting polymorphisms in a uridine

userul for Screening non-vigurals for a patient, where the drugs activity, for optimising drug desages for a patient, where the drugs cactivity, for optimising drug desages for a patient, where the drugs of activity of the drug is effected by its level of gruntland and the activity of the drug is effected by its level of gruntland in the DNA and determining the number of TA repeats or promoter. Thus the DNA haid amplified comprises all or part of in the promoter. Thus the DNA haid maplified comprises all or part of the promoter. The DNA is amplified by a polymerase chain reaction and the under of TA repeats is determined by gel electrophoresis or by sequencing the amplified DNA. The polymorphism comprises an allele consisting of five TA repeats (TA) 5, six TA repeats (TA) 5, (TA) Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, involves determining number of thymidine-adenine repeats in the promoter. Human uridine diphosphate glucuronosyltransferase gene polymorphism #12. Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat; uridine diphosphate glucuronosyltransferase gene promoter; UGTLA1; drug dosage optimisation; xenobiotic sensitivity. useful for screening individuals for variation in glucuronidation .. 0 1.3%; Score 14; DB 1; Length 15; 100.0%; Pred. No. 2.3e+02; tive 0; Mismatches 0; Indels Sequence 15 BP; 8 A; 0 C; 0 G; 7 T; 0 U; 0 Other; Example 6; Page 2; 13pp; English Rienzo AD, Iyer L, Ratain MJ; BP. 01-FEB-2002; 2002US-00061693 99US-00251274 1813 TATATATATATA 1826 AAL50678 standard; DNA; 15 (first entry) Query Match
Best Local Similarity 100.0
Matches 14; Conservative 14 rararararara 1 (ARCH-) ARCH DEV CORP. WPI; 2002-740095/80. US2002115097-A1. 16-FEB-1999; Homo sapiens 16-JAN-2003 22-AUG-2002 AAL50678; RESULT 325 AALSO678

ID AALS

AAC AALS

XXX AALS

DE Huma

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The invention comprises a method for detecting polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter (preferably UGTALAI). The method involves determining the number of thymidine-adenine (TA) repeats in the promoter — as the number of TA repeats correlates with expression of the UGT gene. The method of the invention is useful for detecting polymorphisms in a UGT gene promoter. The method of the invention is also useful in optimising drug dosages and predicting an individual's sensitivity to xenobiotics for drugs and xenobiotics that are glucuronidated by UGT. The present DNA sequence represents a UGT gene
diphosphate glucuronosyltransferase (UGT) gene promoter (preferably UGT1A1). The method involves determining the number of thymidine-adenine (TA) repeats in the promoter - as the number of TA repeats correlates with expression of the UGT gene. The method of the invention is useful for detecting polymorphisms in a UGT gene promoter. The method of the invention is also useful in optimising drug dosages and predicting an individual's sensitivity to xenobiotics for drugs and xenobiotics that are glucuronidated by UGT. The present DNA sequence represents a UGT gene TA repeat polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene promoter, useful for optimizing drug dosages for a patient, involves determining number of thymidine-adenine repeats in the promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human uridine diphosphate glucuronosyltransferase gene polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, polymorphism, TA repeat, ds, UGT, thymidine-adenine repeat, uridine diphosphate glucuronosyltransferase gene promoter, UGTLA1, drug dosage optimisation, xenobiotic sensitivity.
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                                                                                                                                                                                                                                                     Query Match 1.3%; Score 14; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 2.3e+02; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                 Sequence 15 BP; 8 A; 0 C; 0 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15 BP; 8 A; 0 C; 0 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 6; Page 2; 13pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratain MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВÞ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-00251274.
                                                                                                                                                                                                                                                                                                                                            1813 TATATATATATA 1826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-2002; 2002US-00061693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AALS0678 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                 1 TATATATATATA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ARCH-) ARCH DEV CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Iyer 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-740095/80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2002115097-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAL50678;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 326
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The present sequence represents the preferred target sequence for an enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves the human a-myb sequence at the base position indicated in the descriptor line. The c-myb sequence was screened for optimal ribozyme target sites using a computer folding algorithm, and regions of the mRNA which did not form secondary folding structures and contained potential ribozyme activities optimised by either varying the length of the binding arms or by modification to prevent degradation by nucleases. The ribozymes cleave the c-myb sequence and can be used to prevent smooth muscle cell hyperproliferation in restenosis, especially after coronary angioplasty,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New enzymatic nucleic acid molecules - cleave RNA produced by e.g. c-myb, for treating restenosis or cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                       Human c-myb hammerhead ribozyme target sequence (nt. position 2898)
                                                                                                                                                                                                              Enzymatic nucleic acid, hammerhead, ribozyme, cleavage, human, smooth muscle cell; hyperproliferation; restenosis; cancer; c-myb;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jarvis T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17 BP; 7 A; 1 C; 0 G; 0 T; 9 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.3%; Score 14; DB 1; Le 1.00.0%; Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Pred. No. 2.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stinchcomb DT, Draper K, Mcswiggen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 78; 128pp; English.
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ID AAT27921 standard; DNA; 17 BP
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95US-00373124.
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1813 TATATATATATA 1826
                                                                                                   AAT81559 standard; RNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                              (RIBO-) RIBOZYME PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 richarararara 2
                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                    coronary angioplasty; ss
               WPI; 1996-010927/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                      18-MAY-1995;
                                                                                                                                                                                                                                                                                  Ношо варіеля
                                                                                                                                                                                                                                                                                                             W09531541-A2
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                                                                                                                                                                                                                                                                                                                                         23-NOV-1995
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1.3%; Score 14; DB 1; Length 15; 100.0%; Pred. No. 2.3e+02; tive 0; Mismatches 0; Indels

Conservative

Local Similarity ses 14; Conserv

Best Loc Matches

Query Match

(LYNX-) LYNX THERAPEUTICS INC

01-SEP-2000; 2000US-0654187P.

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Detecting polymorphisms between 2 nucleic acid samples, esp. in microsatellite regions, comprises digesting the nucleic acid to generate fragments. Jigating adaptor segments to their ends, amplifying them using primer directed amplification and comparing the prods. to detect differences. The primers used in the amplification comprise a primer consisting of a perfect cpd. simple sequence repeat (SSN), and an adaptor segment. The present sequence complementary to an adaptor segment. The present sequence is an example of a SSR primer. The method is partic, useful for genome fingerprinting, i.e. for genetic trait marking and germplasm comparisons
                                                                                                                                                                                                                                                                                                                                                                                    Modified amplified fragment length polymorphism assay - for detection of polymorphism esp. in micro:satellite regions.
                                           Detection; polymorphism; perfect compound simple sequence repeat; adaptor directed primer; genome; genetic; fingerprinting; amplified fragment length polymorphism assay; microsatellite region; genetic trait marking; germplasm comparisons; 5'-anchored; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide sequence identified using ligation-based DNA sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
1.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence signature; nucleotide sequencing; ss.
             5'-anchored simple sequence repeat primer CGG(CA)6.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 BP; 7 A; 8 C; 2 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 77; 173pp; English
                                                                                                                                                                                                                                                                                       (DUPO ) DU PONT DE NEMOURS & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH74947 standard; DNA; 17 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-FEB-2000; 2000US-0182454P.
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                                                                                                                                                                                                                        95WO-US015150.
                                                                                                                                                                                                                                                         94US-00346456
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                                                                                                                                                                                                                                                                                                                        Vogel JM;
                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-277795/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200161044-A1
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                                                                                                                                                          WO9617082-A2
                                                                                                                                                                                                                                                         28-NOV-1994;
                                                                                                                                                                                                                          21-NOV-1995;
                                                                                                                                                                                                                                                                                                                          Morgante M,
                                                                                                                                                                                           06-JUN-1996
                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH74947;
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AAH74947
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                                                                                                                                                                                                                The specification describes a method for determining a nucleotide sequence signature. The method comprises obtaining optical measurements with values indicating each nucleotide in a group of nucleotide positions, adjusting the values until the ratio of highest value in the set to next highest values in the set is at least a predetermined factor, and generating a base call for a position in the group based on results after the adjustment of values. The method is used for determining a signature of a nucleotide sequence, and for determining a nucleotide sequence of a polynucleotide from a series of optical measurements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic, antiviral, neuroprotective, nootropic, neuroleptic, ss;
primer, probe, tumour suppression, tumour reversion, apoptosis;
virus resistance, transgenic animals, Alzheimer's disease, schizophrenia;
                                                                                                                      Determining nucleotide sequence signature, by obtaining optical values for each nucleotide position in a group, adjusting them to get ratio of final highest values near predetermined factor, generating base call.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.3%; Score 14; DB 1; Length 17; ilarity 100.0%; Pred. No. 2.5e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumour suppression/reversion associated nucleotide #5823.
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17 BP; 7 A; 1 C; 4 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 712; 771pp; French
                                                                                                                                                                                        Disclosure, Fig 120; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tuijnder M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR ENGINES LAB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-SEP-2001; 2001FR-00011981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-SEP-2002; 2002WO-IB004219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2245 TCTAGTTGAAATA 2258
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                                                                                              WPI; 2001-522608/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003040369-A2
                                                              Corcoran KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                           nvention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Matches
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fragments of at least 15 consecutive nucleotides of these nucleotides, a fragments of at least 15 consecutive nucleotides of these nucleotides, a sequence having at least 80% identity, after optimal alignment, with the nucleotides, or the complement, or corresponding RNA, of the nucleotides, or the complement, or corresponding RNA, of the nucleotides. The nucleotides are used as probes or primers for detecting, clantifying and/or amplifying nucleotides involved in tumour suppression or reversion, apoptosis and or viral resistance, to produce recombinant polypeptides, and to prepare transgenic animals, as experimental models. The nucleotides (also vectors containing them and cells containing the vectors), the encoded polypeptides and antibodies (AD) against the polypeptide are useful for prevention and/or treatment of viral infections or diseases characterized by development of tumours or cell degeneration (e.g. Alzheimer's disease or schizophrenia).

Analysis of the expression of the nucleotides can be used for diagnosis and/or prognosis of these diseases. The nucleotides and polypeptides can be used to screen for their specific interactive molecules, the nucleotide for prevention also be used to screen for their specific interactive molecules.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bnzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogène; translocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; atheroselerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial ischaemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat ICAM hammerhead ribozyme target sequence (nt. position 2911).
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1.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence 17 BP; 4 A; 2 C; 2 G; 9 T; 0 U; 0 Other;
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94US-00218934.
94US-00222795.
94US-00227958.
94US-00228041.
94US-00228041.
94US-0025136.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-APR-1994;
18-MAY-1994;
06-JUL-1994;
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03-APR-1997
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X88888888888888888888888
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The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the nucleotide base position indicated in the DE line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve thair nuclease resistance. The ribozymes clave the ICAM-1 target sequences and thereby inhibit ICAM-1 expression, making them useful for reducing transplant rejection and alleviating symptoms in patients with rheumatoid arthritis, asthma and other inflammatory disorders. (Updated on 25-WAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                    mb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
Usman N, Wincott FE, Woolf T;
                                                                                                                                                                                                                                                                                                                                                                                                Ribozymes having modified bases and methods for producing them - for use in inhibiting disease related genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human c-myb hammerhead ribozyme target sequence (nt. position 2527).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enzymatic nucleic acid, hammerhead, ribozyme, cleavage, human; smooth muscle cell; hyperproliferation; restenosis; cancer; c-myb; coronary angioplasty; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.3%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 2.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17 BP; 2 A; 7 C; 0 G; 0 T; 8 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 204; 407pp; English.
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         94US-00292620.
94US-00293520.
94US-00303039.
94US-00311486.
94US-00311749.
94US-00316771.
94US-00334847.
94US-00334847.
94US-00334847.
94US-00334847.
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                                                                                                                                                                                                                                                                 (RIBO-) RIBOZYME PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 88.2
Les 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-351090/45.
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                                                                                                  28-SEP-1994;
03-OCT-1994;
07-OCT-1994;
11-OCT-1994;
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                                                                                                                                                                                                                                                                                               Stinchcomb
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Modak A,
Tracz D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT81448;
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Matches
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Example 1; Page .77; 173pp; English
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96US-00584040.
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                                                                                                                                                                                                                                                                                                                      1.3%;
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                                                                                                                                                                                                                                                                                                                                                                                 1789 ATATTGTGTGTGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX69800 standard; RNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Foetal liver kinase 1; ss.
                                                                                                                                                                                                                                                                                                                   Query Match 1.3
Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mcswiggen J,
                                                                                                                                                                                                                                                           germplasm comparisons
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX69800
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                                                                                                                                                                                                                                                                                     The present sequence represents the preferred target sequence for an enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves the human c-myb sequence at the base position indicated in the descriptor line. The c-myb sequence was screened for optimal ribozyme target sites using a computer folding algorithm, and regions of the mRNA which did not form secondary folding structures and contained potential ribozyme cleavage sites were identified. Ribozymes were synthesised and their activities optimised by either varying the length of the binding arms or by modification to prevent degradation by nucleases. The ribozymes cleave hyperproliferation in restenosis, especially after coronary angioplasty, and in cancers
                                                                                                                                                                                                                New enzymatic nucleic acid molecules - cleave RNA produced by e.g. c-\pi y b, for treating restenosis or cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detection; polymorphism; perfect compound simple sequence repeat; adaptor directed primer; genome; genetic; fingerprinting; amplified fragment length polymorphism assay; microsatellite region; genetic trait marking; germplasm comparisons; 5'-anchored; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 13.8; DB 1; Length 17;
Pred. No. 2.7e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5'-anchored simple sequence repeat primer VHVH(TG)6.5.
                                                                                                                                                       Jarvis T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17 BP; 8 A; 1 C; 0 G; 0 T; 8 U; 0 Other;
                                                                                                                                                       Stinchcomb DT, Draper K, Mcswiggen J,
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                                                                                                                                                                                                                                                               Claim 1; Page 75; 128pp; English.
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Best Local Similarity 88.2%;
Matches 15; Conservative
                                               95WO-US006368
                                                                          94US-00245466
95US-00373124
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                                                                                                                         (RIBO-) RIBOZYME PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-277795/28
                                                                                                                                                                                      WPI; 1996-010927/01
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                                                18-MAY-1995;
                                                                                            13-JAN-1995;
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                23-NOV-1995
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RESULT 333 AAT27920

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                                                                                                                                                                                                                    Detecting polymorphisms between 2 nucleic acid samples, esp. in microsatellite regions, comprises digesting the nucleic acid to generate fragments, ligating adaptor segments to their ends, amplifying them using primer directed amplification and comparing the prods. to detect differences. The primers used in the amplification comprise a primer directed primer, comprising of a perfect cpd. simple sequence repeat (SSR), and an adaptor segment. The present sequence complementary to an adaptor segment. The present sequence is an example of a SSR primer, which is modified amplified fragment polymorphism assay, which is partic. useful for genome fingerprinting, i.e. for genetic trait marking and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1; XDR; hammerhead ribozyme; hairpin ribozyme; cleavage; tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease; fms-like tyrosine kinase 1; Kinase insert domain containing receptor;
Modified amplified fragment length polymorphism assay - for detection of polymorphism esp. in micro:satellite regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid molecule modulating VEGF receptor(s) gene expression or stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 17;
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Pred. No. 2.7e+02;
4; Mismatches 0;
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Best Local Similarity
               Matches
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(preferably human) having a condition associated with the level of the fms-like tyrosine kinase i (flt-1), kinase insert domain containing receptor (KDR) and/or foeral liver kinase 1 (flk-1) (e.g. tumour angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAX67275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention
                                                                                                                                                                                                                                                                                                                                                                                  Vascular endothelial growth factor receptor; VBGF receptor; flt-1; flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage; tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease; fms-like tyrosine kinase 1; kinase insert domain containing receptor;
                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                           Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #732.
                                                                                                                              1.3%; Score 13.8; DB 1; Length 17; 5.9%; Pred. No. 2.7e+02; tive 14; Mismatches 2; Indels
                                                                                                         Sequence 17 BP; 0 A; 1 C; 0 G; 0 T; 16 U; 0 Other;
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                                                                                                                                                                                       1864 CTTTTTATTTTTTT 1880
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96US-00584040
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                                                                                                                                                                                                                                                                                 AAX73299 standard; RNA; 17
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foetal liver kinase 1; ss
                                                                                                                                                              Conservative
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                                                                                                                                   Query Match
Best Local Similarity
Matches 1; Conserv
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11-JAN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus sp.
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1.3%; Score 13.8; DB 1; Length 17;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage; tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease; fms-like tyrosine kinase 1; kinase insert domain containing receptor;
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70.6%; Pred. No. 2.7e+02;
iive 3; Mismatches 2; Indels
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                                                                                       1643 CCTTAAGTCAGAACAGC 1659
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96US-00584040.
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les 10; Conservative
                                    12; Conservative
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11-JAN-1996;
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ID AAV
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Human, c-raf, A-raf, B-raf, hammerhead ribozyme, hairpin ribozyme; target, substrate, catalyst, modulation; expression; Raf gene; delivery; screening; identification; synthesis, deprotection; purification; cancer; inflammation, psoriasis; non-hepatic ascites; infection; genetic drift; restenoess; rhumatoid arthritis; ss. target site nucleotide position 2903. 97US-0046059P. 97US-0049002P. 97US-0051718P. 98WO-US009249 (first entry) Homo sapiens WO9850530-A2 18-FEB-1999 05-MAY-1998; Human C-raf 09-MAY-1997 AAV91401;

9703-0056808P. 9703-0061321P. 9703-0061324P. 9703-0064866P. 9703-0068212P. (RIBO-) RIBOZYME PHARM INC.

Burgin A; Kisich K, Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Thompson J, Workman CT, Beaudry A, Sweedler D;

WPI; 1999-009494/01.

Identifying new catalytic nucleic acid that modulates selected processes - especially ribozymes that cleave Raf RNA for treating cancer, restenosis, and also new ribozymes and modified nucleoside triphosphates used as antiviral agents and synthons.

Claim 177; Page 154; 259pp; English.

capable of medulating a process in a biological system. The method capable of modulating a process in a biological system. The method comprises: (a) introducing into the system a random library of nucleic comprises: (a) introducing into the system a random library of nucleic confactalysts (NAC) having a substrate binding domain (SBD), comprising a random sequence, and a catalytic domain (CD); and (b) identifying NAC in systems where modulation has occurred and/or determining the sequence of ar least part of the SBDs in such systems. Nucleic acid molecules with cendonuclease activity and catalytic activity, from the present invention, are used to modulate gene expression in plant and mammalian cells and to cleave target nucleic acid, particularly for treating systemic diseases caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic ascites and infection. They may also be used to detect genetic drift and custant cancer, restenosis, psoriasis of the Raf gene, are used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or center modifications in addition associated with the level of c-raf. Introduction of super/phosphate modifications in discasses stability against nuclease and cutivity AAV99022 to AAV93877 represent NACE that can be used in the method has been developed for the identification of a nucleic acid method, specifically for modulating the expression of a Raf gene

Sequence 17 BP; 3 A; 1 C; 2 G; 0 T; 11 U; 0 Other;

Gaps ö Query Match
1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 29.4%; Pred. No. 2.7e+02;
Matches 5; Conservative 10; Mismatches 2; Indels

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AAUUUUGUUUUUAUUGC 17

AAX18370 standard; DNA; 17

AAX18370

11-MAY-1999

AAX18370;

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Peptides having at least two new nucleotides - useful as primers in RT-
                                  RT-PCR primer; DNA sequence determination; gene sequence analysis;
                         RT-PCR primer of the invention SEQ ID 11
                                                                                         97JP-00208312.
                                                                                                    (TAKI ) TAKARA SHUZO CO
                                                                                                                WPI; 1999-183822/16
                                                          JP11032765-A.
                                                                                           18-JUL-1997;
                                                                     09-FEB-1999
                                               Synthetic.
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This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta any; ,or (X)m5'-(agamma) k-(delta-N3'), where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thywine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine or vytosine; N = adenine, guanine, cytosine or thymine; gamma = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, quanine and/or cytosine. The new nucleotides are useful as primers for KT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene Disclosure; Page 11; 19pp; Japanese. sequences

Sequence 17 BP; 2 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Gaps 0 1.3%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 2.78+02; ive 0; Mismatches 2; Indels Query Match 1.3 Best Local Similarity 88.2 Matches 15, Conservative

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AAA36022 standard; DNA; 17 BP. AAA36022; AAA36022/c

(first entry) 26-JUL-2000 Human genomic SNP allele specific oligonucleotide SEQ ID NO:79

Human, single nucleotide polymorphism, SNP; genotyping; DNA analysis; allele specific oligonucleotide, ASO; reduced complexity genome; RCG; genomic classification; identification; DNA fingerprinting; tumour characterisation; hybridisation; SN

1870 ATTITIGITITIAATGC 1886

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WO200018960-A2
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Landers JE,
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                                                                                                                                                                                                                                                                                                                                           Detection of single nuclectide polymorphisms in genomes by preparation and analysis of reduced complexity genomes, useful for genotyping, fingerprinting and determining allele frequency of SNPs.
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88.2%; Pred. No. 2.7e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17 BP; 6 A; 4 C; 2 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                    (MASI ) MASSACHUSETTS INST TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 55; 111pp; English
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Best Local Similarity 88.2
Matches 15; Conservative
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         Homo sapiens
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A method has been developed for detecting the presence or absence of a single nucleotide polymorphism (SNP) allele in a genomic sample. The method comprises preparing a reduced complexity genome (RCG) from the genomic sample and annalysing the RCG for the presence or absence of a SNP allele. The method can be used to characterise a tumour, to generate a genomic pattern for an individual genome or to generate a genomic classification code for a genome. The method can be used to assess whether a subject is a risk for developing a disease or to identify a set of SNP alleles associated with a disease. The method can also be used to perform linkage analysis. AAA35944 to AAA35947 represent sequences used in the exemplification of the present invention. AAA35948 to AAA3632 represent nucleotide sequences containing SNPs
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                                                                                                                                 Detection of single nucleotide polymorphisms in genomes by preparation and analysis of reduced complexity genomes, useful for genotyping, fingerprinting and determining allele frequency of SNPs.
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88.2%; Pred. No. 2.7e+02;
iive 0; Mismatches 2;
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Charest
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Housman DE,
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Best Local Similarity 88.2
Matches 15; Conservative
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       Jordan B,
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Length 17;

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A method has been developed for detecting the presence or absence of a single nucleotide polymorphism (SNP) allele in a genomic sample. The method comprises preparing a reduced complexity genome (RCG) from the genomic sample and analysing the RCG for the presence or absence of a SNP allele. The method can be used to characterise a tumour, to generate a genomic pattern for an individual genome or to generate a genomic classification code for a genome. The method can be used to assess whether a subject is at risk for developing a disease or to identify a set of SNP alleles associated with a disease. The method can also be used to perform linkage analysis. AAA35944 to AAA35947 represent sequences used in the exemplification of the present invention. AAA35948 to
method comprises preparing a reduced complexity genome (RCG) from the genomic sample and analysing the RCG for the presence or absence of a SNP allele. The method can be used to characterise a tumour, to generate a genomic pattern for an individual genome or to generate a genomic pattern for an individual genome or to generate a genomic a subject is at risk for developing a disease or to identify a set of SNP alleles associated with a disease. The method can also be used to perform linkage analysis. AAA35944 to AAA35947 represent sequences used in the exemplification of the present invention. AAA35948 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detection of single nucleotide polymorphisms in genomes by preparation and analysis of reduced complexity genomes, useful for genotyping, fingerprinting and determining allele frequency of SNPs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; single nucleotide polymorphism; SNP; genotyping; DNA analysis; allele specific oligonucleotide; ASO; reduced complexity genome; RCG; genomic classification; identification; DNA fingerprinting; tumour characterisation; hybridisation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genomic SNP allele specific oligonucleotide SEQ ID NO:29.
                                                                                                                                                                                                                                                                  Length 17;
                                                                                                                                                                                                                                                                Score 13.8; DB 1; Length 1:
Pred. No. 2.7e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                     AAA36632 represent nucleotide sequences containing SNPs
                                                                                                                                                                                                                              Sequence 17 BP; 6 A; 4 C; 2 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Housman DE, Charest A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MASI ) MASSACHUSETTS INST TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 54; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                    1379 TGGTTTGAAGAATGTTA 1395
                                                                                                                                                                                                                                                                    1.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US022283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA35972 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                           17 recerrehada arerra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jordan B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-293181/25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA35972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 342
AAA35972/c
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with a target sequence and contain at least one phosphoro(di)[hioate (III., having endonuclease activity. (A), and more generally any catalytic link, having endonuclease activity. (A), and more generally any catalytic nucleic acid (A) that modulates expression of the oestrogen receptor gene, are used to treat cancer [particularly of breast or endometrium). (C) in vivo or by transforming cells ex vivo and implanting treated cells, or for other conditions associated with levels of oestrogen receptor. (C) particularly for the high selectivity for targeted RNA, (A) can also be used to correlate inhibition of gene expression with alterations in phenotype, (C) particularly for identification of therapeutic targets, and as research cragents (for RNA, in the same way that restriction endonucleases are used with DNA). The combination of modifications in (A) improves (AAA214747 represent oestrogen receptor hardrens sequences, and AAA2148 to AAA22010 represent their corresponding target sequences. (C) AAA22148 to AAA22010 represent their corresponding target (C) AAA22010 represent their corresponding target (C) AAA22010 represent cestrogen receptor hardrens and C) sequences, and AAA26107 to AAA26107 to AAA26107 represent their corresponding target (C) and C) a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acids that interact, and optionally cleave, target sequences,
                                                                                                                                                                                                                                                                                                                                                                                                                      Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1948.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide; gene expression modification; cancer; phosphorothioate; endonuclease;
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes nucleic acids (A) that interact
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Score 13.8; DB 1; Length 1 Pred. No. 2.7e+02; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mcswiggen JA, Karpeisky A, is T, Woolf T, Haeberli P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anticancer; breast cancer; endometrium cancer; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thompson JD, Beigelman L, Mcswit
Reynolds M, Zwick M, Jarvis T,
Matulic-Adamic J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 77; Page 79; 148pp; English
                                                                                                      1395
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  1.3%;
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                                                                                                        1379 TGGTTTGAAGAATGTTA
                                                                                                                                                     17 reserreaasaarerra
                                                                                                                                                                                                                                                                           AAA25450 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                              (first entry)
          Query Match
Best Local Similarity 88.2
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used to treat cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-013248/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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23-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                              19-JUL-2000
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                                                                                                                                                                                                                                                                                                                               AAA25450;
                                                                                                                                                                                                                                 RESULT 343
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ID AAA2
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DB 1; Length 17;

1.3%; Score 13.8;

Query Match

Sequence 17 BP; 6 A; 4 C; 2 G; 5 T; 0 U; 0 Other

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Gaps
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Best Local Similarity 88.2%; Pred. No. 2.7e+02; Matches 15; Conservative 0; Mismatches 2; Indels
                                                                1865 TITITATITITATI 1881
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rtititrititiii 17

AAA25180 standard; DNA; 17 BP. RESULT 344

(first entry)

19-JUL-2000

Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1678.

Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide; gene expression modification; cancer; phosphorothioate; endonuclease; anticancer; breast cancer; endometrium cancer; ss.

Homo sapiens.

28-OCT-1999

99WO-US008547. 19-APR-1999;

98US-0082404P. 98US-00103636. 23-JUN-1998;

RIBO-) RIBOZYME PHARM INC.

Bellon L; Karpeisky A, Haeberli P; Thompson JD, Beigelman L, Mcswiggen JA, F Reynolds M, Zwick M, Jarvis T, Woolf T, Matulic-Adamic J;

WPI; 2000-013248/01

nucleic acids that interact, and optionally cleave, target sequences, used to treat cancer

Claim 77; Page 71; 148pp; English.

The present invention describes mucleic acids (A) that interact stably with a target sequence and contain at least one phosphoro(di)thioate link, having endonuclease activity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the oestrogen receptor gene, are used to treat cancer (particularly of breast or endometrium), in vivo or by transforming cells ex vivo and implanting treated cells, or for other conditions associated with levels of estrogen receptor. Because of the high selectivity for targeted RNA, (A) can also be used to correlate inhibition of gene expression with alterations in phenotype, particularly for identification of the restriction endonucleases are reagents (for RNA, in the same way that restriction endonucleases are used with DNA). The combination of modifications in (A) improves resistance to nucleases, binding affinity and/or activity. AAAA23503 to AAA2593 to AAA2592 represent ceptor hancehording target sequences.

AAA25931 to AAA26105 represent oestrogen receptor hairpin ribozyme sequences.

AAA25931 to AAA26107 to AAAA6618 represent their corresponding target sequences. AAAA26219 to AAAA2621 to Expresent other ribozyme sequences and entitions oligonucleotides used in the exemplification of the present

Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

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Score 13.8; DB 1; Length 17;
Pred. No. 2.7e+02;
0; Mismatches 2; Indels
    Query Match
Best Local Similarity 88.2%;
Matches 15; Conservative (
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Gaba

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Retroviral expression vector, useful in gene therapy, contains a promoter from a human endogenous retrovirus to provide cell-specific expression.
                                                                                                                      Cell-specific expression, tissue-specific expression, gene therapy, LTR;
U3-R segment, long terminal repeat, retroviral expression vector;
                                                                                                                                                                                                                                          (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.
                                                                                                         Human retrovirus HERV LTR PCR primer #31.
                                                                                                                                                                                                                                                                                                                    Disclosure; Page 27; 67pp; German
                                                                                                                                                                                                                                                            Baust
1865 TITITATITIGITIT 1881
         1 Tritightintatiti 17
                                                        AAA98232 standard; DNA; 17 BP.
                                                                                                                                                                                                           39-MAR-2000; 2000WO-EP002064
                                                                                                                                                          Human endogenous retrovirus
                                                                                                                                                                                                                                                           Leib-Moesch C, Schoen U,
                                                                                         (first entry)
                                                                                                                                                                                                                                                                            WPI; 2000-587442/55.
                                                                                                                                          PCR primer; ss.
                                                                                                                                                                           WO200053789-A2.
                                                                                                                                                                                                                            10-MAR-1999;
                                                                                         30-JAN-2001
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                                                                          AAA98232;
                                          RESULT 345
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This invention describes a novel retroviral expression vector (A) containing DNA sequences (I) for packaging vector RNA and for cell-containing DNA sequences or peptides encoding by heterologous DNA specific expression contain a cell-containing the sequences controlling cell-specific expression contain a cell-capecific and elucaryotic cells containing (A); (b) prokaryotic and elucaryotic cells containing (A); (c) entroded for a containing a retroviral expression vector RNA derived from (A); (e) a containing a retroviral expression vector RNA derived from (A); (e) a containing a retroviral expression cell (G); (f) a method for incorporating protein-encoding nucleic acid sequences into a eukaryotic cell by infection with the virions of (d); (f) a method for incorporating containing (A) and a packaging cell line, that contains at least one infection with a packaging cell line, that contains at least one (receip genes for gene therapy and to produce virions for introducing (I) into the chromosomal DNA of eukaryotic cells, preferably mammalian and specifically human. (A) retain the advantages of usual retroviral contains at sequences with all the signal structures required for transcription in a contain region within the U3-R sequence, they do not introduce any new viral sequences into the genome and recombination will not create new contains and recoving and sequences, they do not introduce any new viral sequences into the genome and recombination will not create new contains and recovering and sequences in a packaging contains and recombination will not create new contains and recovering and recovering and sequences in a packaging contains and recombination will not create new contains and recovering and sequences and sequences in the contains and recombination will not recate new contains and recovering and sequences and sequences and s types of retrovirus. The promoters provide cell or tissue specific expression, according to which HERV they are derived from

Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

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                                 Gaps
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1.3%; Score 13.8; DB 1; Length 17;
88.2%; Pred. No. 2.7e+02;
ative 0; Mismatches 2; Indels
                                    Conservative
      Query Match
Best Local Similarity
Matches 15; Conserv
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The present sequence is that of a phosphorothioate oligonuclectide containing 20 T nucleobases, each having a 2'-methoxyethoxy group on its containing 20 T nucleobases, each having a 2'-methoxyethoxy group on its produced according to the methods of the invention. The invention produced according to the methods of the invention of mixed backbone oligomeric, or chimeric, compounds having phosphoiseter internucleoside linkages in addition to phosphorothoate and/or phosphoramidate internucleoside linkages. The methods also include incorporation of nermothosphate internucleoside linkages. The methods utilise H-phosphonate internucleoside linkages. The methods utilise H-phosphorothioate, phosphorotamidate to boranophosphate internucleoside linkages. Each contiguous region is subsequently oxidized to phosphorothioate, phosphoroamidate or boranophosphate internucleoside linkages prior to further elongation. Mixed backbone oligomeric compounds of the invention are prepared using novel oxidation steps that oxidize a region of 1 or more H-phosphonate configurated regions of 1 or more H-phosphonate internucleoside linkages without degrading existing linkages that have been previously oxidized region of 1 or more H-phosphonate been previously oxidized a region of 1 or more H-phosphonate been previously oxidized a region of 1 or more H-phosphonate configured in the nucleoside compounds of the invention are prepared using primers in PCR, probes, linkers, gene fragments and for other diagnostic reters on e.g. blological tissue, fluid, cells etc., as research reagents,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Preparation of mixed backbone oligomeric compounds useful as e.g. primers for diagnostic tests, involves oxidation of H-phosphonate internucleoside linkages to phosphodiester internucleoside linkages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= b
/note= "phosphorothioate internucleoside linkages"
                                                                                                                                                                                                                                                                                         Phosphorothioate oligonucleotide; H-phosphonate chemistry; ss
                                                                                                                                                                                                                                                                                                                                                                                                                   a "2'-methoxyethoxy modified thymidine"
                                                                                                                                                                                                                                                          2'-Methoxyethoxy-modified phosphorothioate oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
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1. 19
1. 19
1. 4.4ag= a
1. 10cte= "2'-methoxyeth
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1865 TITITATITITET 1881
                                                                                                                                  AAA50197 standard; DNA; 17 BP
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                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and as antiviral agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ISIS-) ISIS PHARM INC.
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modified_base
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                                                                                                                                                                                                                                                                                                                                      Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapa
             Gaps
                                                                                                                                                                                                                          erythropoietin; granulocyte colony stimulating factor;
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             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17 BP; 8 A; 0 C; 3 G; 6 T; 0 U; 0 Other;
88.2%; Pred. No. 2.7e+02;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                         Mcswiggen J;
                                                                                                                                                                                                       Hammerhead ribozyme substrate #1290.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hammerhead ribozyme substrate #644.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 37; Page 85; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1760 AGCCAGATTTTTAAAA 1776
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                                                                                                                                                                                                                                                                                                                                             11-APR-2000; 2000WO-US009721
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                                                                                                                             AAF02995 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                               (RIBO-) RIBOZYME PHARM INC
                                        1865 TITITATITITGITIT
                                                                                                                                                                                (first entry)
  Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                              interferon alpha; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interferon alpha
                                                                                                                                                                                                                                                                                              WO200061729-A2.
                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                        AAF02995;
                                                                                                                                                                                                                                                                                                                                                                                                                         Blatt L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                       RESULT 347
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1.3%; Score 13.8; DB 1; Length 17;

Query Match

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The present invention relates to human testis expressed Patched like C protein (HTPL, see ABV7875 to ABV78762 and ABB98519 to ABB98520). HTPL protein (HTPL, see ABV7875 to ABV78762 and ABB98519 to ABB98520). HTPL consider the single base pair changes introduces a premature stop codon in HTPL-8 (S for short) compared to HTPL-16, for long). HTPL codon in HTPL-8 (S for short) compared to HTPL-16, for long). HTPL codon in HTPL-8 (S for short) expension with the Patched protein. The shared errotural features strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was important in regulating male germ cell development, and the HTPL gene was useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of therapy and manufacture of a medicament for treatment or prevention of HTPL. Such disorders include disorders of testis, or adrenal, and the HTPL Such disorders include disorders of testis, or adrenal, and the HTPL protein marker and potential therapeutic acids are collingally useful diagnostic markers and potential therapeutic acids are male infertility and cancer. The present oligonucleotide was used in an example from the invention
                                                                                                                                                                                                                Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAPP-E; human; pregnancy associated plasma protein E; abortive; contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis; dysgenetic pregnancy; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.3%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 2.7e+02; 7ative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17 BP; 3 A; 2 C; 3 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human PAPP-Ea associated 17-mer SEQ ID 389.
                                                                                                                                                                                                                                                                                                              Example 2; Page 599; 718pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2160 AAGCATTTGTTTCTACT 2176
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30-JAN-2001; 2001WO-US000669.
23-MAY-2001; 2001US-00864761.
09-OCT-2001; 2001US-0327898P.
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(SHAN/) SHANNON M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
hes 15; Conserv
                                                                                                                                                                               WPI; 2002-676582/73.
                                                                                         (AEOM-) AEOMICA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2002102252-A1.
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                                                                                                                                         Zhan J;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                              Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, gene therapy, tumour suppressor; HTPL; chromosome 10p12.1; human testis expressed Patched like protein; testis; adrenal; liver; male germ cell development; bone marrow; brain; kidney; lung; placenta; prostate; skeletal muscle; colon; male infertility; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
         Ribozyme, erythropoietin; granulocyte colony stimulating factor; interferon alpha; ss.
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                                                                                                                                                                                                                                                                                                                                                Mcswiggen J;
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2001WO-US000664.
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2001WO-US000667.
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                                                                                                                                                                                                                                                                                                   (RIBO-) RIBOZYME PHARM INC
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30-JAN-2001; 2
30-JAN-2001; 2
30-JAN-2001; 2
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                                                                                Homo sapiens.
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Query Match

Best Loca: Matches

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ABV82841

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Gaps

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Human PAPP-Ea associated 17-mer SEQ ID 385.
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                                                                                                                                                                                   (GUYY/) GU Y.
(SHAN/) SHANNON M E.
                                                                                                                                                                                             Shannon ME;
  Gu Y, Shannon ME;
                                                                                                                                                           JS2002102252-A1.
                                                                                                                                                                 01-AUG-2002.
                                                                                                                      ABS74859;
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                                                                                                         RESULT 351
ABS74859
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                           This invention describes a novel isolated nucleic acid that encodes one of three new isoforms of human pregnancy associated plasma protein E, harppre. The products of the invention have abortive and contraceptive activity and can be used for gene therapy or in a vaccine. The mucleic acid, polypeptide encoded by it, or antibody to the polypeptide can be used in pharmaceutical compositions or vaccines for preventing or aborting pregnancy. PAPPE is used in the antenatal diagnosis of dysgenetic pregnancies. The nucleic acids are used as probes to assess the level of PAPPE isoform mRNA in chorionic villus samples, and the proteins in chorionic villus samples, to diagnose dysgenetic pregnancies antenatally. This sequence represents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention
                                                                                                                                           New isolated nucleic acid encoding an isoform of human pregnancy associated plasma protein E, for preventing or aborting pregnancy
                                                                                                                                                                                                                                  Example 2; Page 126; 353pp; English
                                                                                WPI; 2002-697817/75
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0; Gaps Query Match
1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels Sequence 17 BP; 2 A; 0 C; 6 G; 9 T; 0 U; 0 Other;

ABS74859 standard; DNA; 17 BP

PAPP-E; human; pregnancy associated plasma protein E; abortive; contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis; dysgenetic pregnancy; primer; ss.

26-MAY-2000; 2000US-0207456P.

WPI; 2002-697817/75.

New isolated nucleic acid encoding an isoform of human pregnancy associated plasma protein E, for preventing or aborting pregnancy

Sxample 2; Page 125; 353pp; English.

This invention describes a novel isolated nucleic acid that encodes one of three new isoforms of human pregnancy associated plasma protein ${\rm E}_{\nu}$

hPAPP-E. The products of the invention have abortive and contraceptive activity and can be used for gene therapy or in a vaccine. The nucleic used in playapetide encoded by it, or antibody to the polypeptide can be used in pharmaceutical compositions or vaccines for preventing or aborting pregnancy. PAPP-E is used in the antenatal diagnosis of the level of PAPP-E is used in the antenatal diagnosis of an aborting pregnancies. The nucleic acids are used as probes to assess the level of PAPP-E isoform mRNA in chorionic villus samples, and the antibodies can be used to assess the expression levels of PAPP-E isoform proteins in chorionic villus samples, to diagnose dysgenetic pregnancies antenatally. This sequence repersents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention

Sequence 17 BP; 1 A; 0 C; 7 G; 9 T; 0 U; 0 Other;

Gaps .. 0 1.3%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 2.7e+02; ive 0; Mismatches 2; Indels ilarity 88.2%; Conservative Local Similarity hes 15; Conserv

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1793 TGTGTGTGTGTGTGT 1809 TGTGTTTGTGAGTGT 17

ABS74862

ABS74862 standard; DNA; 17 BP

ABS74862;

(first entry) 24-DEC-2002

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Human PAPP-Ea associated 17-mer SEQ ID 388.

PAPP-E; human; pregnancy associated plasma protein E; abortive; contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis; dysgenetic pregnancy; primer; ss.

Homo sapiens.

US2002102252-A1

01-AUG-2002.

06-APR-2001; 2001US-00827998.

26-MAY-2000; 2000US-0207456P.

(GUYY/) GU Y. (SHAN/) SHANNON M E.

Shannon ME; Gu Y, WPI; 2002-697817/75.

New isolated nucleic acid encoding an isoform of human pregnancy associated plasma protein E, for preventing or aborting pregnancy

Example 2; Page 126; 353pp; English

This invention describes a novel isolated nucleic acid that encodes one of three new isoforms of human pregnancy associated plasma protein E, hpapp-B. The products of the invention have abortive and contraceptive activity and can be used for gene therapy or in a vaccine. The nucleic acid, polypeptide encoded by it, or antibody to the polypeptide can be used in pharmaceutical compositions or vaccines for preventing or aborting pregnancy. PAPP-E is used in the antenatal diagnosis of dysgenetic pregnancies. The nucleic acids are used as probes to assess the level of PAPP-E isoform mRNA in chorionic villus samples, and the antibodies can be used to assess the expression levels of PAPP-E isoform proteins in chorionic villus samples, to diagnose dysgenetic pregnancies antenatally. This sequence represents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention

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ABS74861;

RESULT 353 ABS74861

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This invention describes a novel isolated nucleic acid that encodes one of three new isoforms of human pregnancy associated plasma protein E, heapp-E. The products of the invention have abortive and contraceptive activity and can be used for gene therapy or in a vaccine. The mucleic acid, polypeptide encoded by it, or antibody to the polypeptide can be used in pharmaceutical compositions or vaccines for preventing or used in pharmaceutical compositions or vaccines for preventing or dysgenetic pregnancies. The nucleic acids are used as probes to assess the level of PAPP-E isoform mRNA in chorionic villus samples, and the antibodies can be used to assess the expression levels of PAPP-E isoform proteins in chorionic villus samples, to diagnose dysgenetic pregnancies antennally. This sequence represents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention
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                                                                                                                                                                                           pregnancy associated plasma protein E; abortive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid encoding an isoform of human pregnancy associated plasma protein E, for preventing or aborting pregnancy.
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88.2%; Pred. No. 2.7e+02;
ative 0; Mismatches 2; Indels
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                                                                                                                                                 Human PAPP-Ea associated 17-mer SEQ ID 384.
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                                                                                                                                                                                                                                               dysgenetic pregnancy; primer; ss.
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                   ABS74858 standard; DNA; 17
                                                                                                            (first entry)
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Matches 15; Conservative
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(SHAN/) SHANNON M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-697817/75
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ABS74860
ID ABS7486
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                                       Score 13.8; DB 1; Length 17;
Pred. No. 2.7e+02;
0; Mismatches 2; Indels
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Sequence 17 BP; 2 A; 0 C; 7 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human PAPP-Ea associated 17-mer SEQ ID 387.
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                                              1.3%;
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                                              Query Match
Best Local Similarity 88.2
Matches 15; Conservative
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(SHAN/) SHANNON M E.
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Gu Y,

RESULT 354

Gaps

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Human, chloride channel calcium activated 1, CLCA1, ss; antiasthmatic; antiinflammatory; chronic obstructive pulmonary disease; CO2P, asthma; chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel isolated nucleic acid that encodes one of three new isoforms of human pregnancy associated plasma protein E, hPAPP-E. The products of the invention have abortive and contraceptive activity and can be used for gene therapy or in a vaccine. The mucleic acid, polypeptide encoded by it, or antibody to the polypeptide can be used in pharmaccutical compositions or vaccines for preventing or aborting pregnancy. PAPP-E is used in the antenatal diagnosis of dysgenetic pregnancies. The nucleic acids are used as probes to assess the level of PAPP-E isoform mRNA in chorionic villus samples, and the proteins can be used to assess the expression levels of PAPP-E isoform proteins in chorionic villus samples, to diagnose dysgenetic pregnancies antenatally. This sequence represents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid encoding an isoform of human pregnancy associated plasma protein E, for preventing or aborting pregnancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 1 A; 0 C; 8 G; 8 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 126; 353pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1794 GIGIGIGIGIGIGIG 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2001; 2001WO-US024970
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                                                                                                                                                                                                                                   06-APR-2001; 2001US-00827998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-697817/75.
                                                                                                                                                                                                                                                                                                                                                                            (GUYY/) GU Y.
(SHAN/) SHANNON M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gu Y, Shannon ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40200211674-A2.
                                                                                                    US2002102252-A1
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                                     Homo sapiens.
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ABK55689/C
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The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (CDPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions contact are related to or will respond to the levels of LCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, casciated with the level of CLCA1, where the invention further comprises associated with the level of CLCA1, where the invention further comprises treatment, for example, oxygen therapy, bronchodilators, corticosteroids, treatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The camine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 RNA in a cell. This sequence represents an electromagnetic acid molecule of the invention
                                                                                                                                                                       Enzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytostatic; immunostimulant; gene therapy; vaccine; human; zinc finger protein; MDZ3; MDZ4; MDZ1; MDZ12; chromosome 7q22.1; chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer; developmental disorder; ss.
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                                                                                Szymkowski DE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.3%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 2.7e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17 BP; 7 A; 1 C; 1 G; 0 T; 8 U; 0 Other;
                                                                                  Thompson J, Mcswiggen J, Mckenzie T, Ayers D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human MDZ7 scanning oligonucleotide SEQ ID 5257.
                                                                                                                                                                                                                                                      Claim 4; Page 54; 152pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1821 TATATGTACAGTTAT 1837
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             (RIBO-) RIBOZYME PHARM INC. (SYNT ) SYNTEX USA LLC. (THOM/) THOMPSON J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-NOV-2003 (first entry)
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Best Local Similarity 88.2
Matches 15; Conservative
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                                                                                                                                         WPI; 2002-217145/27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP1281758-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADB04271;
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                                                                                                          Grupe A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 357
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The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MDZ3, MDZ4, MDZ1, MDZ1. MDZ3 is concoded at chromosome 7022.1, MDZ4 is encoded at chromosome 6p21.3-22.2, MDZ7 is encoded at chromosome 6p21.3-22.2, MDZ7 is encoded at chromosome 16p11 2 and MDZ12 is encoded at chromosome 16p12 or in manufacturing a medicament for treating or preventing a disorder or increased expression or activity of MDZ3, MDZ4, MDZ1, or MDZ12, e.g. cancer or developmental disorders. The nucleic acids and proteins are also useful for diagnosing or monitoring a disease acids can also be used as probes to detect and characterize gross alterations in MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic acids can also be used as probes to detect and characterize gross alterations in MDZ3, MDZ7, or MDZ12 genetic locus. The probes are protein are useful as therapeutic agency or as proteins are useful as therapeutic agents for gene therapy or as proteins are useful as therapeutic agents for gene therapy or as proteins are useful as therapeutic agents for gene therapy or as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9. .10
/*tag= a
/*tag= "Bases 9 and 10 are linked by a butanediol linker
/note= "Bases 9 and 10 are linked by a nutanediol linker
which is represented as B in page 49 and X in page 59,
Fig 9 and 10 of the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H; antisense; ss.
                                                 New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7 or MDZ12, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense oligo #2, to elicit RNase H degradation of target RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.3%; Score 13.8; DB 1; Length 17; ilarity 88.2%; Pred. No. 2.7e+02; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
                                                                                                                                               Example 8; SEQ ID NO 5257; 103pp; English
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1 CTTTTTTTTTTTTTT 17
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                 WPI; 2003-423107/40
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wes 15; Conserv
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Matches
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Min K;

Parniak MA,

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                                                                                              The invention relates to an acyclic linker-containing oligonucleotide comprising at least one modified deoxyribonucleotide. Oligonucleotides of the invention are useful for preventing or decreasing translation, reverse translation, and/or replication of a target RNA in a system. They are useful for selectively preventing gene expression in a sequence-specific manner, for hybridising to complementary RNA such as cellular mRNA or viral RNA, to hybridise to and induce cleavage of complementary RNA. They are also useful therapeutically in formulations or medicaments to prevent or treat a disease characterised by the expression of a particular target RNA. The invention is used in gene therapy. The present sequence is an antisense oligo used to elicit human RNase (ribonuclease) H degradation of target RNA. This sequence is used in the exemplification
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/*tag= b
//note= "Bases 9 and 10 are linked by a butanediol linker
which is represented as B in page 49 and Fig 5 and as X
in page 52, 55 and Fig 6 of the specification"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2'F-ANA antisense oligo #3, to elicit RNase H degradation of target RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel acyclic linker-containing oligonucleotide useful for preventing decreasing translation, reverse transcription and/or replication of a
Novel acyclic linker-containing oligonucleotide useful for preventing decreasing translation, reverse transcription and/or replication of a target RNA in a system, comprises a modified deoxyribonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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/*tea a OTHER
/note= "2'-deoxy-2'-fluoroarabinothymidine"
                                                                                                                                                                                                                                                                                                                                                                    1.3%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                       Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                       Example 2; Page 90; 104pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                           1865 TTTTTTTTTTTT 1881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Damha MJ, Viazovkina E,
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 88.2
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                           of the invention
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modified_base
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The invention relates to an acyclic linker-containing oligonucleotide comprising at least one modified decoxyribonucleotide. Oligonucleotides of the invention are useful for preventing or decreasing translation.

They are useful for selectively or decreasing translation.

They are useful for selectively preventing gene expression in a sequence-specific manner, for hybridising to complementary RNA much as cellular mRNA or viral RNA, to hybridising to and induce cleavage of complementary RNA. They are also useful therapeutically in formulations or medicaments to prevent or treat a disease characterised by the expression of a particular target RNA. The invention is used in gene therapy. The present sequence is an antisense oligo used to elicit human RNase (ribonuclease) and degradation of target RNA. This sequence is used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= b
//note= "Bases 12 and 13 are linked by a butanediol linker
which is represented as B in page 49 and Fig 5 and as X
in page 55 and Fig 6 of the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2'F-ANA antisense oligo #4, to elicit RNase H degradation of target RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
target RNA in a system, comprises a modified deoxyribonucleotide.
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/mod_base= OTHER
/note= "2'-deoxy-2'-fluoroarabinothymidine"
                                                                                                                                                                                                                                                                                              Score 13.8; DB 1; Length 17;
Pred. No. 2.7e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                      Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                  Example 2; Fig 5; 104pp; English
                                                                                                                                                                                                                                                                                                                                                               1881
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                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                            of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antisense; ss.
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 360
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Novel acyclic linker-containing oligonucleotide useful for preventing or decreasing translation, reverse transcription and/or replication of a target RNA in a system, comprises a modified deoxyribonucleotide.

Parniak MA, Min K;

Mangos MM,

Damha MJ, Viazovkina WPI; 2003-421516/39.

(UYMC-) UNIV MCGILL

29-OCT-2002; 2002WO-CA001628. 29-OCT-2001; 2001US-0330719P

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Gaps

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                  The invention relates to an acyclic linker-containing cligonuclectide comprising at least one modified decoxyribonuclectide. Oligonuclectides of the invention are useful for preventing or decreasing translation, reverse transcription and/or replication of a target RNA in a system. They are useful for selectively preventing gene expression in a sequence-specific manner, for hybridising to complementary RNA such as cellular RNA, to hybridise to and induce cleavage of complementary RNA. They are also useful therapeutically in formulations or medicaments to prevent or treat a disease characterised by the expression of a particular target RNA. The invention is used in gene therapy. The present sequence is an antisense oligo used to elicit human RNase (ribonuclease) H degradation of target RNA. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel acyclic linker-containing oligonucleotide useful for preventing or decreasing translation, reverse transcription and/or replication of a target RNA in a system, comprises a modified decxyribonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= b
/note= "Bases 4 and 5 are linked by a butanediol linker
which is represented as B in page 49 and Fig 5 and as X
in page 55 and Fig 6 of the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2'F-ANA antisense oligo #2, to elicit RNase H degradation of target RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                  ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/mod_base= OTHER
/note= "2'-deoxy-2'-fluoroarabinothymidine"
                                                                                                                                                                                                                                                                                Score 13.8; DB 1; Length 17; Pred. No. 2.7e+02; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Min K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parniak MA,
                                                                                                                                                                                                                                                   Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mangos MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Fig 5; 104pp; English
Example 2; Fig 5; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                   1865 TTTTATTTTTT 1881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD56447 standard; DNA; 17 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39-OCT-2002; 2002WO-CA001628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-OCT-2001; 2001US-0330719P
                                                                                                                                                                                                                                                                                     Query Match 1.3%;
Best Local Similarity 88.2%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Damha MJ, Viazovkina E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYMC-) UNIV MCGILL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-421516/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003037909-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antisense; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD56447;
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD56447
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mcgarry191-19.rng

Page 168

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The invention relates to an acyclic linker-containing oligonucleotide comprising at least one modified deoxyribonucleotide. Oligonucleotides of the invention are useful for preventing or decreasing translation, reverse transcription and/or replication of a target RNA in a system. They are useful for selectively preventing gene expression in a sequence-specific manner, for hybridising to complementary RNA such as cellular mRNA, or viral RNA, to hybridishe to and induce cleavage of complementary RNA. They are also useful therapeutically in formulations or medicaments to prevent or treat a disease characterised by the expression of a particular target RNA. The invention is used in gene therapy. The present sequence is an antisense oligo used to elicit human RNase (ribonuclease) H degradation of target RNA. This sequence is used in the exemplification of the invention
              8888888888888888888888888
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Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

0; Gaps 1.3%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 2.7e+02; tive 0; Mismatches 2; Indels 1865 TTTTTTTTTTTTT 1881 15, Conservative Best Local Similarity Query Match Matches ò

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TTTTTTTTTTTTTT 17 g

AAD56450; RESULT 362

AAD56450 standard; DNA; 17

07-AUG-2003 (first entry)

2'F-ANA antisense oligo #5, to elicit RNase H degradation of target RNA.

Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H; antisense; ss

Unidentified

Location/Qualifiers ĸ l. .17 /*tag= modified base

mod base= OTHER misc_feature

/note= "2'-deoxy-2'-fluoroarabinothymidine"
9.10
7*taga.
/hote= "Bases 9 and 10 are linked by a secouridine linker which is represented as 8 in page 49 and X in page 57 and 8 of the specification"

WO2003037909-A1

29-OCT-2002; 2002WO-CA001628.

29-OCT-2001; 2001US-0330719P.

(UYMC-) UNIV MCGILL.

Parniak MA, Min K; Mangos MM, Viazovkina Damha MJ,

WPI; 2003-421516/39.

ö Novel acyclic linker-containing oligonucleotide useful for preventing decreasing translation, reverse transcription and/or replication of a target RNA in a system, comprises a modified deoxyribonucleotide.

Example 2; Fig 7; 104pp; English.

The invention relates to an acyclic linker-containing oligonucleotide comprising at least one modified deoxyribonucleotide. Oligonucleotides of

; 0

Gaps

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y Match 1.3%; Score 13.6; DB 1; Length 15; Local Similarity 92.9%; Pred. No. 2.6e+02; hes 13; Conservative 1; Mismatches 0; Indels

Query Match

Matches

Sequence 15 BP; 7 A; 2 C; 3 G; 2 T; 0 U; 1 Other;

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the invention are useful for preventing or decreasing translation, reverse transcription and/or replication of a target RNA in a system. They are useful for selectively preventing gene expression in a sequence specific manner, for hybridising to complementary RNA such as cellular RNA or viral RNA, to hybridise to and induce cleavage of complementary RNA. They are also useful therapeutically in formulations or medicaments to prevent or treat a disease characterised by the expression of a particular target RNA. The invention is used in gene therapy. The present sequence is an antisense oligo used to cell thuman RNase (ribonuclase) H degradation of target RNA. This sequence is used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, ubiquitin protein ligase E3A; UBE3A; haplotype, SNP; gene therapy; Angelman syndrome; human papilloma virus E6-associated gene; single nucleotide polymorphism; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel genetic variants of ubiquitin protein ligase E3A gene useful in studying expression and function of the protein, and for screening drugs to treat diseases e.g. Angelman syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ubiquitin protein kinase E3A (human papilloma virus E6-associated protein) UBE3A coding sequence and protein. Also described are a number of single nucleotide polymorphisms (SNPs) identified within these fragments. The fragments can be used in the gene therapy of Angelman syndrome and to haplotype the UBE3A gene. The present sequence is an allele specific primer for a coding sequence fragment of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides the sequences of fragments of the human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 1.3%; Score 13.8; DB 1; Length 17; Local Similarity 88.2%; Pred. No. 2.7e+02; les 15; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human UBE3A gene ASO PCR primer SEQ ID NO: 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sausker EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Page 14; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1865 TITITATITITIT 1881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENA-) GENAISSANCE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Pritritirii 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL45668 standard; DNA; 15 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001; 2001WO-US017994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Koshy B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2000; 2000US-0208539P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                        of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 363
ABL456 (8)/C
1D ABL456
XX ABL456
XX ABL456
XX Human, YX Human, YX Human, YX Human, YX Human, YX YX ABL450
XX ABL450
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The invention describes an isolated human pyridoxal (pyridoxine, vitamin B6) kinase, (PDXK) polynucleotide. The polynucleotide is useful in studying the expression and function of PDXK, and in expressing PDXK protein for use in screening for candidate drugs to treat PDXK related diseases and for therapeutic purposes. A transgenic animal is useful for studying expression of the PDXK isogenes in vivo, for in vivo screening and testing of drugs targeted against PDXK protein, and for testing the efficacy of therapeutic agents and compounds for autoimmune polyglandular disease type I. The pulypeptide is useful for studying the effect of the variation on the biological activity of PDXK and the binding affinity of candidate drugs targeting PDXK for the treatment of autoimmune polyglandular disease type I. Genotyping and haplotyping is useful for improving the efficacy and reliability of several steps in the discovery and development of drugs for treating diseases associated with PDXK as a candidate agent for treating a specific condition or disease predicted to be associated with PDXK activity, and in the design of clinical trials of candidate drugs. This sequence is one of 37 (see Alinical trials of candidate drugs. This sequence is one of 37 (see Alinical trials of candidate drugs. This sequence is one of 37 (see Alinical trials of candidate drugs. This sequence is one of 37 (see Alinical trials of candidate drugs. This sequence is one of 37 (see Alinical trials of candidate drugs. This sequence is one of 37 (see Alinical trials of candidate drugs. This sequence is one of 37 (see Alinical trials of candidate drugs. This sequence is one of 37 (see Alinical trials of candidate drugs. This sequence is one of 37 (see Alinical trials of candidate drugs. This sequence is one of 37 (see Alinical trials of candidate drugs. This sequence is one of 37 (see Alinical trials of candidate drugs. This sequence is one of 37 (see Alinical trials of candidate drugs. This sequence is one of 37 (see Alinical trials of candidate drugs.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated human pyridoxal (pyridoxine, vitamin B6) kinase polyNts, useful for therapeutic purposes, for studying the expression and function of the polyNt, and for expressing pyridoxal protein.
                                                                                                                                                                                                                                                                                                                                                                                                   Pyridoxal kinase, pyridoxine, vitamin B6;
PDXK autoimmune polyglandular disease type 1; transgenic animal;
gene therapy; allele specific oligonucleotide; ASO; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                 Pyridoxal (Pyridoxine, vitamin B6) Kinase (PDXK) PCR primer #22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.3%; Score 13.6; DB 1; Length 15; 92.9%; Pred. No. 2.6e+02; ative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15 BP; 7 A; 5 C; 1 G; 1 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 17; Page 13; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENA-) GENAISSANCE PHARM INC.
                                                                                                                                                                                       ABK16961 standard; DNA; 15 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAY-2001; 2001WO-US016909.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-MAY-2000; 2000US-0206664P.
2167 TGTTTCTACTTTGA 2180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Duda A, Koshy B;
                                                                                                                                                                                                                                                                                             26-MAR-2002 (first entry)
                                WPI; 2002-106169/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200190125-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-NOV-2001.
                                                                                                                                                                                                                                           ABK16961;
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                                                                                                                             RESULT 364
                                                                                                                                                          ABK16961
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Detection of eukaryotic pathogens, especially fungal or Plasmodium spp. by detecting telomerase activity.

Claim 5; Col 93-94; 82pp; English.

Blackburn EH, Shay J, Mceachern MJ, West MD, Wright W;

WPI; 1998-041292/04.

(UYCA-) UNIV CALIFORNIA SAN FRANCISCO. (TEXA) UNIV TEXAS SYSTEM:

92US-00882438. 93US-00038766. 9303-00060952

13-MAY-1993; 13-MAY-1992; 24-MAR-1993;

Detection, eukaryotic pathogen, telomeric nucleic acid sequence, telomerase activity, diagnosis, fungal infection, fungus, fungi; malaria, ss.

Saccharomyces cerevisiae.

US5695932-A.

09-DEC-1997.

Fungal telomeric nucleic acid sequence.

(revised)
(first entry)

25-MAR-2003: 08-APR-1998

AAT96304;

AAT96304 Btandard; DNA; 15 BP.

RESULT 365 AAT96304

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The present sequence can be used in a novel method for detecting a eukaryctic pathogen in a patient. The method comprises obtaining a sample of somatic tissue or cells from the patient, determining if telomerase activity is present and correlating this with the presence of the pathogen. The method is useful for diagnosis of fungal infections, especially a fungus of the genus Candida, Kluyveromyces, Saccharomyces, Sporothrix, Coccidioides, Histoplasma, Blastomyces, Pascocidioides, Cryptococcus, Aspergillus, Mucor or Rhizopus, or malarial infections, especially plasmodium vivax, P. ovale, P. malariae or P. falciparum. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.3%; Score 13.4; DB 1; Length 15; Best Local Similarity 93.3%; Pred. No. 2.7e+02; Matches 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15 BP; 0 A; 0 C; 8 G; 7 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF47617 standard; DNA; 15 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2001
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AAF47617/c
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Gaps

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1801 TGTGTGTGTGTA 1814

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13; Conservative

Best Local Similarity

Matches

15 rricidicidicia 2

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Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition; hyperplasia; kidney disease;
                                                                                                                                                                                                                                       Edmondson SR;
                                                                                                                                                                                                               (MURD-) MURDOCH CHILDRENS RES INST.
                                                                                                                                                                                                                                                                                                                                                 Example 7; Page 50; 201pp; English
                                                                                                                                                                                         99US-0140345P.
                                                                                                                                                                21-JUN-2000; 2000WO-AU000693
                                                                                                                                                                                                                                        Werther GA,
                                                                                                                                                                                                                                                              WPI; 2001-041421/05.
                                                                                                                WO200078341-A1.
                                                                                                                                                                                                                                                                                                                            inflammation.
                                                                                          Homo sapiens.
                                                                                                                                                                                       21-NUU-1999;
                                                                                                                                                                                                                                         Wraight CJ,
                                                                                                                                         28-DEC-2000.
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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligomucleoride, (for Insulin-like Growth Factor IGRF) is receptor, IGF binding protein [IGFRF] -2 or IGFRF3), which is capable of inflammation and/or other disorders. The present sequence is an inflormation and/or other disorders. The present sequence is an oligomucleotide which can be used to design the antisense oligomucleotide which can be used to design the antisense oligomucleotides of the present invention (see AAF45151 and AAF45153 - F45161). The method is useful for ameliorating the effects of psoriasis, in tyriasis, ruba, pilaris, serborthoea, keloids, keratosis, neoplasias, soleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brine is skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.3%; Score 13.4; DB 1; Length 15; 33.3%; Pred. No. 2.7e+02; ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15 BP; 6 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.3%;
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es 14; Conservative
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2045 TGTCCTTGGCAGGCT
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Gaps ô

> AAF80919 standard; DNA; 15 AAF80919; RESULT 367

BP

02-MAY-2001 (first entry)

PTGS2 allele specific oligonucleotide probe SEQ ID 25.

Human; prostaglandin-endoperoxide synthase 2; PTGS2; cyclooxygenase 2; single nuclectide polymorphism; SNP; immune-related disorder; arthritis; inflammation; probe; ss.

Homo sapiens

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This invention relates to a polymucleotide sequence that is a polymorphic variant of the human prostaglandin-endoperoxide synthase 2 (PTGS2) gene variant of the human prostaglandin-endoperoxide synthase 2 (PTGS2) gene also referred to as cyclooxygenase 2. The human PTGS2 gene sequence AAPR0896 contains 27 single nucleotide polymorphisms (SNP8). AAPR0896 and AAPR0897 represented by AAPR2199. The invention includes PCR and the PTGS2 gene and coding sequence, and the PTGS2 gene sequence, and to contain a represented by AAPR2199. The invention includes PCR and to contain and probes represented in AAPR0898 - AAPR81151 which are used to isolated and characterise the PTGS2 gene sequence, and to compare the positions of the SNPs. PTGS2 proteins and polymucleotide compressing PTGS2 broteins, for structural analysis or drug-binding studies and also in gene therapy (either consecution or diagnosis, prognosis and also in gene therapy (either consecution polymorphisms and used to determine PTGS2 haplotype and genotype, consecution to determining association between a particular trait, eggenetially for determining association between a particular trait, ergo susceptibility severity or stage. Anti-PTGS2 bathologies are particularly consecuted to susceptibility severity or stage. Anti-PTGS2 antibodies are particularly consecuted as architic tests and treatments for immune related disorders such as architic and inflammation. The polymorphisms may also be used to study expression and biological function of PTGS2. Transgenic soluminals that expression and biological function of PTGS2 ransgenic confecution and profession of pTGS2.
                                                                                                                                                                                                                                                                                                       New nucleic acid containing polymorphisms in the cyclooxygenase-2 gene, for gene therapy of inflammation and for establishing a genotype or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                   Tanguay DA;
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                                                                                                                                                                                                                 Denton RR, Nandabalan K, Sanchis A, Stephens JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 21; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1881
                                                                                                                                                                          (GENA-) GENAISSANCE PHARM INC.
                                                                                    24-JUL-2000; 2000WO-US020114.
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                                                                                                                                                                                                                                                                   WPI; 2001-182805/18.
WO200107662-A1
                                                                                                                                 22-JUL-1999;
                                           01-FEB-2001
                                                                                                                                                                                                                                                                                                                                                               haplotype.
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Matches
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EST polymorphic DNA repeat polynucleotide #83. E ABX79758 standard; cDNA; 15 (first entry) 17-APR-2003 ABX79758; RESULT 368

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BST; expressed sequence tag; ss; polymorphic repeat; tandem repeat; polymorphic marker prediction of ubiquitous simple sequences; POMPO! Rep-X; human; genetic disease; drug-treatment; Machado-Joseph; Haw River syndrome; Huntington's disease; fragile-X syndrome; Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia; spinal atrophy; bulbar atrophy; spinocerebellar ataxia.

sapiens Ношо

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The invention discloses a method for identifying a candidate polymorphic repeat within a coding sequence (expressed sequence tag, EST), which comprises detecting tandem repeats in a target coding sequence, scoring the repeats for polymorphic probability and generating a dataset correlating the repeats with polymorphic probability to identify a candidate polymorphic repeat. The computational methods (polymorphic repeat. The computational methods (polymorphic marker prediction of ubiquitous simple sequences, PowPoUS, and Rep-X) are useful for identifying and detecting candidate polymorphic repeats in human genes, which can be used to understand, treat or eliminate genetic diseases, predispositions or adverse durg-treatment reactions. Examples of diseases linked to nucleotide repeats are Machado-Joseph, Haw River syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis, myotonic dystrophy, hyperandrogensemia, spinal and bulbar attophy and spinocereballar ataxia. The sequences presented in ABX79676-ABX80022 are the polymorphic repeats identified for a search of human BST8
                                                                                                                                                                                                                                                                             Identifying a candidate polymorphic repeat within a coding sequence, funderstanding or treating genetic disease, comprises detecting tandem repeats in a target coding sequence and scoring the repeats for polymorphic probability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diagnostic; Gram-positive bacterium; high G+C content; amplification; mycobacterial infection; PCR; primer; probe; detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.3%; Score 13.4; DB 1; Length 15; Best Local Similarity 93.3%; Pred. No. 2.7e+02; Matches 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15 BP; 9 A; 0 C; 0 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                          Fondon JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23S rDNA helix 54 region probe SEQ ID 37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corynebacterium pseudotuberculosis.
Corynebacterium ulcerans.
                                                                                                                                                                                                                                                                                                                                                                             Example; Col 309; 588pp; English.
                                                                                                                                                                                                       Minna JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1811 TGTATATATATAT 1825
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                                                                                         99US-00475947.
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                                                                                                                                                                 (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                       Wren JD,
                                                                                                                                                                                                                                            WPI; 2003-208818/20.
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                                                                                         31-DEC-1999;
                                                                                                                              31-DEC-1999;
                US6472154-B1
                                                   29-OCT-2002
                                                                                                                                                                                                     Garner HR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABX94519;
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This invention describes a novel method for the diagnostic detection and/or identification of Gram-positive bacteria that have a high G+C content, especially Mycobacteria. The method comprises subjecting a sample to nucleic acid amplification using the PGR primers represented in ABX94483-ABX9492. The amplification mixture, or part of it, is then tested for hybridisation to at least one of the probes represented in ABX94493-ABX94524 which can be immobilised on a solid phase or used in kit form. The specified primers/probes provide highly specific detection of particular Gram positive bacteria, which are difficult to differentiate by morphological or biochemical tests and/or those which take a long time to test because of their slow growth
                                                                                               Detecting and identifying Gram-positive bacteria of high G/C content, useful particularly for diagnosis of mycobacterial infection, by specific amplification and hybridization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treating condition associated with cell senescence or increased rate of cell proliferation, by administering to cell an agent that derepresses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell proliferation, cell senescence; telomere length; telomerase activity; cel replication; neoplasia; cancer; age-related macular degeneration; Alzheimer's disease; atherosclerosis; telomerase inhibitor; immortalised cell; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Telomere length and/or telomerase activity related polynucleotide #51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.3%; Score 13.4; DB 1; Length 15; Best Local Similarity 93.3%; Pred. No. 2.7e+02; Matches 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15 BP; 0 A; 0 C; 8 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shay J, Wright W, Blackburn EH;
                                                                                                                                                                         Claim 1b; Fig 2B; 34pp; German.
(HAIN-) HAIN LIFESCIENCE GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1793 TGTGTGTGTGTGT 1807
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93US-00060952.
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(SHAY/) SHAY J.
(WRIG/) WRIGHT W.
(BLAC/) BLACKBURN E H.
                                                                 WPI; 2003-140491/13.
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                                 Weizenegger M;
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13-MAY-1993;
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telomerase in the senescing cells or that reduces loss of telomere

Disclosure; Page 50; 86pp; English.

The invention describes a method use for treating increased rate of proliferation of a cell or extending the ability of a cell to replicate, or treating a disease associated with cell sensecence. The method comprises administering an agent to reduce loss of telomera length within the sensecing cells. The method is useful for treating a condition associated with an increased rate of proliferation of a cell extending the ability of a cell to replicate, or for treating a condition condition associated with cell sensecence e.g. neoplasia. A second method disclosed in the invention is useful for treating a condition associated with an elevated level of telomerase activity within a cell e.g. cancer. This of isclosed is a method useful for treating a condition associated with an increased rate of proliferation in a cell in an individual e.g. age-related macular degeneration, astrocytes associated with Alzheimer's equence represents a polymuclecule used in the study of telomera length centering and telomerase activity described in the invention

Sequence 15 BP; 0 A; 0 C; B G; 7 T; 0 U; 0 Other;

/ Match 1.3%; Score 13.4; DB 1; Length 15; Local Similarity 93.3%; Pred. No. 2.7e+02; Local Similarity 93.3%; Pred. No. 2.7e+02; Length 1; Indels of Mismatches 1; Indels 1792 TIGIGIGIGIGIGI 1806 1 recrerererere 15 Query Match Matches ģ 셤

RESULT 371 AAT81559

AAT81559 standard; RNA; 17 BP.

AAT81559;

14-DEC-1997 (first entry)

Human c-myb hammerhead ribozyme target sequence (nt. position 2898).

Enzymatic nucleic acid; hammerhead; ribozyme; cleavage; human; smooth muscle cell; hyperproliferation; restenosis; cancer; c-myb; coronary angioplasty; ss.

Homo sapiens.

WO9531541-A2.

23-NOV-1995.

95WO-US006368. 18-MAY-1995;

95US-00373124. 94US-00245466 18-MAY-1994; 13-JAN-1995;

(RIBO-) RIBOZYME PHARM INC.

Stinchcomb DT, Draper K, Mcswiggen J, Jarvis T;

WPI; 1996-010927/01.

New enzymatic nucleic acid molecules - cleave RNA produced by e.g. c-myb, for treating restenosis or cancer.

Claim 1; Page 78; 128pp; English.

The present sequence represents the preferred target sequence for an enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves the human c-myb sequence at the base position indicated in the descriptor

ö line. The c-myb sequence was screened for optimal ribozyme target sites using a computer folding algorithm, and regions of the mENA which did not form secondary folding structures and contained potential ribozyme cleavage sites were identified. Ribozymes were synthesised and their activities optimised by either varying the length of the binding arms or by modification to prevent degradation by nucleases. The ribozymes cleave hyperproliferation in restenosis, especially after coronary angiophasty, and in cancers Gapa ö 1.3%; Score 13.4; DB 1; Length 17; 46.7%; Pred. No. 2.9e+02; tive 7; Mismatches 1; Indels Sequence 17 BP; 7 A; 1 C; 0 G; 0 T; 9 U; 0 Other; 1813 TATATATATATAT 1827 2 UAUAUAUAUAUACAU 16 Local Similarity 46.7 Query Match Matches

88888888888888

RESULT 372

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AAA10358

AAA10358 standard; DNA; 13

AAA10358;

03-JUL-2000 (first entry)

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Gaps

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DNA ligand binding assay competitor oligonucleotide, SEQ ID NO:41.

Nucleic acid ligand binding assay; duplex formation; stability; detectable signal; competition assay; competitor oligonucleotide; ds.

Synthetic.

WO200015848-A1.

23-MAR-2000

99WO-US020719. 10-SEP-1999; 98US-00151890. 11-SEP-1998;

(GENE-) GENELABS TECHNOLOGIES INC.

Schroth GP, Bruice TW,

WPI; 2000-271478/23.

Determining binding affinity of a ligand to an oligonucleotide sequence in double stranded form, comprises measuring the effect of adding increasing amounts of a ligand on a signal generated by two indicator oligonucleotides of the duplex.

Example 3; Page 19; 78pp; English.

The invention relates to new methods of determining the binding affinity of a ligand to an oligomucleotide sequence, particularly to a duplex. The ligand is typically a metal lon, a small organic or inorganic molecule, a protein or a multi-protein complex. The methods comprise measuring the protein or a multi-protein complex. The methods comprise measuring the ceffect of adding inoreasing amounts of a ligand on a signal generated by two indicator oligomucleotides of the duplex. In the absence of ligand, conditions are such that the oligomucleotides exist primarily in single stranbilises the duplexs, such that duplex formation is favoured. One of the indicator oligomucleotides contains a first group capable of producing a detectable signal, while the other indicator oligomucleotide contains a second group that on hybridisation of the two indicator molecules, will detectably alter the signal produced by the first group. The signal independence of decreased on hybridisation. For example, the pairs of signalling groups used could be a radioactive group and a contillant (where an increase in signal intensity indicates that

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hybridisation has taken place) or a fluorophore and a fluorescence quencher (where a reduction in signal intensity indicates that the training intensity indicates that the hybridisation has occurred). Other methods of the invention comprise a crand diplacement assay, where the ability of an unlabelled displacement strand to displace one of the oligomolectides in the duplex is determined in the absence and presence of ligand; and a competition assay, where an unlabelled single or double-stranded competition of ignounclectide is added to the ligand-bound indicator duplex, and the effect on the signal produced from the indicator duplex, and the methods are useful for determining the binding affinity of a ligand to an oligomuclectide sequence. They are particularly useful for determining callicity binding affinities of various ligands to various oligomuclectide sequences. The sequences, particularly double-stranded oligomuclectide sequences. The sasays allow rapid and convenient determination of mucleic acid binding specificities. Sequences AAA10342-A10391 represent competitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide SEQ ID NO 88229 for detecting SNP TSC0022170.
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1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                     Seguence 13 BP; 0 A; 0 C; 7 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                        present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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ABC88212
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1779 TATATTGTAAATA 1791 (first entry) 1 Trrradadrriar 13 Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG WPI; 2001-657177/75. WO200177384-A2. Homo sapiens. 21-FEB-2002 18-OCT-2001 Query Match ABF52648; Matches RESULT 374 ABF52648 ð This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, artdiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 ABC00010-ABC09989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 ö Gaps Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status. ô Claim 1; SEQ ID NO 88229; 29pp + Sequence Listing; German. Berlin K; Olek A, Piepenbrock C, WPI; 2001-657177/75

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                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                     Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide SEQ ID NO 152645 for detecting SNP TSC0038583.
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                                                                                                                                                                                                                                           Query Match
1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                             Sequence 13 BP; 5 A; 0 C; 0 G; 8 T; 0 U; 0 Other;
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                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                 Oligonucleotide SEQ ID NO 98289 for detecting SNP TSC0024420.
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                                      ABC98272 standard; DNA; 13 BP
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                                                                      ABC98272;
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cancer also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                    Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                      Claim 1; SEQ ID NO 91710; 29pp + Sequence Listing; German
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                                           Piepenbrock C,
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Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

Piepenbrock C,

WPI; 2001-657177/75.

Claim 1; SEQ ID NO 190379; 29pp + Sequence Listing; German.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99899 and ABT00010-ABIS2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; BS; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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  ABC12933 standard; DNA; 13 BP.
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                                      1.2%; Score 13; DB 1; Length 13; 100.0%; Pred. No. 2.7e+02;
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Sequence 13 BP; 10 A; 1 C; 0 G; 2 T; 0 U; 0 Other;
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Matches 13; Conservative 0; Mismatches
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                                                    This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, coingomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Claim 1; SEQ ID NO 12940; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.2%; Score 13; DB 1; Length 13;
100.0%; Pred. No. 2.7e+02;
tive 0; Mismatches 0; Indels
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Matches 13; Conservative
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RESULT 381 ABC12933/c

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretracted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form par of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                           Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 88054; 29pp + Sequence Listing; German.
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                                                                                06-APR-2001; 2001WO-IB000713.
                                                                                                                07-APR-2000; 2000DE-01019173.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99989, ABH00010-ABH99899 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                      Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                           Claim 1; SEQ ID NO 119128; 29pp + Sequence Listing; German.
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100.0%; Pred. No. 2.7e+02;
tive 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 13; Conservative
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WPI; 2001-657177/75.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99999, ABF00010-ABF99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NoTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at
central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99889, ABF00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fib.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosie; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligomucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABC0010-ABF99989, ABH00010-ABH99989 and ABI00010-ABIS2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                 Oligonuclectide SEQ ID NO 160100 for detecting SNP TSC0040305.
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1778 TTATATTGTAAAT 1790
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Query Match
1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels

06-APR-2001; 2001WO-IB000713.

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting call type differentiation. ABC0010 -ABC99989, ABR00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form par of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                  Oligonucleotide SEQ ID NO 161492 for detecting SNP TSC0040647.
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21-FEB-2002 (first entry)
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                                                      1.2%; Score 13; DB 1; Length 13; 100.0%; Pred. No. 2.7e+02; tive 0; Mismatches 0; Indels
Sequence 13 BP; 11 A; 1 C; 0 G; 1 T; 0 U; 0 Other;
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                                                                                 Best Local Similarity 100.0
Matches 13; Conservative
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WO200177384-A2

18-OCT-2001

Homo sapiens.

ABC55255;

Query Match

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF32073 data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at
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1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels
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                               07-APR-2000; 2000DE-01019173
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                                                                                                   Olek A, Piepenbrock C,
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                                                                 (EPIG-) EPIGENOMICS AG
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cyclosine methylation status in chemicaally pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABF99899 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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100.0%; Pred. No. 2.7e+02;
tive 0; Mismatches 0; Indels
                             Claim 1; SEQ ID NO 58824; 29pp + Sequence Listing; German.
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Matches 13; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid [PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABI22073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic
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100.0%; Pred. No. 2.7e+02;
tive 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels
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                                                      Sequence 13 BP; 5 A; 0 C; 2 G; 6 T; 0 U; 0 Other;
             ftp.wipo.int/pub/published_pct_sequences
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Matches 13; Conserv
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                                                                                                                                                                                                                                                                                              RESULT 391
ABF60102/c
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Claim 1; SEQ ID NO 37127; 29pp + Sequence Listing; German.

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central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ABC79591/c
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                                                                                                                                                                                                                                                                        Oligonucleotide SEQ ID NO 17787 for detecting SNP TSC0003802.
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Best Local Similarity
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                               RESULT 392
ABC17780
ABC1771
XX
AC ABC1771
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AC ABC1771
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DT 20-FEB
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DY Oligon
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Matches
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ABC98273/C
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory) contral nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                       Claim 1; SEQ ID NO 98290; 29pp + Sequence Listing; German.
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1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels
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This invention describes novel oligonucleotide primers or peptide nucleic
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                                       set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                           Claim 1; SEQ ID NO 79608; 29pp + Sequence Listing; German
                                                                                                                                                                                                                                                          Seguence 13 BP; 6 A; 6 C; 0 G; 1 T; 0 U; 0 Other;
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          Piepenbrock
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                              WPI; 2001-657177/75
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic diseoders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC099889, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic form part of the printed specification, but they wipo int/pub/published_pct_sequences
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1.2%; Score 13; DB 1; Length 13; 100.0%; Pred. No. 2.7e+02; /ative 0; Mismatches 0; Indels

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                   Oligonucleotide SEQ ID NO 152646 for detecting SNP TSC0038583.
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Pred. No. 2.7e+02;
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SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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1.2%; Score 13; DB 1; Length 13; 100.0%; Pred. No. 2.7e+02; ative 0; Mismatches 0; Indels
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1766 ATTTTTAAAATT 1778

RESULT 398 ABF52649/c ID ABF52649 standard; DNA; 13 XX

Sequence 13 BP; 5 A; 0 C; 0 G; 8 T; 0 U; 0 Other;

WO200177384-A2

Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                             This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 for prepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but they obtained in electronic format from WIPO at
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Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                Claim 1; SEQ ID NO 5406; 29pp + Sequence Listing; German.
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Mismatches

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Berlin K;

Score 13; DB 1; Length 13; Pred. No. 2.7e+02;

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ABF38750 standard; DNA; 13

ABF38750

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                                                                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification ftp.wipo.int/pub/published_pot_sequences
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1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels
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                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                          Oligonucleotide SEQ ID NO 138747 for detecting SNP TSC0034761
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100.0%; Pred. No. 2.7e+02;
ative 0; Mismatches 0;
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Matches 13; Conservative
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21-FEB-2002
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ABH52395/c
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1.2%; Score 13; DB 1; Length 13; 100.0%; Pred. No. 2.7e+02; rative 0; Mismatches 0; Indels

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; Ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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nes 13; Conservative
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Berlin K;

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acid (PNA) oligomers for detecting single nucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 represent the oligomers described in the invention. NOTE: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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100.0%; Pred. No. 2.7e+02;
ive 0; Mismatches 0; Indels
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1.2%; Score 13; DB 1; Length 13; 100.0%; Pred. No. 2.7e+02; ative 0; Mismatches 0; Indels

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Sequence 13 BP; 2 A; 0 C; 4 G; 7 T; 0 U; 0 Other;

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and (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomers for detecting single nucleotides polymorphisms (SNP) oligomers are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF0010-ABF9989, ABF00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form par of the printed specification, but was obtained in electronic format from WIPO at
                               invention describes novel oligonucleotide primers or peptide nucleic
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13 rrrraaaarraa 1 g

ABH52394 standard; DNA; 13 BP ABH52394; RESULT 407

(first entry) 22-FEB-2002 Oligonucleotide SEQ ID NO 252371 for detecting SNP TSC0061564.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C,

WPI; 2001-657177/75

Berlin K;

Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 252371; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABE99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form par of the printed specification, but the was obtained in electronic format from WIPO at

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Length 13;
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Query Match
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Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0;
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Sequence 13 BP; 6 A; 3 C; 0 G; 4 T; 0 U; 0 Other;

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and dycosine methylation status in chemically pretreated genomic DNA. The coligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99889, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a
                                                                                                                                                               This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosts and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                Claim 1; SEQ ID NO 88053; 29pp + Sequence Listing; German.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABF9989 and ABI00010-ABI82073 the represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; SS; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                           Oligonuclectide SEQ ID NO 5118 for detecting SNP TSC0001711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 5118; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                          SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                        Oligonucleotide SEQ ID NO 20164 for detecting SNP TSC0004136.
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       Mismatches
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         Matches 13; Conservative
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ABC20147/c
ID ABC201
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Berlin K;

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                          Oligonucleotide SEQ ID NO 5405 for detecting SNP TSC0001818.
                        Query Match
1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels
Sequence 13 BP; 7 A; 6 C; 0 G; 0 T; 0 U; 0 Other;
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ABC05127 standard; DNA; 13 BP

ABC05127

RESULT 415
ABC05127/c
ID ABC0511
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1868 TTATTTTTTT 1880

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Query Match Best Local Similarity 100. Matches 13; Conservative

methylation status.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF0010-ABF9989, ABR0010-ABF9989, ABR0010-ABF9989, and ABI0010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but form witho.int/pub/published_pct_sequences SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status. Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine Oligonucleotide SEQ ID NO 5405 for detecting SNP TSC0001818. 1.2%; Score 13; DB 1; Length 13; 100.0%; Pred. No. 2.7e+02; ive 0; Mismatches 0; Indels Claim 1; SEQ ID NO 5405; 29pp + Sequence Listing; German. Sequence 13 BP; 7 A; 0 C; 0 G; 6 T; 0 U; 0 Other; Berlin K; ABC05414 standard; DNA; 13 BP 06-APR-2001; 2001WO-IB000713. 100.0%; 07-APR-2000; 2000DE-01019173 06-APR-2001; 2001WO-IB000713 07-APR-2000; 2000DE-01019173 1814 ATATATATATA 1826 (first entry) 1 ATATATATATA 13 Matches 13; Conservative Dlek A, Piepenbrock C, Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG WPI; 2001-657177/75 (EPIG-) EPIGENOMICS WPI; 2001-657177/75 Best Local Similarity 40200177384-A2 Homo sapiens 20-FEB-2002 18-OCT-2001 ABC05414; RESULT ò

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic diseases. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE099989, ABF00010-ABE99989, ABH0010-ABH99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence
                                                          This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting call type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at
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                               Claim 1; SEQ ID NO 5405; 29pp + Sequence Listing; German.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ABF90383 standard; DNA; 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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Berlin K;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and merabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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acid; cytosine methylation; cardiovascular; primer; 8s; system; gastrointestinal; respiratory; immune; metabolic.
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100.0%; Pred. No. 2.7e+02;
tive 0; Mismatches 0; Indels
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Best Local Similarity 100.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The coligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09939, ABC00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 -ABC9989, ABF00010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073 data for this patent did not form part of the printed specification, but the pub/published_pot_sequences
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Query Match 1.2%; Score 13; DB 1; Length 13; Best Local Similarity 100.0%; Pred. No. 2.7e+02; Matches 13; Conservative 0; Mismatches 0; Indels
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Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

Piepenbrock C,

Olek A,

WPI; 2001-657177/75

(EPIG-) EPIGENOMICS AG

06-APR-2001; 2001WO-IB000713 07-APR-2000; 2000DE-01019173

WO200177384-A2

18-OCT-2001

Claim 1; SEQ ID NO 260343; 29pp + Sequence Listing; German.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF0010-ABF9989, ABH0010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                     oligonuclectides, useful for diagnosis and cell typing, is to detect single-nuclectide polymorphisms and cytosine
                                                                     Oligonucleotide SEQ ID NO 190359 for detecting SNP TSC0046817.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 190359; 29pp + Sequence Listing; German.
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                                           (first entry)
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                                                                                                                                                                                                                                                                                                                 (EPIG-) EPIGENOMICS AG
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les 13; Conserv
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                                                                                                                                                                  Homo sapiens.
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Matches
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1.2%; Score 13; DB 1; Length 13;
100.0%; Pred. No. 2.7e+02;
rative 0; Mismatches 0; Indels
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                                                                                                                                                                                                    ABC28588 standard; DNA; 13 BP
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                                                                                                              1 GATTTTTTAAAT 13
       Query Match
Best Local Similarity 100.0
Matches 13; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABIS2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Gaps

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1.2%; Score 13; DB 1; Length 13; 100.0%; Pred. No. 2.7e+02; ative 0; Mismatches 0; Indels

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Ното варіепв

Oligonucleotide SEQ ID NO 260343 for detecting SNP TSC0063217.

22-FEB-2002 (first entry)

ABH60366;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF8073 tepseant the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but thow, was obtained in electronic format from WIPO at
                 Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                          Claim 1; SEQ ID NO 28605; 29pp + Sequence Listing; German.
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Sequence 13 BP; 6 A; 0 C; 1 G; 6 T; 0 U; 0 Other;

ö Query Match 1.2%; Score 13; DB 1; Length 13; Best Local Similarity 100.0%; Pred. No. 2.7e+02; Matches 13; Conservative 0; Mismatches 0; Indels 1818 ATATATATATA 1830 ð

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1 ATATATATATATA 13

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ABC13480 standard; DNA; 13 BP ABC13480;

20-FEB-2002 (first entry)

Oligonucleotide SEQ ID NO 13487 for detecting SNP TSC0003116.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG.

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 13487; 29pp + Sequence Listing; German.

This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The

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Query Match 1.2%; Score 13; DB 1; Length 13; Best Local Similarity 100.0%; Pred. No. 2.7e+02; Matches 13; Conservative 0; Mismatches 0; Indels

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oligomers are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99889, ABH00010-ABH99988 and ABI00010-ABB182073
-ABC99989, Ligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fip.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                              Sequence 13 BP; 9 A; 0 C; 0 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                          Oligonucleotide SEQ ID NO 43082 for detecting SNP TSC0012784.
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                                                                          ABC43065 standard; DNA; 13 BP
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1766 ATTTTTTAAATT 1778
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This invention describes novel oligonucleotide primers or peptide nucleic and (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, coingomers are also used for detecting cell type differentiation. ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC000010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC000010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC000010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010-ABC00010
                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide SEQ ID NO 58823 for detecting SNP TSC0015758.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNB) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                       This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prereated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF0010-ABF8989, ABH0010-ABH9989 and ABI00010-ABI82073 are present the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
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Claim 1; SEQ ID NO 260344; 29pp + Sequence Listing; German.
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RESULT 434 ABH60367,

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic
                                                                                                                 Oligonucleotide SEQ ID NO 104281 for detecting SNP TSC0026066.
                           ABF04284 standard; DNA; 13 BP.
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                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                         Query Match
1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels
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                             Sequence 13 BP; 0 A; 0 C; 7 G; 6 T; 0 U; 0 Other;
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Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal respiratory, central nervous system, cardiovascular and metabolic diseorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                        Claim 1; SEQ ID NO 104281; 29pp + Sequence Listing; German.
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set ot oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
Olek A, Piepenbrock
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                                       This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99899 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Claim 1; SEQ ID NO 106847; 29pp + Sequence Listing; German.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, certical nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
              range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABF00010-ABE99989, ABF00010-ABE99989, ABF00010-ABE99989 and ABI00010-ABE9073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but typ.wipo.int/pub/published_pct_sequence
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABF9989, and ABI00010-ABI32073 represent the oligomers described in the invention. NOTE: The sequence and one form part of the printed specification, but was obtained in electronic formmat from WIPO at
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 89; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                    Oligonucleotide SEQ ID NO 213164 for detecting SNP TSC0010105.
                                                                                                                   06-APR-2001; 2001WO-IB000713
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       22-FEB-2002 (first entry)
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC09989, ABF00010-ABF99989, ABF00010-ABF99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF99989 and ABI00010-ABF99999 are chis patent did not form part of the printed specification, but was obtained in electronic format from WIPO at Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status. Claim 1; SEQ ID NO 213164; 29pp + Sequence Listing; German. Sequence 13 BP; 8 A; 0 C; 0 G; 5 T; 0 U; 0 Other;

1.2%; Score 13; DB 1; Length 13; 100.0%; Fred. No. 2.7e+02; trive 0; Mismatches 0; Indels 13; Conservative Query Match Best Local Similarity

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ABF04285 standard; DNA; 13 RESULT 444

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Oligonucleotide SEQ ID NO 104282 for detecting SNP TSC0026066 (first entry) 21-FEB-2002

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prerreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and merabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but fitp.wipo.int/pub/published_pct_sequences Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status. .. 0 Claim 1; SEQ ID NO 104282; 29pp + Sequence Listing; German. 0; Indels 1.2%; Score 13; DB 1; Length 13; 100.0%; Pred. No. 2.7e+02; rative 0; Mismatches 0; Indels Sequence 13 BP; 7 A; 3 C; 0 G; 3 T; 0 U; 0 Other; Berlin K; 07-APR-2000; 2000DE-01019173 06-APR-2001; 2001WO-IB000713 Best Local Similarity 100. Matches 13; Conservative Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG WPI; 2001-657177/75 Query Match

ABF96135 standard; DNA; 13 BP. 1849 TAPAGTTGTTTGT 1861 13 TAAAGTTGTTTGT 1 ABF96135; RESULT 445 ò

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Gaps

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic Oligonucleotide SEQ ID NO 196132 for detecting SNP TSC0048267. 22-FEB-2002 (first entry)

Homo sapiens

WO200177384-A2.

06-APR-2001; 2001WO-IB000713. 18-OCT-2001.

07-APR-2000; 2000DE-01019173 (EPIG-) EPIGENOMICS AG Berlin K; olek A, Piepenbrock C,

WPI; 2001-657177/75

Set of oligonucleotides, useful for diagnosis and cell typing, is

represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fit, wipo.int/pub/published_pct_sequences

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Seguence 13 BP; 7 A; 1 C; 0 G; 5 T; 0 U; 0 Other;

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC09010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 tappement the oligoners described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                Claim 1; SEQ ID NO 196132; 29pp + Sequence Listing; German.
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Sequence 13 BP; 7 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

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1.2%; Score 13; DB 1; Length 13; 100.0%; Pred. No. 2.7e+02; ative 0; Mismatches 0; Indels
                                                                  2202 TTATTTGTTGAGA 2214
                 Best Local Similarity 100.0
Matches 13; Conservative
                                                                                                  TTATTTGTTGAGA 1
                                                                                                  13
   Query Match
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0; Gaps

ABF61049 standard; DNA; 13 BP. ABF61049;

(first entry) 22-FEB-2002

Oligonuclectide SEQ ID NO 161046 for detecting SNP TSC0040548.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG

Berlin K; Piepenbrock C, olek A,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 161046; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, axidovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABI82073

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Gaps

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Match 1.2%; Score 13; DB 1; Length 13; Local Similarity 100.0%; Pred. No. 2.7e+02; Les 13; Conservative 0; Mismatches 0; Indels

Query Match

Matches

1794 GTGTGTGTGTG 1806

1 crerererere 13

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method for determining the relative binding affinities of a ligand to different oligonucleotides. A mixture is formed from two oligonucleotides, one carrying a label and a second containing a group that alters the signal from the label, when the sequences hybridise. In the absence of the ligand, the oligonucleotides exist mainly in single-stranded form and the signal is recorded in this state. The ligand is then added and the signal measured again, and the effect binding affinities of the ligands are determined by comparing their effects. Sequences ABK70559-ABK70629 represent oligonucleotides used for determining relative binding affinities of ligands.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Determining relative affinity of ligands for oligonucleotides, from ability to separate a duplex of oligonucleotides, one labeled and the other having a signal modifying group.
                                   Gaps
                                   ö
 Length 13;
                               0; Indels
                                                                                                                                                                                                                                                                               Ligand binding affinity determining oligonucleotide #32.
0uery Match
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13 BP; 0 A; 0 C; 7 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENE-) GENELABS TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Col 16; 51pp; English.
                                                                                                                                                                                 ABK70590 standard; DNA; 13 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-00151890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-00393783
                                                                                                                                                                                                                                                                                                                 Ligand binding affinity; ss.
                                                                 1774 AAAITIAIAITGI 1786
                                                                                                                                                                                                                                               15-JUL-2002 (first entry)
                                                                                        13 AAATTTATATTGT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schroth GP, Bruice TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-380936/41.
                                                                                                                                                                                                                                                                                                                                                                                 US6355428-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                   ABK70590;
                                                                                                                                                   RESULT 447
                                                                                                                                                                 ABK7059(
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for

Fondon JW

99US-00475947. 99US-00475947.

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The invention discloses a method for identifying a candidate polymorphic repeat within a coding sequence (expressed sequence tag, EST), which comprises detecting tandem repeats in a target coding sequence, scoring the repeats for polymorphic probability and generating a dataset che repeats for polymorphic probability and generating a dataset correlating the repeats with polymorphic probability to identify a correlating the repeats with polymorphic probability to identify a correlating of ubiquitous simple sequences, POMPOUS, and Rep-X) are useful for identifying and detecting candidate polymorphic repeats in human genes, which can be used to undearstand, treat or eliminate genetic diseases linked to mucleotide repeats are Machado-Joseph, Haw River syndrome, Huutington's disease, fragile-X syndrome, Fordersch's ataxis, syndrome, Fordersch's ataxis, mytonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and spinocerebellar ataxia, The sequences presented in ABX79676-ABX80022 are the polymorphic repeats identified for a search of human ESTS
                                                                                                                                                                                                                                                Identifying a candidate polymorphic repeat within a coding sequence, inderstanding or treating genetic disease, comprises detecting tandem repeats in a target coding sequence and scoring the repeats for polymorphic probability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15 BP; 9 A; 0 C; 0 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                 Example, Col 309; 588pp; English
                                                                                                                                                                                Garner HR, Wren JD, Minna JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.2%
Dest Local Similarity 100.0
Matches 13; Conservative
                                                                                                                                           (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                      WPI; 2003-208818/20
                                                                     31-DEC-1999;
                                                                                                         31-DEC-1999;
US6472154-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New assay for determining relative binding affinities of a ligand to different oligonucleotide sequences is useful to determine nucleic acid binding specificities and base pair determinants of particularly ligands.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to methods for determining relative binding affinities of a ligand to different oligonucleotide sequences, using indicator oligonucleotide pairs having a signal and a signal-altering group attached in direct or competitive binding assays. The method is used to determine nucleic acid binding specificities and base pair determinants of particular ligands. The present sequence is a competitor oligonucleotide used to illustrate the method of the invention
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                                                                                                                                                                                          Competitive binding assay; binding affinity; ligand; indicator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.2%; Score 13; DB 1; Length 13;
100.0%; Pred. No. 2.7e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 13 BP; 0 A; 0 C; 7 G; 6 T; 0 U; 0 Other;
                                                                                                                                                    Competitor oligo used in the invention #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENE-) GENELABS TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Col 11; 32pp; English.
                                           AAD45600 standard; DNA; 13 BP
                                                                                                                                                                                                                                                                                                                                                                                                 98US-00151890.
                                                                                                                                                                                                                                                                                                                                                               98US-00151890
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                                                                                                                   (first entry)
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Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schroth GP, Bruice TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-626078/67.
                                                                                                                                                                                                                                                  Unidentified.
                                                                                                                                                                                                                                                                                        JS6420109-B1.
                                                                                                                                                                                                                                                                                                                                                               11-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                   11-SEP-1998;
                                                                                                                     27-DEC-2002
                                                                                 AAD45600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
         RESULT 448
                               AAD45600
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Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; intranslocation; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; philadelphia chromosome; inflammation; autoimmune disease; atheroselerosis; myocardial infarction; stroke, restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial ischaemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS; human immunodeficiency virus; acquired immune deficiency syndrome;
                                                                                                                                                                                                                                                                Human relA hammerhead ribozyme target sequence (nt. position 562).
                                                                                                                   5014/c
AAT55014 standard; RNA; 15 BP.
1814 ATATATATATA 1826
                                                                                                                                                                                                               (revised)
(first entry)
                                       13
                                       1 Ararararara
                                                                                                                                                                                                                 25-MAR-2003
18-APR-1997
                                                                                                                                                                              AAT55014;
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Homo sapiens

EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat; polymorphic marker prediction of ubiquitous simple sequences; POMPOUS; Rep-X; human; genetic disease; drug-treatment; Machado-Joseph; Haw River syndrome; Huntington's disease; fragile-X syndrome; Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia; spinal atrophy; bulbar atrophy; spinocerebellar ataxis.

Ното варіепв

EST polymorphic DNA repeat polynucleotide #83

CXXXEXEXEXEXEXXXX

(first entry)

17-APR-2003

ABX79758;

ABX79758 standard; cDNA; 15

ABX79758

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Gaps

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1.2%; Score 13; DB 1; Length 15; 100.0%; Pred. No. 3e+02; artive 0; Mismatches 0; Indels

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Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; dironic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; atherosolarosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial; keumasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
                                                                                                                                                 Mouse relA hammerhead ribozyme target sequence (nt. position 562).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94US-00201109.
94US-00218934.
94US-00224483.
94US-00224483.
94US-002245736.
94US-00291432.
94US-00291632.
94US-00291632.
94US-00291632.
94US-00311486.
94US-00303039.
94US-00311486.
94US-00311486.
94US-00311486.
94US-00314397.
94US-00314397.
94US-00314397.
94US-00314397.
94US-00314397.
94US-00314397.
94US-00314397.
94US-00314337.
94US-0031493.
                                AAT54825 standard; RNA; 15 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (RIBO-) RIBOZYME PHARM INC.
                                                                                                    (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-MAY-1994;
06-JUL-1994;
15-AUG-1994;
16-AUG-1994;
17-AUG-1994;
02-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-SEP-1994;
23-SEP-1994;
23-SEP-1994;
28-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9523225-A2.
                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-FEB-1995;
                                                                                                    25-MAR-2003
07-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-AUG-1995
                                                                    AAT54825;
RESULT 451
AAT54825/c
                                                   The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves relA mRNA at the nucleotide base position indicated in the DE line. The relA gene product is a subunit of the transcriptional regulator NF-kappa and is implicated specifically in the indiction of inflammatory responses. Regions of the mRNA that do not form secondary folding structures and that contain operation and pairs in the prospectives and that contain were designed and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes are designed to cleave the target sequences and thereby inhibit relA expression, making them potentially useful for treating rheumatoid arthritis, restenosis and asthma as well as for increasing clearace to transplanted tissues. The potential inmunosuppressive properties of a ribozyme that cleaves relA mRNA means that uses are limited to local delivery, acute indications or ex vivo treatment. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       b DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
Usman N, Wincott FE, Woolf T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ribozymes having modified bases and methods for producing them - for use in inhibiting disease related genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15 BP; 2 A; 4 C; 4 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 228; 407pp; English.
                                                                       94US-00201109.
94US-00218934.
94US-00224483.
94US-00224481.
94US-00229132.
94US-00291433.
94US-00291433.
94US-00391832.
94US-00391832.
94US-0031837.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-351090/45.
                                                                                                                                                                                                                                                                                                                                                            28-SEP-1994;
03-OCT-1994;
07-OCT-1994;
                                                                                                                                                                                                                                                                                                         08-SEP-1994;
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Stinchcomb Grimm S, Modak A, Tracz D,

11-OCT-1994 04-NOV-1994

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Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
Tracz D, Usman N, Wincott FE, Woolf T;
                                                                                                                                                                                                                                                                                                   Ribozymes having modified bases and methods for producing them - for use in inhibiting disease related genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 225; 407pp; English
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TCACCTGGAAGCA 3

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The present sequence represents a preferred target sequence for an constant conclete acid (i.e. a ribozyme) which cleaves relA mRNA at the concleotide base position indicated in the DE line. The relA gene product is a subunit of the transcriptional regulator NP-kappaB and is implicated specifically in the induction of infibammatory responses. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes are designed to cleave the target sequences and thereby inhibit relA expression, making them potentially useful for treating rheumatoid arthritis, restenosis and aschma as well as for increasing tolerance to transplanted tissues. The potential is munosuppressive properties of a ribozyme that cleavers relA mRNA means that uses are limited to local delivery, acute indications or ex vivo treatment. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; ILD-5; ICAM-1; intercellular adhesion molecule; rell A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation, chronic myelogenous leukaemia; CMY, cancer; Philadelphia chromosome; inflammenton; autoimmune disease; atherosclerosis; myocardial infarction; stroke; restenosis; transplant rejection; heumatoid arthritis; psoriasis; myocardial ischaemaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse relA hammerhead ribozyme target sequence (nt. position 1664).
                                                                                                                                                                                                                                                                                                                                                                                             1.2%; Score 13; DB 1; Length 15;
100.0%; Pred. No. 3e+02;
rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                     Sequence 15 BP; 2 A; 4 C; 4 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2152 TCACCTGGAAGCA 2164
                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 452
QQ
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The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves relA mRNA at the enzymatic nucleotide base position indicated in the DE line. The relA gene product is a subunit of the transcriptional regulator NF-kappaB and is implicated specifically in the induction of inflammatory responses. Regions of the man secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes are designed to cleave the target sequences and thereby inhibit relA expression, making them potentially useful for treating rheumatoid arthritis, restenosis and asthma as well as for increasing tolerance to transplanted tissues. The potential immited to local delivery, acute indications or ex vivo treatment. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                         b DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
Karpelsky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
Favco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
Usman N, Wincott FE, Woolf T;
                                                                                                                                                                                                                                                                                                                                                                                                Ribozymes having modified bases and methods for producing them - for use in inhibiting disease related genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chemokine receptor; interleukin-8 compound inhibitor; chromosome 7p22; inflammation; wound healing; neutropaenia; myeloid leukaemia; tumour; toxin delivery; hypermegakaryocytopoietic disease; polycythaemia vera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.2%; Score 13; DB 1; Length 15;
100.0%; Pred. No. 3e+02;
tive 0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15 BP; 2 A; 4 C; 4 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 226; 407pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3-nitropyrrole-containing primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ90176 standard; cDNA; 15 BP.
             94US-00311486.
94US-00311749.
94US-00316437.
94US-00319492.
94US-0031893.
94US-00337608.
94US-00357577.
                                                                                                                                                                                                         95US-003B0734.
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                                                                                                                                                                                                                                         (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0°
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-351090/45.
                                                                                                                                                                                                                                                                           Stinchcomb DT,
                                                                03-OCT-1994;
07-OCT-1994;
11-OCT-1994;
                                                                                                                                                      28-NOV-1994;
                                                                                                                                                                         16-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-MAY-2000
                                                                                                                                                                                                         30-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer; ss.
                                                                                                                                                                                                                                                                                            Grimm S,
Modak A,
Tracz D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ90176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ90176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
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/*tag= a /note= "Optionally A, T, G, C or 1-(2-deoxy-D-ribfuranosy1)-3-nitropyrrole"

99WO-US012829 98US-00106800 99US-00236166

Location/Qualifiers

mcgarry191-19.rng

Page 207

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New nucleic acid encoding chemokine receptor, useful for diagnosis and
treatment of e.g. neutropenia, inflammation and leukemia.
                                                               WPI; 2000-170907/15
                                                        HYSE-) HYSEQ INC.
                      WO200000515-A2
Key
modified_base
                                                22-JAN-1999;
                                     29-JUN-1999;
                                             :9-JUN-1998;
                              06-JAN-2000.
```

in the sequence represents a 3-nitropyrrole-containing primer which is used in the course of the invention. The invention relates to a polymulceotide sequence which encodes a human cheend invention. The invention relates to a polymulceotide sequence which encodes a harman foetal liver spleen cDNA is derived from a human foetal liver spleen cDNA interaction for cell binding sites. The chemokine receptor gene on the short arm of chromosome 7 at 7p22. The polymulceotide competition for cell binding sites. The chemokine receptor gene is competition for cell binding sites. The chemokine receptor gene is competition for cell binding sites. The chemokine receptor gene is competition of antisense or triplex-forming molecules for chromosome/gene mapping or in the recombinant production of polypeptides and the cortor of production of antisense or triplex-forming molecules for the control of production of antisense or triplex-forming molecules for the control of production of antisense or triplex-forming molecules for the control of specific antibodies, also for purification, detection or modulation of interleukin-8-type chemokines (for diagnosis or prognosis, or monitoring conference in sequence can also be used as molecular weight markers or food supplements, and to screen compound libraries for specific binding conference and also be used as molecular weight markers or food supplements, potential agonists or antagonists Antibodies raised against the chemokine receptor polypeptide sequence are used to detect or purify the polypeptide and antibodies are also used to premote the healing of wounds. The colypeptide and antibodies are also used to prevent correct myeloid (associated with hyperproliferation of preparation correct myeloid associated with hyperproliferation of preparation of preparation of preparation of associated with hyperproliferation of preparation of preparation of secured as associated with hyperproliferation of preparation of preparation of carry toxing to tuning the proper propagation of preparation of sequence represents a 3-nitropyrrole-containing primer which is used Example 2; Page 52; 138pp; English carry toxins to tumour cells

Sequence 15 BP; 0 A; 2 C; 2 G; 10 T; 0 U; 1 Other;

Gaps ö 1.2%; Score 13; DB 1; Length 15; 92.9%; Pred. No. 3e+02; 1; Indels 0; Mismatches Local Similarity 92.9 Query Match Best Loca. Matches

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ABK55502 standard; DNA; 15 BP ABK55502; RESULT 454 ABK5502 ID ABK: XX AC ABK: XX DT 18-5

(first entry) 18-JUN-2002

Selectin L Lymphocyte Adhesion Molecule 1 (SELL) oligonucleotide #38 Human; Selectin L Lymphocyte Adhesion Molecule 1; SELL; neonatal pertussis; whooping cough; haplotyping; primer; allele-specific oligonucleotide; ss.

Homo sapiens,

WO200216654-A1

28-FEB-2002;

27-AUG-2001; 2001WO-US026675

25-AUG-2000; 2000US-0228262P

(GENA-) GENAISSANCE PHARM INC

Bieglecki KM, Kliem SE, Koshy B, Kumar AM; Anastasio AE,

WPI; 2002-292071/33.

Novel genetic variants of selectin L lymphocyte adhesion molecule 1 (SELL) gene useful for therapeutic purposes and for expressing SELL protein useful in identifying drugs to treat whooping cough.

Claim 17; Page 14; 137pp; English.

The invention relates to an isolated polymucleotide (I) comprising a uncleotide sequence which is a polymorphic variant of a reference or uncleotide sequence which is a polymorphic variant of a reference sequence for Selectin Liyaphocyte Adhesion Molecule 1 (SELL) gene. SELL sequence for Selectin Liyaphocyte Adhesion Molecule 1 (SELL) gene. SELL olypeptide is useful for screening for drugs targeting the polypeptide. Or haplotype pair of SELL gene. These are useful in developing diagnostic tests and therapeutic treatments for neonatal pertussis (whooping cough). Collisions of SELL protein for use in screening for candidate drugs to treat diseases related to SELL activity. The polymorphism and haplotype data cree whooping cough, screening for such drugs and reducing bias in clinical trials of such drugs. Establishing the SELL haplotype of clinical trials of several steps in the discovery and development of an individual is useful for improving the efficiency and reliability of several steps in the discovery and development of curs in the discovery and development of pertussis (whooping cough). The haplotyping method is useful to validate predicted to be associated with SELL activity e.g. neonatal consists of the series associated with SELL activity e.g. neonatal consists of a compounds targeting sepecific condition or disease predicted to be associated with SELL activity. The method is also useful or stease predicted to be associated with SELL activity e.g. detecting which of the SELL haplotypes or haplotype pairs present in individual consonist activity of candidate drugs ergeting SELL is useful in the disease population with the specific condition or the binding affinity of candidate drugs targeting SELL is useful in the binding affinity of candidate drugs targeting sell activity of candidate curson and in assays to measure the binding affinity of candidate drugs candidate drugs ergeting the sell of the server and sell provided and server and sell perpension or the binding affinities of one or more candidated a protein, ABK55465-ABK55559 represent SELL gene allele-specific oligonucleotides of the invention

Sequence 15 BP; 2 A; 5 C; 4 G; 3 T; 0 U; 1 Other;

Gaps .; 0 1.2%; Score 13; DB 1; Length 15; 86.7%; Pred. No. 3e+02; tive 1; Mismatches 1; Indels Query Match
Best Local Similarity 86.،،
...ماه 23. Conservative

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1584 GCCCCAGTGACAGCT 1598 decembereday 15

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RESULT 455

mcgarry191-19.rng

3-nitropyrrole containing oligonucleotide #2.

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The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12799.ACH5081, whose sequence was determined by the technique of SBH Gequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antiscense DNA or RNA. The purified polypoptide is useful for generating antiscense DNA or RNA. The purified polypoptide is an example of an oligonucleotide containing a 3-nitropyrrole base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jones LW,
                                                                                                                                                                     Primer, ss; sequencing by hybridisation, SBH; 3-nitropyrrole; genome mapping; biodiversity; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stache-Crain B, Dickson MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15 BP; 0 A; 2 C; 2 G; 10 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            analogue which may be used in the SBH technique
                                                                                                                                3-nitropyrrole containing oligonucleotide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Page 16; 44pp; English.
                  ACH50832 standard; DNA; 15 BP.
                                                                                                                                                                                                                                                                                                                                                                                   30-JUL-2001; 2001US-00918995.
                                                                                                                                                                                                                                                                                                                                               10-JUL-2001; 2001US-00918995
                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      (DRMA/) DRMANAC R T.
(LABA/) LABAT I.
(STAC/) STACHE-CRAIN B.
(DICK/) DICKSON M C.
(JONE/) JONES L W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drmanac RT, Labat I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-615964/58
                                                                                                                                                                                                                                                                     US2003073623-A1.
                                                                                             13-OCT-2003
                                                                                                                                                                                                                                                                                                          17-APR-2003.
                                                                                                                                                                                                                                Synthetic.
ACH50832
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Gaps ..

1.2%; Score 13; DB 1; Length 15; 92.9%; Pred. No. 3e+02; tive 0; Mismatches 1; Indels

1863 CCTTTTTATTTTG 1876

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Query Match Best Local Similarity 92.9³ Matches 13, Conservative

15 CCTTTTTTTTG 2

Gaps ; 0 1.2%; Score 13; DB 1; Length 15; 92.9%; Pred. No. 3e+02; 1; Indels 0; Mismatches Query Match
Best Local Similarity 92.9
Matches 13; Conservative

1863 CCTTTTTATTTTG 1876

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RESULT 456 ACH50833/c ID ACH50833 standard; DNA; 15 BP XX AC ACH50833; XX DT 13-OCT-2003 (first entry)

Human, pharmacological, hypotensive, antilipaemic, vasotropic, laxative, dermatological, antidepressant, tranquilliser; antiinflammatory; eczema, antiulcer; antimigraine; neuroprotective; antiparkinsonian; analgesic;

Human CD40L antisense oligonucleotide SEQ ID NO:67.

AZZXBXBX

09-OCT-2003 (first entry)

ACF63345;

ACF63345 standard; DNA; 16 BP.

RESULT 457 ACF63345

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The invention relates to an isolated polymucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SEH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polymucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (RST) for in forensice, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as cligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide protein, or in generating antished containing a 3-nitropyrrole base analogue which may be used in the SBH technique
                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
                                                                                                                                                                                                                                                                                                                                                                                 Jones LW;
                                                Primer, 88; sequencing by hybridisation; SBH; 3-nitropyrrole; genome mapping; biodiversity; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                 Stache-Crain B, Dickson MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15 BP; 10 A; 2 C; 2 G; 0 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Page 16; 44pp; English.
                                                                                                                                                                                                            30-JUL-2001; 2001US-00918995.
                                                                                                                                                                                                                                             30-JUL-2001; 2001US-00918995.
                                                                                                                                                                                                                                                                                                                  m.
                                                                                                                                                                                                                                                                                                                                                                                   Drmanac RT, Labat I,
                                                                                                                                                                                                                                                                                               LABAT I.
STACHE-CRAIN
                                                                                                                                                                                                                                                                                                              (STAC/) STACHE-CRAIN
(DICK/) DICKSON M C.
(JONE/) JONES L W.
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-615964/58.
                                                                                                                                                                                                                                                                               DEMANAC R T.
                                                                                                                                       US2003073623-A1.
                                                                                                                                                                          17-APR-2003.
                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                               (DRMA/)
(LABA/)
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gynaecological; virucide; vulnerary; antiarthritic; antipsoriatic; cold; antimicrobial; cytostatic; litholytic; pathological disorder; depression; abnormal appetite; hypertension; hypercholesterolaemia; hyperlipidaemia; erectile dysfunction; anxiety; stress; inflammatory bowel syndrome; ulcerative colltis; Crohn's disease; renal stone; gall stone; migraine; constipation; headache; seizure; multiple sclerosis; polywyositis; fibromyalgia; Parkinson's disease; anyotrophic lateral sclerosis; trauma; chronic pain; pre-menstrual syndrome; sinusitis; carpal tunnel syndrome; rosacea; arthritis; psoriaeis; prostatis; inflammation; heart burn; infection; colon cancer; malignant melanoma; skin disorder; antisense oligonucleotide; ss.
                                                                                                                                                                                                                                                                                                                                                                         Composition with a modified oligonucleotide useful for treating a patient with a pathological disorder such as abnormal appetite, hypertension, eczema, anxiety, stress, and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; Page 9; 173pp; English
                                                                                                                                                                                                                                                                                                                          Thompson T;
                                                                                                                                                                                                                                               .0-JUL-2002; 2002WO-US021664.
                                                                                                                                                                                                                                                                       10-JUL-2001; 2001US-0303820P
                                                                                                                                                                                                                                                                                                 (OLIG-) OLIGOS ETC INC
                                                                                                                                                                                                                                                                                                                          Dale RMK, Arrow A,
                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-221709/21
                                                                                                                                                                                             WO2003006478-A1.
                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                     23-JAN-2003
                                                                                                                                                                   Synthetic
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The present invention describes a composition (I) suitable for administration in a mammal, which comprises a modified oligonucleotide for administration in a mammal, which comprises a modified oligonucleotide scontaining 7 or more contiguous ribose groups linked by achiral 5-3' internucleoside phosphate linkages, where the modified oligonucleotide is complementary to a region of a gene associated with a pathological disorder. Also described: (1) as commentational supplement comprising (II); and (2) a cosmetic composition comprising (II); where the modified oligonucleotide is complementary to a creation of a gene associated with a skin disorder. (1) and (1) and (1) and (1) and (1) and (1) and (2) a cusplementary in a nutrilingual complementary to a creation of a gene associated with a skin disorder. (1) and (1) 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16 BP; 4 A; 3 C; 5 G; 4 T; 0 U; 0 Other;
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Gaps

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Query Match 1.2%; Score 12.8; DB 1; Length 16; Best Local Similarity 87.5%; Pred. No. 3.3e+02; Matches 14; Conservative 0; Mismatches 2; Indels

2200 GTTTATTTGTGAGAG 2215

ð

1 Gritaririciraaak 16

Seguence 16 BP; 5 A; 0 C; 3 G; 8 T; 0 U; 0 Other;

The sequences given in AAQ27960-86 are primers which were used in the construction of the DNA encoding a Staphylococcus protease. The protease are also AAQ27987) specifically cleaves the peptide bond at the C-terminus of the glutamic acid residue in polypeptide

i of

Novel protease prepd. using Bacillus or Saccharomyces host - capable cleaving peptide bond at carboxyl terminus of glutamic acid residues polypeptide(s).

Disclosure; Page 4; 25pp; Japanese.

Polymerase chain reaction; PCR; amplify; Staphylococcus; ss.

91JP-00024633. 90JP-00040398.

19-FEB-1991;

03-AUG-1992.

20-FEB-1990;

JP04211370-A.

Synthetic.

(SHIO) SHIONOGI & CO LTD.

WPI; 1992-304938/37

AAQ27968 standard; DNA; 16 BP.

RESULT 458

4AQ27968

(first entry)

11-FEB-1993 Primer V810.

AAQ27968;

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Homo sapiens fetal kidney clone AK647 secreted protein gene 3' end.
                                                                                     Secreted protein; fetal kidney; ds.
                 AAX07568 standard; cDNA; 16 BP.
                                                                                                                                                           98WO-US013530
                                                                                                                                                                             97US-00885610
                                                   21-JUN-1999 (first entry)
                                                                                                                                                                                              (GEMY ) GENETICS INST INC.
                                                                                                        Homo sapiens
                                                                                                                         WO9900405-A1
                                                                                                                                                           29-JUN-1998;
                                                                                                                                                                             30-JUN-1997;
                                                                                                                                          07-JAN-1999
RESULT 459
                 BXXXXXXXXXXXXXXXXXXXXXXXXX
                                                                                                                                                           ö
                                                                                                                                                           Gaps
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1.2%; Score 13; DB 1; Length 16; 100.0%; Pred. No. 3.1e+02; tive 0; Mismatches 0; Indels

1688 TGACACTGTTCAG 1700 rcacacretrcas 16

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Local Similarity 100. les 13; Conservative

Matches

Query Match

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The sequence is that of the 3' end of a sequence encoding a secreted protein from a human fetal kidney clone AK296. Such a sequence is predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Although no supporting data is given. Suggested activities in clude nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as proliferation/differentiation activity, hemmatopojeeis regulating activity, chematocopieeis regulating activity, chematocopieeis regulating activity, chematocopiecis activity, activity, haemostatic and thrombolytic activity, chematocopiecis activity, anti-inflammatory activity, anti-inflammatory activity, and tumour inhibition activity. It is also stated to be useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           feolation of satellite sequences from genomic DNA for use as DNA markers comprises isolating a library with high homogeneity by DNA fragmentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention provides a novel method for isolation of satellite sequences from genomic DNA that comprises fragmentation of the DNA by a
                                                                                                   derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Satellite sequence; DNA fragmentation; microsatellite DNA; DNA marker;
                                                                                               lynuclèotides encoding secreted human proteins - are derived fro
kidney or adult retina CDNA libraries, used as, e.g. potential
                Treacy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.2%; Score 12.8; DB 1; Length 16; 87.5%; Pred. No. 3.3e+02; tive 0; Mismatches 2; Indels
                Racie LA, Merberg D,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16 BP; 16 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES
                Lavallie ER,
                                                                                                                                                                    Disclosure; Page 54; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 5; Page 15; 35pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H. discus derived sequence #28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1865 TTTTTTTTTTTT 1880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-JP003551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98JP-00232153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ98510 standard; DNA; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Takahashi H, Sekino M;
                Mccoy JM, I
Agostino MJ;
                                                                                               New polynucleotides
foetal kidney or adu
                                                                  WPI; 1999-095671/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haliotis discus; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haliotis discus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAR-2000
                  Jacobs K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ98510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16
                                  Evans C,
                                                                                                                                     vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Gaps

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method which is not dependent on base sequences, then selection of the satellite sequences from the obtained genomic library of high homogeneity. The method is useful for the isolation of microsatellite DNA sequences which can be used as DNA markers. The new method markedly improves the efficiency of isolation of satellite sequences in comparison to prior art methods which are reliant on base sequences. Sequences AAZ98483-514 represent sequences from Haliotis discus, used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes nucleoside derivatives (I) with photolabile protecting groups. (I) are used to synthesize oligonucleotides using the photolithographic nucleic acid chip method, particularly where these are intended for performing enzymatic reactions initiated from a free 3'-hydroxy (especially solid-phase polymerase reactions or ligase reactions, but also reverse transcription, cDNA synthesis etc.), also for hybridization testing, sequencing and in DNA computing. (I) are produced with high selectivity by reaction with a mild acylating agent that has high specificity for the 3'-position, without significant side-reactions (Cf. more reactive acylating agents such as chloroformates)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                groups, useful in s, e.g. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA chip; primer; nucleoside derivative; photolabile protecting group; photolithographic nucleic acid chip; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleoside derivatives with photolabile protecting groups, oligonucleotide synthesis, particularly on solid phases, e.g. hybridization testing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.2%; Score 12.8; DB 1; Length 16;
llarity 87.5%; Pred. No. 3.3e+02;
Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                             1.2%; Score 12.8; DB 1; Length 16; 87.5%; Pred. No. 3.3e+02; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16 BP; 16 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                 Sequence 16 BP; 8 A; 6 C; 2 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 9; 48pp; German.
                                                                                                                                                                                                                                                                         1793 TGTGTGTGTGTGTG 1808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-APR-1999; 99DE-01015867.
28-JAN-2000; 2000DE-01003631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-APR-2000; 2000WO-DE001148
                                                                                                                                                                                                                                                                                                                                                                                                  AAC66068 standard; DNA; 16
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 87.5
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hoheisel J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-679457/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA chip primer #4
                                                                                                                               of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200061594-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC66068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beier M,
                                                                                                                                                                                                                                                                                                                                                                                 AAC66068/c
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The present invention relates to an analytical support, to which a number of oligonucleotides are labelled with a fluorescent compound, the fluorescence of which varies when the oligonuclectide hybridises to its complement. The analytical support is useful in hybridisation testing for identification of specific nucleic acids, such as genomic sequencing, detecting mutations or pharmaceutical development. The present oligonuclectide was used to illustrate the
                                                                                                                                                                                                                                                                                                                                                F1 (CH2) 6-PO-thymine, where F1 is flavine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Support for hybridization analysis of nucleic acids for sequencing techniques, comprises an array of oligonucleotides having a label where the fluorescence changes follow hybridization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tch al Similarity 87.5%; Pred. No. 3.3e+02; 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                 Analytical support; genomic sequencing; mutation detection; pharmaceutical development; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dueymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cuzin M, Peltie P, Fontecave M, Decout JL,
                                                                                                                                                                                                                                                                                                                                  /mod_base= OTHER
/note= "OTHER = F1(CH2)6-PO-
and PO is a phosphate group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.
                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 12; 33pp; French.
TTTTTTTTTTTT 1880
                                                                                                   ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-FEB-2000; 2000FR-00002236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-FEB-2000; 2000FR-00002236
                                                                                                   ABA04585 standard; DNA; 16
                             TTTTTTTTTTTT
                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-628265/73.
                                                                                                                                                                                        Oligonucleotide #5.
                                                                                                                                                                                                                                                                                             Key
modified base
                                                                                                                                                                                                                                                                                                                                                                                             FR2805348-A1
                                                                                                                                                         15-FEB-2002
                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                               ABA04585;
   1865
                           16
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                                                                                     ABA04585
                                                                       RESULT
                                                                                                                               ò
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Conjugate of oligonucleotide, minor groove binder and latent fluorophore, useful for detecting specific nucleic acids, e.g. for single-nucleotide mismatch discrimination.

Vermeulen NMJ;

(EPOC-) EPOCH BIOSCIENCES INC

Dempcy RO, Afonina IA, WPI; 2001-328656/34.

99US-00428236.

26-OCT-1999;

26-OCT-2000; 2000WO-US029786

WO200131063-A1.

03-MAY-2001.

/*tag= a /note= "thymine modified by a minor groove binder (2-dimethylaminonaphthalene-6- sulfonamide"

Location/Qualifiers

Key modified_base

Synthetic

ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore; hybridisation; detection; fluorescence; probe; ss.

Oligonucleotide-minor groove binder complex.

(first entry)

09-JUL-2001

```
The present sequence is that of an oligonucleotide (ODN)-minor groove binder (MGF) complex. MGBs bind in a non-intercalating manner to the minor groove of non-single-stranded DNA, RNA or thair hybrids. ONN-MGB-LF winch binds similarly to the MGB but in an intercalating manner, or lies in the minor groove, or is oriented in some other way to the DNA molecule by MGBs such that it becomes fluorescent (or its fluorescent properties change detectably). The conjugates are used as hybridisation probes and amplification primers for fluorescent detection of specifically PCR, for single-nucleotide mismatch discrimination, target or signal amplification, array-based assays and sequencing, including detection of double-stranded DNA by triplex formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore; hybridisation; detection; fluorescence; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 1.2%; Score 12.8; DB 1; Length 16; Local Similarity 87.5%; Pred. No. 3.3e+02; hes 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide portion of ODN-MGB-LF conjugate.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 101; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1865 TITIBITITITI 1880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF30880 standard; DNA; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF30880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
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S
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Gaps

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1865 TTTTTTTTTTTT 1880

à

Local Similarity

Matches

AAF30895 standard; DNA; 16 BP.

RESULT 463 AAF30895 AAF30895

EXXX

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The present sequence is that of the oligonucleotide (ODN) component of an ODN-MGB (minor groove binder)-IF (latent fluorophore) conjugate of the invention. MGBs bind in a non-intercalating manner to the minor groove of non-single-stranded DNA, RNA or their hybrids, while a LF binds similarly but in an intercalating manner, or lies in the minor groove, or is oriented in some other way to the DNA molecule by MGB, such that it becomes fluorescent for its fluorescent properties change detectably). The conjugates are used as hybridisation probes and amplification primers for fluorescent detection of specifically hybridising sequences, for analysis or diagnosis, especially (real-time) PCR, for single-nucleotide mismatch discrimination, target or signal amplification, array-based assays and sequencing, including detection of double-stranded DNA by triplex formation. Many different targets can be detected a single reaction vessel. The present targets can be detected a single reaction vessel. The present obn-MGB-IF conjugate was used to demonstrate hybridisation-triggered fluorescence. Upon hybridisation to the complementary target sequence there was an increase in fluorescence cypield, measured as the ratio of the fluorescence emitted by the hybrid between the ODN-MGB-IF conjugate sequence to the stranded) ODN-MGB-IF,
                                                                                                                                                                                                                                                                                 Conjugate of oligonucleotide, minor groove binder and latent fluorophore, useful for detecting specific nucleic acids, e.g. for single-nucleotide mismatch discrimination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                  Vermeulen NMJ;
                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 58; 105pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1865 TTTTTTTTTTTT 1880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH42481 standard; DNA; 16 BP.
                                                                                                                                                                             (EPOC-) EPOCH BIOSCIENCES INC.
                                                                                                          26-OCT-2000; 2000WO-US029786
                                                                                                                                            99US-00428236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                  Dempcy RO, Afonina IA,
                                                                                                                                                                                                                                                      WPI; 2001-328656/34
                                    WO200131063-A1
                                                                                                                                            26-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2001
                                                                       03-MAY-2001
 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH42481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 465
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ઠે
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ö Gaps ô Query Match
1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels

Oligonuclectide used to produce branched chain compounds.

Branched chain compound; nucleic acid synthesis; primer extension; reverse transcription; nucleic acid hybridization; nucleic acid amplification; ss.

Synthetic.

Location/Qualifiers Key nodified base

/*tag=

```
: .3
*tag= c
'note= "branch present"
           /*tag= b
/note= "COOH attached"
"COOH attached"
         modified_base
  misc_feature
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EP1111068-A1

27-JUN-2001.

99EP-00125484 21-DEC-1999;

99EP-00125484 21-DEC-1999;

(LION-) LION BIOSCIENCE AG. (VBCG-) VBC GENOMICS GMBH.

Mueller M; Schmidt W, Hiller R, Huber M,

WPI; 2001-466959/51.

Branched compounds useful in e.g. nucleic acid synthesis reaction comprises nucleic acid moieties optionally extended by a polymerase

Example 1; Page 10; 31pp; English

The specification describes branched compounds containing nucleic acid moieties optionally extended by a polymerase. The branched chain compounds of the invention are used in nucleic acid synthesis reaction, primer extension reaction, reverse transcription reaction of RNA into DNA, nucleic acid hybridization experiment (for identifying sequence of nucleic acid, and nucleic acid amplification experiment (for analysing the expression pattern of genes). The compounds are also used in solid-phase enzymatic reactions. The present sequence was used in the course of the invention to produce branched chain compounds

Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

0; Gaps Query Match
1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels

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1865 TITITATITITE 1880

ò g RESULT 466

ABA97402 standard; DNA; 16 BP. ABA97402; Nucleotide sequence of oligomer # 1 used to test thermal stability.

18-JUN-2002 (first entry)

Protein nucleic acid molecule; PNA; ds

Synthetic

WO200168673-A1.

20-SEP-2001.

13-MAR-2001, 2001WO-US008111

14-MAR-2000; 2000US-0189190P. 30-NOV-2000; 2000US-0250334P.

(ACTI-) ACTIVE MOTIF

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This invention relates to oligonuclectide analogues comprising a protein nucleic acid molecule (PNA) monomer. They are used in the detection and separation of nucleic acid molecules and as probes, primars, linkers, adapters and antisense agents on solid supports. Modifications enhance their use as capture and detection probes e.g. by the incorporation of biothin digordgenen, radioStoppes, fluorescent labels such as labining used for enhancing or inhibiting the activity of an enzyme or calludar activity. The compounds are stable to nucleases and proteases, have high affinity, binding specificity and solubility. The polyamide backbone of FNAs is resistant to both nucleases and proteases. Concentration. The compounds are relatively simple to synthesize and are used in a wide variety of applications. This sequence represents a DNA concentration. The compounds are relatively simple to synthesize and are used in a wide variety of applications. This sequence represents a DNA coligoner which is used to represent the thermal stability of the
                                                                                                                                                             Oligonucleotides analogs useful in detection, separation and purification of nucleic acid molecules, comprise monomers, dimers and oligomers.
                          Efimov V, Fernandez J, Archdeacon D, Archdeacon J;
Chakhmakhcheau O, Buryakova A, Choob M, Hondorp K;
                                                                                                                                                                                                                                            Example 17; Page 118; 197pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oligomers of the invention
                                                                                                        WPI; 2002-041177/05.
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1.2%; .Score 12.8; DB 1; Length 16; 87.5%; Pred. No. 3.3e+02; ative 0; Mismatches 2; Indels 1865 TTTTTTTTTTTT 1880 Conservative Best Local Similarity Matches 14; Conserv Query Match ò D

1 Tritritrititi 16

Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

AADS6451 standard; DNA; 16 BP 07-AUG-2003 (first entry) AAD56451; RESULT 467

2'F-ANA antisense oligo #6, to elicit RNase H degradation of target RNA Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H; antisense; ss. /mod_base= OTHER /note= "2'-deoxy-2'-fluoroarabinothymidine" Location/Qualifiers ...16 *tag= a modified_base Unidentified

misc_feature

8 . .9
/*tag= b
//note= "Bases 8 and 9 are linked by two secouridine
linkers which is represented as S in page 49 and X in
page 57 and Fig 7 and 8 of the specification"

WO2003037909-A1

08-MAY-2003

29-OCT-2002; 2002WO-CA001628

29-OCT-2001; 2001US-0330719P

(UYMC-) UNIV MCGILL.

Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;

Novel acyclic linker-containing oligonucleotide useful for preventing or decreasing translation, reverse transcription and/or replication of a target RNA in a system, comprises a modified deoxyribonucleotide.

Example 2; Fig 7; 104pp; English.

The invention relates to an acyclic linker-containing oligonucleotide comprising at least one modified deoxyribonucleotide. Oligonucleotides of the invention are useful for preventing or decreasing translation.

They are useful for selectively preventing of a target RNA in a system. They are useful for selectively preventing gene expression in a sequence-specific manner, for hybridising to complementary RNA such as cellular mRNA or viral RNA. They are also useful therapeutically in formulations or medicaments to prevent or treat a disease characterised by the expression of a particular target RNA. The invention is used in gene therapy. The present sequence is an antisense oligo used to elicit human RNase (tibonuclease) if degradation of target RNA. This sequence is used in the exemplification of the invention

Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

0; Gaps Query Match 1.2%; Score 12.8; DB 1; Length 16; Best Local Similarity 87.5%; Pred. No. 3.3e+02; Matches 14; Conservative 0; Mismatches 2; Indels

1865 TITITATITATIT 1880

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0; Gaps

RESULT 468 AAL54078

AAL54078 standard; DNA; 16 BP.

AAL54078;

06-MAR-2003 (first entry)

Oligo-homodeoxyribonucleotide sequence, oligo dT.

Detection, single-stranded sensor, detectable fluorescence emission; forensic testing, paternity testing, tissue typing, hereditary disorder, human population genetics; human evolutionary history; cystic fibrosis; human haplotype diversity; Tay-Sachs; sickle-cell anaemia; ss.

Unidentified.

WO200284271-A2

24-OCT-2002.

16-AFR-2002; 2002WO-US012176

16-APR-2001; 2001US-00836579.

(REGC) UNIV CALIFORNIA. (CHAJ/) CHA J N.

Stucky GD; Cha JN, Morse DE,

WPI; 2003-103378/09.

Detecting polynucleotides, for pharmacogenetic testing, comprises contacting a target polynucleotide with a complementary single-stranded sensor polynucleotide and an agent that allows the sensor to fluoresce upon excitation.

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Example 1; Page 25; 41pp; English
                                                       04-DEC-2003
                                                                             21-AUG-2003
                                                                  Synthetic.
                                                     ADB68519;
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The invention relates to a novel assay for detecting a polymucleotide in a sample, which comprises: contacting a sample suspected of containing a target polymucleotide with a predetermined single-stranded sensor polymucleotide complementary to the target polymucleotide, in a solution comprising an agent that is a nonaqueous solvent that allows the sensor comprising an agent that is a nonaqueous solvent that allows the sensor polymucleotide, and detectable fluorescence emission. The sensor polymucleotide, and detecraning fluorescence emission. The sensor polymucleotide, and detecraning fluorescence emission. The comparison is controlled to detecting a single or double-stranded target of different applications including pharmacogenetic testing, wide variety of different applications including pharmacogenetic testing, forensic resting to identify the species or individual which was the course of a forensic specimen, in anthropological setting, paternity testing for compatibility between prospective issue or blood conors and patients and in screening for hereditary disorders. The method is alsease, drug or medication, and other applications include confidence in allows and alterations of human evolutionary history and characterisation of human haplotype diversity. The method is useful for detecting polymucleotide sequences from contaminants or pathogens including pateria, yeast, and viruses to detect single nucleotide confidence associated with particular alleles or subsets of nucleotide sequences associated with increased risk of diseases or this polymucleotide sequences represents an oligonucleotide sequence represents an oligonucleotide sequence represents an oligonucleotide sequence represents an oligonucleotide sequence used in a fluorescence technique of the invention
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ö Gaps ö Query Match
1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

1865 TITITATITITI 1880

ADB68519 standard; DNA; 16 BP

DNA hybridisation oligomer SEQ ID 9. (first entry)

hydroxyproline nucleic acid; HypNA; PNA; peptide nucleic acid; gene expression; respiration; secretion; signalling; ion-channel activity; cell motility; developmental phenotype; tumour regression; hybridisation; ss.

/*tag= a /note= "Optional N-terminal acetyl" Location/Qualifiers misc_difference

WO2003068798-A2

07-FEB-2003; 2003WO-US003904.

09-FEB-2002; 2002US-00072975

(ACTI-) ACTIVE MOTIF

Choob M; Archdeacon D, Archdeachon J, Fernandez J, Efimov V,

Method of inhibiting expression of genes or RNA transcripts, useful for therapy and determining effects of genes, by administering oligomers containing hydroxyproline nucleic acid.

Example 17; Page 233; 240pp; English

The invention relates to a novel method of inhibiting the expression of one or more genes or RNA transcripts by administering at least one oligonuclectide analogue that includes at least one hydroxyproline nucleic acid (HypNA) monomer to a cell or organism or their extracts. Oligonuclectides of the invention may be used to monitor properties including gene expression, respiration, secretion, signalling, innermence expression, respiration, secretion, signalling, innergensision. Furthermore, they may be utilised to determine the effects of particular genes, as antisense or homologous recombination constructs eg. for creating animal models of disease and finally, for increasing the activity of some enzymes, such as polymerases. The current sequence is that of the DNA hybridisation oligomer SEQ ID 9, cit he invention. This sequence may also comprise a peptide nucleic acid (PNA)

Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

ô Gaps . Query Match
1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels

1865 TTTTTTTTTTTT 1880 1 tritiritititititi

g

AAT81558 standard; RNA; 17 BP.

14-DEC-1997 (first entry)

Human c-myb hammerhead ribozyme target sequence (nt. position 2896)

Bnzymatic nucleic acid; hammerhead; ribozyme; cleavage; human; smooth muscle cell; hyperprollferation; restenceis; cancer; c-myb; coronary angioplasty; ss.

WO9531541-A2

Homo sapiens

23-NOV-1995.

94US-00245466. 95US-00373124. 95WO-US006368. 18-MAY-1995; 18-MAY-1994; 13-JAN-1995;

(RIBO-) RIBOZYME PHARM INC.

Stinchcomb DT, Draper K, Mcswiggen J, Jarvis T; WPI; 1996-010927/01.

New enzymatic nucleic acid molecules - cleave RNA produced by e.g. c-myb, for treating restenosis or cancer.

Claim 1; Page 78; 128pp; English.

The present sequence represents the preferred target sequence for an enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves

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The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (CDPD), chronic bronchistis, asthmat, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, hence, are useful for treatment of a patient having a condition associated with the level of CLCA1, where the invention further comprises
                                                                                                                                                                                                                                                                                                             ö
the human c-myb sequence at the base position indicated in the descriptor line. The C-myb sequence was screened for optimal ribozyme target sites using a computer folding algorithm, and regions of the mANA which did not form secondary folding structures and contained potential ribozyme activates sites were identified. Ribozymes were synthesises are their activities optimised by either varying the length of the binding arms or by modification to prevent degradation by nucleases. The ribozymes cleave the c-myb sequence and can be used to prevent smooth muscle cell hyperproliferation in restenosis, especially after coronary angioplasty, and in cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, chloride channel calcium activated 1; CLCA1; ss; antiasthmatic; antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma; chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ensymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma.
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Œ;
                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                 Query Match . 1.2%; Score 12.8; DB 1; Length 17; Best Local Similarity 43.8%; Pred. No. 3.4e+02; Matches 7; Conservative 7; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ayers D,
                                                                                                                                                                                                                                 Sequence 17 BP; 7 A; 1 C; 0 G; 0 T; 9 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human CLCAl gene enzymatic nucleic acid #60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thompson J, Mcswiggen J, Mckenzie T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 54; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                    1811 TGTATATATATATA 1826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001; 2001WO-US024970.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2000; 2000US-0224383P
                                                                                                                                                                                                                                                                                                                                                                             (RIBO-) RIBOZYME PHARM INC.
(SYNT ) SYNTEX USA LLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK55689 standard; RNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-217145/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (THOM/) THOMPSON J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200211674-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The mucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased calls or to detect the presence of CLCAI RNA in a cell. This sequence represents an enzymatic nucleic acid molecule of the invention
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1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                              Length 17;
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                                                                                                                                                         Sequence 17 BP; 7 A; 1 C; 1 G; 0 T; 8 U; 0 Other;
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1.2%; Score 12.8; DB 1;
Best Local Similarity 37.5%; Pred. No. 3.40+02;
Matches 6; Conservative 8; Mismatches 2;
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This invention describes novel oligomucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99389, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; SB; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                 Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
         Oligonucleotide SEQ ID NO 182712 for detecting SNP TSC0045154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 182712; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                        SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                         Oligonucleotide SEQ ID NO 115461 for detecting SNP TSC0028934.
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                                                                                                         RESULT 473
ABF15464/c
ID ABF15464 standard; DNA; 13 BP.
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Conservative
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Query Match
1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels
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ABF82715 standard; DNA; 13 BP

RESULT 474 **ABF82715** (first entry)

22-FEB-2002

ABF82715

1239 GATTCACATCTCA 1251

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13 RATTCACATCTCA 1

07-APR-2000; 2000DE-01019173.

Olek A, Piepenbrock C,

(EPIG-) EPIGENOMICS

06-APR-2001; 2001WO-IB000713

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This invention describes novel oligonucleotide primars or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; $8; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Best Local Similarity 92.3
Matches 12; Conservative
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                                             This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF9989, ABH00010-ABH99999 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels
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                 Claim 1; SEQ ID NO 68383; 29pp + Sequence Listing; German.
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RESULT 478

ABC14215/

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99989, ABH00010-ABF99989, ABH00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                    SNP; single_nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels
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                                                                   ABF96635 standard; DNA; 13
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1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels
                                                                                                             Similarity 92.3%; Score 12.6; DB 1; Length 13; Similarity 92.3%; Pred. No. 3e+02; 12; Conservative 1; Mismatches 0; Indels
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                                                                   Sequence 13 BP; 8 A; 2 C; 0 G; 2 T; 0 U; 1 Other;
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was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99889, ABH00010-ABH99889 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic formmat from WIPO at
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1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels
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                                                                                                                       Claim 1; SEQ ID NO 89619; 29pp + Sequence Listing; German.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99999, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form with MIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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Seguence 13 BP; 6 A; 5 C; 0 G; 1 T; 0 U; 1 Other;

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Score 12.6; DB 1; I
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92.3%; Pred. No. 3e+02;
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Matches 12; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 tepseent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but fip.wipo.int/pub/published_pct_sequences
                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Set of oligonucleotides, useful for diagnosis and cell typing, addesigned to detect single-nucleotide polymorphisms and cytosine
                                                                        Oligonucleotide SEQ ID NO 182711 for detecting SNP TSC0045154.
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                                    (first entry)
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ABF82714;
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 data for this patent did not form part of the printed specification, but typo.int/pub/published_pct_sequences

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

Olek A, Piepenbrock C,

WPI; 2001-657177/75

(EPIG-) EPIGENOMICS

06-APR-2001; 2001WO-IB000713 07-APR-2000; 2000DE-01019173

18-OCT-2001.

Claim 1; SEQ ID NO 25123; 29pp + Sequence Listing; German.

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Gaps

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Query Match 1.2%; Score 12.6; DB 1; Length 13; Best Local Similarity 92.3%; Pred. No. 3e+02; Matches 12; Conservative 1; Mismatches 0; Indels

1767 ITTITAAAATTI 1779

8

1 rrrrrraaaarry 13

Sequence 13 BP, 4 A; 0 C; 0 G; 8.T; 0 U; 1 Other;

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic
                                                                                       Oligonucleotide SEQ ID NO 225427 for detecting SNP TSC0054949.
                                                                                                                                                                                                                                                                                                       Berlin K;
                     ABH25450 standard; DNA; 13 BP.
                                                                                                                                                                                                                                  06-APR-2001; 2001WO-IB000713.
                                                                                                                                                                                                                                                         07-APR-2000; 2000DE-01019173.
                                                                  22-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                               (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                     WO200177384-A2.
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                                             ABH25450;
RESULT 487
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Gaps

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92.3%;

Local Similarity 92.3 nes 12, Conservative

1766 ATTTTTTABARTT 1778

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13 RTTTTTAAAATT 1

WPI; 2001-657177/75

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

WO200177384-A2

Oligonucleotide SEQ ID NO 25123 for detecting SNP TSC0006116.

(first entry)

20-FEB-2002

BXSXXXXXXXXXX

ABC25106;

ABC25106 standard; DNA; 13 BP.

RESULT 486 ABC25106

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a rarge of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010
                                                                                                                            This invention describes novel oligonucleotide primars or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999, ABF00010-ABF99999, ABF00010-ABF99999, ABF00010-ABF99999 and ABI00010-ABF9073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but fire wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide SEQ ID NO 164971 for detecting SNP TSC0006375.
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                                                                                            Claim 1; SEQ ID NO 225427; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                      1.2%; Score 12.6; DB 1; Length 13; 92.3%; Pred. No. 3e+02; tive 1; Mismatches 0; Indels
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                                                                                                                      Sequence 13 BP; 1 A; 0 C; 1 G; 10 T; 0 U; 1 Other;
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ftp.wipo.int/pub/published_pct_sequences
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Matches 12; Conservative
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Best Local Similarity 92.33
Matches 12, Conservative
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1774 AAATTTATATTGT 1786

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ABC59000 standard; DNA; 13 BP 21-FEB-2002 (first entry)

Oligonucleotide SEQ ID NO 59017 for detecting SNP TSC0015817.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2.

18-OCT-2001

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG.

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 59017; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

Sequence 13 BP; 6 A; 0 C; 0 G; 6 T; 0 U; 1 Other;

Gaps ö Query Match
1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels

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RESULT 491

ABC59000 standard; DNA; 13 BP ABCS9000/c ID ABCS: XX AC ABCS: XX DT 21-FI XX DE Olige

ABC59000;

21-FEB-2002 (first entry)

Oligonucleotide SEQ ID NO 59017 for detecting SNP TSC0015817.

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peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Set of oligonucleotides, useful for diagnosis, and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                               Homo sapiens.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE9989, ABH00010-ABE9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at was obtained in electronic format from Wl ftp.wipo.int/pub/published_pct_sequences

Claim 1; SEQ ID NO 59017; 29pp + Sequence Listing; German.

Sequence 13 BP; 6 A; 0 C; 0 G; 6 T; 0 U; 1 Other;

Gaps ó / Match 1.2%; Score 12.6; DB 1; Length 13; Local Similarity 92.3%; Pred. No. 3e+02; length 13; Conservative 1; Mismatches 0; Indels Query Match Matches

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ò g RESULT 492

ABH39478 standard; DNA; 13 BP. X # X D X B X S X M M X B X B X B X Y X B

22-FEB-2002 (first entry)

Oligonuclectide SEQ ID NO 239455 for detecting SNP TSC0058411.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2

18-OCT-2001.

06-APR-2001; 2001WO-IB000713

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABF9989 and ABI00010-ABF82073 tepresent the oligoners described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                               oligonucleotides, useful for diagnosis and cell typing, i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide SEQ ID NO 47735 for detecting SNP TSC0013684.
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                                                                 Berlin K;
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07-APR-2000; 2000DE-01019173.
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Best Local Similarity 92.55
Best Local 2; Conservative
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                                                                 Olek A, Piepenbrock C,
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                                (EPIG-) EPIGENOMICS AG.
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                                                                                                                                                 designed to detect s
methylation status.
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                                                                                                  WPI; 2001-657177/75
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at
         This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cartival nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting call type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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0; Gaps

Oligonucleotide SEQ ID NO 115462 for detecting SNP TSC0028934.

(first entry)

21-FEB-2002

ABF15465;

ABF15465 standard; DNA; 13 BP.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABC0010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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designed to detect single-nucleotide polymorphisms and cytosine
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1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels
                                     . Match 1.2%; Score 12.6; DB 1; Length 13; Local Similarity 92.3%; Pred. No. 3e+02; ls Conservative 1; Mismatches 0; Indels
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Sequence 13 BP; 1 A; 0 C; 1 G; 10 T; 0 U; 1 Other;
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methylation status
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Matches
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; SS; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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1793 TGTGTGTGTGT 1805

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1 TGTGTGTGTGY 13

RESULT 496

WPI; 2001-657177/75.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 160172; 29pp + Sequence Listing; German.
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Best Local Similarity 92.3
Matches 12; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a
                                                                                                                                                       This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABR0010-ABR9989, ABR0010-ABR9989, ABR0010-ABR9899, and ABI0010-ABR9203 are described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                          Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels
                                                                                                                      Claim 1; SEQ ID NO 239456; 29pp + Sequence Listing; German.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, coingomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                              Sequence 13 BP; 8 A; 0 C; 0 G; 4 T; 0 U; 1 Other;
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Query Match Best Local Similarity

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                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                         ABC59001 standard; DNA; 13 BP.
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AC ABC8
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Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prerreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form at from NIPO at
                                                                                                                                                                                                                     Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                              07-APR-2000; 2000DE-01019173.
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                                                                             SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                          Oligonucleotide SEQ ID NO 89620 for detecting SNP TSC0022467.
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  21-FEB-2002 (first entry)
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
                                                                                                     Oligonucleotide SEQ ID NO 47736 for detecting SNP TSC0013684.
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                       ABC47719 standard; DNA; 13 BP.
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RESULT 504
ABC47719/c
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide SEQ ID NO. 28734 for detecting SNP TSC0008353.

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Query Match 1.2%; Score 12.6; DB 1; Length 13; Best Local Similarity 92.3%; Pred. No. 3e+02; Matches 12; Conservative 1; Mismatches 0; Indels

1817 TATATATATGT 1829

13 TATATATATGY 1

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Sequence 13 BP; 7 A; 0 C; 1 G; 4 T; 0 U; 1 Other;
data for this patent did not form part of the F was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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AAT9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                  Claim 1; SEQ ID NO 47736; 29pp + Sequence Listing; German.
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Best Local Similarity
Matches 12; Conserv
         methylation status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detection of eukaryotic pathogens, especially fungal or Plasmodium spp. by detecting telomerase activity.
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1.2%; Score 12.6; DB 1; Length 13; 92.3%; Pred. No. 3e+02; tive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fungal telomeric nucleic acid sequence
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(TEXA ) UNIV TEXAS SYSTEM.
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                                                             Matches 12; Conservative
                                                                                                                                                     Saccharomyces cerevisiae
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           Query Match
Best Local Similarity
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24-MAR-1993;
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08-APR-1998
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RESULT 507 AAV95611

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The invention describes a method use for treating increased rate of proliferation of a cell or extending the ability of a cell to replicate, or treating a disease associated with cell sensecence. The method comprises administering an agent to reduce loss of telomera length within the senseding cells. The method is useful for treating a condition in the senseding cells. The method is useful for treating a condition associated with an increased rate of proliferation of a cell extending the ability of a cell to replicate, or for treating a disease or condition associated with cell sensecence e.g. neoplasia. A second method isclosed in the invention is useful for treating a condition associated with an elevated level of telomerase activity within a cell e.g. cancer. Also disclosed is method useful for diagnosis of a condition associated with an increased rate of proliferation in a cell in an individual e.g. age-related macular degeneration, astrocytes associated with Alzheimer's disease and endothelial cells associated with atherosclerosis. This sequence represents a polymuclecide used in the study of telomere length and telomerase activity described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating condition associated with cell senescence or increased rate of cell proliferation, by administering to cell an agent that derepresses telomerase in the senescing cells or that reduces loss of telomere
telomerase activity; cel replication; neoplasia; cancer; age-related macular degeneration; Alzheimer's disease; atherosclerosis; telomerase; telomerase inhibitor; immortalised cell; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.2%; Score 12.4; DB 1; Length 14; 92.9%; Pred. No. 3.3e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14 BP; 0 A; 0 C; 8 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blackburn EH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 51; 86pp; English.
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                                                                                                                                                                                                                                                                               92US-00882438.
93US-00038766.
93US-00060952.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shay J, Wright W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1793 TGTGTGTGTGTG 1806
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Best Local Similarity 92.9°
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              (SHAY/) SHAY J.
(WRIG/) WRIGHT W.
(BLAC/) BLACKBURN E H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-066896/06
                                                                                                                                                                                                                                                                                                                                                                      WEST/) WEST M D. SHAY/) SHAY J. WRIG/) WRIGHT W.
                                                                                                                                              US2002127634-A1.
                                                                                                                                                                                                                                                                               13-MAY-1992;
24-MAR-1993;
13-MAY-1993;
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22-APR-1997
                                                                                                                                                                                                                                     05-JUN-1995;
                                                                                                                                                                                          12-SEP-2002
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                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          West MD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes an enzymatic nucleic acid molecule which specifically cleaves RNA derived from a c-fos gene. AAV95401 to AAV95540 and AAV95554 to AAV95554 represent hammerhead ribozymes and hairpin ribozymes, respectively, which specifically cleave human c-fos. AAV95261 to AAV95400 and AAV9558 to AAV95628 represent human c-fos target cancer associated with elevated levels of c-fos oncogene, especially leukaemias, neuroblastomas and lung, breast and colon cancers. The ribozymes may also be used as diagnostic tools to examine genetic drift and mutations within diseased cells, or to detect the presence of c-fos RNA in a cell
                                                                                                                                                                                                                                                                                   Human; c-fos; hammerhead ribozyme; hairpin ribozyme; target site; cancer;
oncogene; leukaemia; neuroblastoma; diagnosis; genetic drift; mutation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enzymatic nucleic acid molecules which specifically cleave RNA derived from a c-fos gene - useful for treating conditions related to levels of -fos, especially cancer.
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                                                                                                                                                                                                                                        Human c-fos target sequence nucleotide position 756.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jarvis I, Mcswiggen JA, Stinchcomb DT;
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                                                                                                          AAV95611 standard; RNA; 14 BP.
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                                                                                                                                                                                                                                                                                                                                    diseased cell; ss.
                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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24-DEC-1997;
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Gaps

ABX50033

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gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; intercellular adhesion molecule; rel A; tumour necrosis factor; TNR-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogeneus leukaemia; CML; cancer; philadelphia chromosome; inflammation; autoimmune disease; atherosclerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial ischaemia; Kawasaki disease; septic shock; HIV; human immunodefliciency virus; acquired immune defliciency syndrome; AIDS;
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94US-00293520.
94US-00300000.
94US-00311486.
94US-00311749.
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940S-00316771.
940S-00321993.
940S-00334847.
940S-00334847.
940S-0033516.
940S-00355177.
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94US-00291932.
94US-00291433.
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94US-00222795
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23-SEP-1994;
23-SEP-1994;
                                                                                                            Mus musculus
                                                                                                                               W09523225-A2
                                                                                                                                                                                                                              15-APR-1994;
15-APR-1994;
18-MAY-1994;
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03-OCT-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grimm S,
Modak A,
Tracz D,
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The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves interleukin-5 (IL-5) mRNA at the nucleotide base position indicated in the DE line. Regions of the mRNA that do not form secondary folding structures and that contain potential harmershead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their unclease resistance. The ribozymes cleave the IL-5 target sequences and thereby inhibit IL-5 expression, making them useful for treating chronic asthma, e.g. by inhibiting the synthesis of IL-5 in lymphocytes and preventing the recruitment and activation of cosinophils. The ribozymes can also be used to treat eosinophila (related to parasitic infection or with pulmonary infiltration) and L-tryptophan-associated b DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
Usman N, Wincott FE, Woolf T; Ribozymes having modified bases and methods for producing them - for use in inhibiting disease related genes. Claim 2; Page 221; 407pp; English.

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                                                                                     Gaps
eosinophilia-myalgia syndrome. (Updated on 25-MAR-2003 to correct PI
field.)
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                                                                                                                                                                                                                                                                                                  RSV 1B hammerhead ribozyme target sequence (nt. position 421).
                                                            Query Match
1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 3.5e+02;
Matches 11; Conservative 2; Mismatches 1; Indels
                                      Sequence 15 BP; 8 A; 1 C; 3 G; 0 T; 3 U; 0 Other;
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94US-00224795.
94US-00224795.
94US-00227958.
94US-00271280.
94US-00271280.
94US-00291832.
94US-00292620.
94US-00293520.
94US-00293520.
94US-00393520.
94US-0031749.
94US-00314397.
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                                                                                                                 1956 AAAGCATGAAATGG 1969
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                                                                                                                               1 AAAGCAUAAAAUGG 14
                                                                                                                                                                                                     AAT56843 standard; RNA; 15
                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                     (revised)
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17-AUG-1994;
19-AUG-1994;
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25-MAR-2003
04-APR-1997
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30-JAN-1995
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5-APR-1994
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04-APR-1994
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                        Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
Tracz D, Usman N, Wincott FE, Woolf T;
                                                                                                                                                                           The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves mRNA coding for a protein of respiratory syncytial virus (RSV) at the nucleotide base position indicated in the DE line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and haliphin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes cleave the target sequences and can be used for treatment and diagnosis of RSV infection. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct PI
                                                                                                                methods for producing them - for use
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                             Query Match
1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                       Sequence 15 BP; 7 A; 5 C; 0 G; 0 T; 3 U; 0 Other;
                                                                                                                  Ribozymes having modified bases and me in inhibiting disease related genes.
                                                                                                                                                         Claim 2; Page 265; 407pp; English.
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94US-00222795.
94US-00224483.
94US-00227958.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT54631 standard; RNA; 15
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(first entry)
     (RIBO-) RIBOZYME PHARM INC.
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                                                                                          WPI; 1995-351090/45
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04-APR-1994;
07-APR-1994;
15-APR-1994;
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22-APR-1997
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The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves interleukin-5 (II-5) mRNA at the nucleotide base position indicated in the DE line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes cleave the II-5 target sequences and thereby inhibit II-5 expression, making them useful for treating chronic asthma, e.g. by inhibiting the synthesis of II-5 in lymphocytes and preventing the recruitment and activation of essimphils. The expression is essimated to parabilic infection or with pulmonary infiltration) and L-tryptophan-associated essimphilia—myalgia syndrome. (Updated on 25-MAR-2003 to correct PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
Tracz D, Usman N, Wincott FB, Woolf T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ribozymes having modified bases and methods for producing them - for use in inhibiting disease related genes.
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94US-00228041.
94US-00245736.
94US-00291930.
94US-00291433.
94US-00292620.
94US-00300000.
94US-00303039.
94US-003117486.
94US-003117486.
                                                                                                                                                                                                                                                                                                                       9405-00316771.
9405-00319492.
9405-00321993.
9405-00337608.
9405-00345516.
9405-00345517.
9405-00362333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1284 TTATTTAATCTGT 1297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .:|:::|| :|::
UUAUUUAAUUCUGU 15
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Best Local Similarity 35.7
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-351090/45.
                                                                                                                                                              19-AUG-1994;
02-SEP-1994;
08-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
25-MAR-1997
                                                                                                                                                                                                                                                                                                                          03-OCT-1994;
07-OCT-1994;
11-OCT-1994;
                                                                                                          16-AUG-1994;
17-AUG-1994;
                                                                                                                                                                                                                                                                   23-SEP-1994
                                                                                                                                                                                                                                                                                                   28-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT52173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 512
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correct PI field.)

Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; transbocation, chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation, autoimmune disease; atherosclexosis; myocardial infarction; stroke; restenosis; reangelphat rejection, rheumatoid arthris; psoriasis; myocardial ischaemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS; 9405-00227558 9405-00228641. 9405-00245736. 9405-00291932. 9405-00291433. 9405-0029620. 9405-0029620. 9405-00390000. 9405-00390303. 9405-00311486. 94US-00218934. 94US-0022795. 94US-00224483. 94US-00314397. 94US-00316771. 94US-00319492. 94US-00321993. 94US-00334847. 94US-00363233. 95US-00380734. 94US-00337608, 95WO-IB000156 WPI; 1995-351090/45. Homo sapiens. WO9523225-A2. 30-JAN-1995; 23-FEB-1995; 15-AUG-1994; 02-SEP-1994; 08-SEP-1994; 23-SEP-1994; 17-AUG-1994 07-OCT-1994 11-OCT-1994 04-NOV-1994 31-AUG-1995 07-APR-1994 28-SEP-1994 03-OCT-1994 .0-NOV-1994 28-NOV-1994 9-AUG-1994 16-DEC-1994 Stinchcomb Grimm S, Modak A, Tracz D,

(RIBO-) RIBOZYME PHARM INC.

b DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW; Karpeisky A, Kistch K, Matulic-Adamic J, Mcswiggen JA; Ravco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD; Usman N, Wincott FE, Woolf T;

Ribozymes having modified bases and methods for producing them - for use in inhibiting disease related genes.

Claim 2; Page 175; 407pp; English.

The present sequence represents a preferred target sequence for an enzymatic nuclected acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the nuclected base position indicated in the DB line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozymes cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes cleave the ICAM-1 target sequences and thereby inhibit ICAM-1 expression, making them useful for reducing transplant rejection and alleviating symptoms in patients with rheumatoid archritis, asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to

Gaps ö 1.2%; Score 12.4; DB 1; Length 15; 42.9%; Pred. No. 3.5e+02; ive 7; Mismatches 1; Indels Sequence 15 BP; 2 A; 0 C; 6 G; 0 T; 7 U; 0 Other; 1801 TGTGTGTGTGTA 1814

1 ucucucuancucua 14

RESULT 513 AAF47616/c ID AAF476

AAF47616 standard; DNA; 15 BP

AAF47616;

(first entry) 30-MAR-2001

IGFBP3 oligonucleotide #1036.

Antisense therapy, antiproliferative, antinflammatory, antipsoriatic, cytostatic, dermatological, cardiant, virucide, ophthalmological, keloid, skin disorder, insulin-like Growth Factor I receptor; IGF-1, pityriasis; IGF binding procein, IGFB-2, IGFBP3, inflammation, psoriasis, pityriasis, growth factor mediated cell proliferation, ichthyosis, serborrhoea, ruba, keratosis, neoplasia, scleroderma, wart, skin cancer, sclerotic disease, hypermeovascular condition; hyperplasia, kidney disease, neovascular condition of the retina, ss.

Homo sapiens.

WO200078341-A1.

21-JUN-2000; 2000WO-AU000693.

21-JUN-1999; 99US-0140345P.

(MURD-) MURDOCH CHILDRENS RES INST.

Edmondson SR; Wraight CJ, Werther GA,

WPI; 2001-041421/05.

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.

Example 7; Page 50; 201pp; English.

The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisorders. The method comprises contacting the skin with an receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the artisense oligonucleotide which can be used to design the artisense oligonucleotide which can be used to design the artisense of proriasis, in the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, inchipyosis, pityriasis, ruba, pitaris, serborrhoea, keloids, keratosis, neoplasis, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood cueses are also any other hyperplasia

Sequence 15 BP; 6 A; 4 C; 4 G; 1 T; 0 U; 0 Other;

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Gaps
                                                   ö
                                                1; Indels
Query Match
1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels
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AAF50118 standard; DNA; 15 AAF50118

RESULT 514

BP. AAF50118;

IGF-I oligonucleotide #1078. 30-MAR-2001 (first entry)

Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; Keloid; skin discorder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; plaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasis; kidney disease; neobascular condition; hyperplasis; kidney disease;

Homo sapiens.

21-JUN-2000; 2000WO-AU000693.

21-JUN-1999;

(MURD-) MURDOCH CHILDRENS RES INST.

Wraight CJ, Werther GA, Edmondson SR;

WPI; 2001-041421/05.

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.

Example 8; Page 67; 201pp; English.

The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonuclectide, [for Insulin-like Growth Factor [IGF] - creeptor, IGF binding protein [formalin-like Growth Factor IGF] - inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an inflammation and/or other disorders. The present sequence is an oligonuclectide which can be used to design the antisense oligonuclectide which can be used to design the antisense oligonuclectide is useful for ameliorating the effects of psoriasis, rothlyosis, pityriasis, ruba, pilaris, serborthoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, charin or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperplasia

Sequence 15 BP; 3 A; 4 C; 3 G; 5 T; 0 U; 0 Other;

ö Gaps ö Query Match 1.2%; Score 12.4; DB 1; Length 15; Best Local Similarity 92.9%; Pred. No. 3.5e+02; Matches 13; Conservative 0; Mismatches 1; Indels

1983 AATTCTGCTCAGAT 1996 1 ACTTCTGCTCAGAT 14 d

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AAF46653 standard; DNA; 15 BP AAF46653/

AAF46653;

30-MAR-2001 (first entry)

Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; selin disporder; insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBD3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichhyosis; serborrhoea; ruba; keratosis; neophasia; gcleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neoblation of the retina; se. IGFBP3 oligonucleotide #73

Homo sapiens.

WO200078341-A1

21-JUN-2000; 2000WO-AU000693

21-JUN-1999; 99US-0140345P.

(MURD-) MURDOCH CHILDRENS RES INST.

Edmondson SR; Wraight CJ, Werther GA,

WPI; 2001-041421/05

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.

Example 7; Page 44; 201pp; English.

The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulia-like Growth Factor [IGF]-1.

The present is binding protein [IGFB]-2 or IGFB], which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotide which can be used to design the antisense oligonucleotide of the present invention (see AAP45151 and AAP45153-75161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, plaris, serborrhoea, Keratosis, reapplatas, scleroderma, warts, benign growths, cancers of the Skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other selerotic brain or skin, growth factor-mediated malignancies, other selerotic condition of the inside of blood vessels or any other hyperplasia

Sequence 15 BP; 4 A; 7 C; 3 G; 1 T; 0 U; 0 Other;

ö Query Match
1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels

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Gaps

2047 ICCIIGGCAGGCIG 2060

à g

15 TGCTTGGCAGGCTG

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Antisense therapy; antiproliferative; antinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; opthbalmological; Keloid; skin disorder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilatis; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keatoosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hypermeovascular condition; hyperplasis, kidney disease; neovascular condition of the retina; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                       Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                                                                                                                                                                                                                                                                           Edmondson SR;
                                                                                                                                                                                                                                                                                                                                                 (MURD-) MURDOCH CHILDRENS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 7; Page 58; 201pp; English
            AAF48749 standard; DNA; 15 BP
                                                                                                                                                                                                                                                                                                                           99US-0140345P.
                                                                                    IGFBP3 oligonucleotide #2169.
                                                                                                                                                                                                                                                                                                   21-JUN-2000; 2000WO-AU000693
                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                           Werther GA,
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-041421/05
                                                                                                                                                                                                                                                    WO200078341-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inflammation.
                                                                                                                                                                                                                                                                                                                            21-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                            Wraight CJ,
                                                            30-MAR-2001
                                    AAF48749;
AAF48749/C
```

The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises concacting the skin with an antisense oligomuclectide, (for Insulan-IRe Growth Factor [IGF] receptor, IGF binding protein [IGFBP] - 2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, oligomuclectide which can be used to design the antisense oligomuclectide which can be used to design the antisense oligomuclectides of the present invention (see AAF4151 and AAF45153-F55161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pliaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovacular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood other hyperplasia

Sequence 15 BP; 6 A; 1 C; 3 G; 5 T; 0 U; 0 Other;

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Gaps
                                   ;
0
1.2%; Score 12.4; DB 1; Length 15; 92.9%; Pred. No. 3.5e+02; Ive 0; Mismatches 1; Indels
                   Local Similarity 92.9%;
les 13; Conservative
       Query Match
                        Best Loca
Matches
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1495 ATCAGATAGCATCT 1508

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AAF47618/c ID AAF47618 standard; DNA; 15 BP RESULT 517

30-MAR-2001 (first entry) AAF47618;

IGFBP3 oligonucleotide #1038.

Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin discorder; Insulin-11ke Growth Factor 1 receptor; IGF 1; pityriasis; IGF binding proctein; IGFBP-2; IGFBP9; inflammation; psoriasis; prowth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keatoolsis, neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neoblation of the retina; ss.

Homo sapiens.

WO200078341-A1

28-DEC-2000

21-JUN-2000; 2000WO-AU000693.

99US-0140345P. 21-JUN-1999; (MURD-) MURDOCH CHILDRENS RES INST.

Werther GA, Edmondson SR; Wraight CJ,

WPI; 2001-041421/05

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.

Example 7; Page 50; 201pp; English

that

The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonuclectide, (for Inmulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inhibiting or reducing growth factor mediated cell proliferation, oligonuclectide which can be used to design the antisense oligonuclectide which can be used to design the antisense oligonuclectides of the present invention (see AAF45151 and AAF45153 or 19545161). The method is useful for ameliorating the effects of psoriasis, chthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovacular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia

Sequence 15 BP; 5 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Gaps ö 1.2%; Score 12.4; DB 1; Length 15; 92.9%; Pred. No. 3.5e+02; tive 0; Mismatches 1; Indels Query Match Best Local Similarity 92.9 Matches 13; Conservative

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2045 TGTCCTTGGCAGGC 2058

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AAF46654 standard; DNA; 15 RESULT 518

30-MAR-2001 (first entry)

AAF46654;

HX Y X H

Antisense therapy, antiproliferative, antinflammatory, antipsoriatic; cytostatic, dermatological; cardiant; virucide; ophthalmological; Keloid; skin disorder; Insulin-11ke Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilatis; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; Keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition; hyperplasia; kidney disease; Homo sapiens.

WO200078341-A1

21-JUN-2000; 2000WO-AU000693.

99US-0140345P. 21-JUN-1999; MURD-) MURDOCH CHILDRENS RES INST.

Werther GA, Edmondson SR;

WPI; 2001-041421/05

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.

Example 7; Page 44; 201pp; English

The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an anticontaction (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFB]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, of inhibiting or reducing growth factor mediated cell proliferation, of inhibiting or reducing growth factor mediated cell proliferation, of inhibiting or reducing growth factor mediated cell proliferation, of information and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotide which can be used to design the affects of psoriasis, refinely. The method is useful for ameliorating the effects of psoriasis, richthyosis, pityriasis, ruba, pilaris, serborthoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, the branch of sease, hyperproliferation of the inside of blood wessels or any other hyperplasia

Sequence 15 BP; 4 A; 6 C; 4 G; 1 T; 0 U; 0 Other;

Gaps . 0 1.2%; Score 12.4; DB 1; Length 15; 92.9%; Pred. No. 3.5e+02; tive 0; Mismatches 1; Indels Query Match
Best Local Similarity 92.9
Matches 13; Conservative

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AAF50117 standard; DNA; 15 AAF50117

30-MAR-2001

IGF-I oligonucleotide #1077.

Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;

cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition of the retina; ss.

Homo sapiens.

WO200078341-A1.

21-JUN-2000; 2000WO-AU000693

21-JUN-1999;

(MURD-) MURDOCH CHILDRENS RES INST.

Wraight CJ, Werther GA,

Edmondson SR;

WPI; 2001-041421/05

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or infiammation.

Example 8; Page 67; 201pp; English

The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotide which can be used to design the antisense oligonucleotide of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, inchayosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, soleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, disease, kidhey disease, hyperproliferation of the inside of blood vessels or any other hyperplasia

Sequence 15 BP; 3 A; 4 C; 2 G; 6 T; 0 U; 0 Other;

.. 0 Query Match 1.2%; Score 12.4; DB 1; Length 15; Best Local Similarity 92.9%; Pred. No. 3.5e+02; Matches 13; Conservative 0; Mismatches 1; Indels

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1983 AATTCTGCTCAGAT 1996 Actricificacian 15 AAF53695 standard; DNA; 15 BP.

RESULT 520

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30-MAR-2001 (first entry)

IGF-I oligonucleotide #4655.

Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;

Homo sapiens

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Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                                                                                                                                                                                                         The present invention relates to a method for ameliorating the effects of
keratosis, neoplasia, scleroderma; wart, skin cancer, sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition of the retina; ss.
                                                                                                                                                                                 Werther GA, Edmondson SR;
                                                                                                                                                         (MURD-) MURDOCH CHILDRENS RES INST.
                                                                                                                                                                                                                                                                                   Example 8; Page 91; 201pp; English.
                                                                                                                                     99US-0140345P.
                                                                                                               21-JUN-2000; 2000WO-AU000693.
                                                                                                                                                                                                       WPI; 2001-041421/05.
                                                                   WO200078341-A1.
                                                                                                                                                                                                                                                               inflammation.
                                                                                                                                     21-JUN-1999;
                                             Homo sapiens
                                                                                                                                                                                 Wraight CJ,
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skin disorders. The method comprises contacting the skin with an antisense aligonuclectide, (for Insulin-like Growth Factor [10F]-1 receptor, 10F binding protein [10F]-1, or 10FBP3]-3 or 10FBP3], which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an aligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, inchthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic Sequence 15 BP; 2 A; 5 C; 1 G; 7 T; 0 U; 0 Other; vessels or any other hyperplasia

Gaps ö Query Match 1.2%; Score 12.4; DB 1; Length 15; Best Local Similarity 92.9%; Pred. No. 3.5e+02; Matches 13; Conservative 0; Mismatches 1; Indels

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2236 TTGCACCTTTCTAG 2249 rrrcaccrrrcrag 15

8 g

AAF53696 standard; DNA; 15 BP AAF53696; RESULT 52

(first entry) 30-MAR-2001 IGF-I oligonucleotide #4656.

Antisense therapy; antiproliferative; antinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; opthalmological; keloid; skin disorder; Insulin-like Growth Factor I receptor; IGP-1; pityrlasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hypermeovascular condition; hyperplasia; kidney disease; neoblasis condition; the retina; ss.

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The present invention relates to a method for amelicrating the effects of skin disorders. The method comprises contacting the skin with an antisense alignmenteride, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotide which can be useful for ameliorating the effects of psoriasis, 1040nucleotide which present invention (see AAF$5151 and AAF$5153 or F$5161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, tuba, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a neoplasias scleroderma, warts, benign growths, cancers of the skin, a brian or skin, growth factor-mediated malignancies, other sclerotic candidor and a mecvascular condition of the retina, brian or skin, growth factor-mediated malignancies, other sclerotic candidor and proper proliferation of the inside of blood
                                                                                                                                                                                                                                                                                                                                                                Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15 BP; 2 A; 4 C; 2 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                          Edmondson SR;
                                                                                                                                                                                                                             (MURD-) MURDOCH CHILDRENS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 8; Page 91; 201pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vessels or any other hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2236 TIGCACCTITCIAG 2249
                                                                                                                                  21-JUN-2000; 2000WO-AU000693
                                                                                                                                                                                99US-0140345P
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                                                                                                                                                                                                                                                                          Wraight CJ,, Werther GA,
                                                                                                                                                                                                                                                                                                                          WPI; 2001-041421/05
                                        WO200078341-A1
                                                                                                                                                                                21-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                           inflammation.
                                                                                        28-DEC-2000
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AAF48471 standard; DNA; 15 BP GFBP3 oligonucleotide #1891. 30-MAR-2001 (first entry) RESULT 522 AAF48471/c

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Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin discorder; lineulin-like.Growth; Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFB-2; IGFBP3; inflammation; psoriasis; pilatis; growth factor mediated cell'proliferation; ichthyosis; serborrhoea; ruba; keratosis; neophasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasis, kidney disease; neobascular condition; hyperplasis, kidney disease;

Homo sapiens

WO200078341-A1

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The present invention relates to a method for ameliorating the effects of antisense oligonucleotide, (for Insulin-like Growth Factor [IGF] antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]) and receptor, IGF binding protein [IGFBP] - or IGFBP3), which is capable inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF4151 and AAF45153-15151). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pitaris, serborthoea, keloids, keratosis, hepinasis, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood
                                                                                                                                                                                                                                                               Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15 BP; 2 A; 3 C; 1 G; 9 T; 0 U; 0 Other;
                                                                                                                              (MURD-) MURDOCH CHILDRENS RES INST.
                                                                                                                                                                                                                                                                                                                                                                            Example 7; Page 56; 201pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vessels or any other hyperplasia
                                        21-JUN-2000; 2000WO-AU000693.
                                                                                     99US-0140345P
                                                                                                                                                                           Werther GA,
                                                                                                                                                                                                                      WPI; 2001-041421/05
                                                                                     21-JUN-1999;
                                                                                                                                                                         Wraight CJ,
28-DEC-2000
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1.2%; Score 12.4; DB 1; Length 15; 92.9%; Pred. No. 3.5e+02; ttive 0; Mismatches 1; Indels 2248 AGTIGAAAATAAAG 2261 15 AGATGAAAATAAAG 2 Query Match Best Local Similarity 92.9 Matches 13; Conservative g ò

AAF48748 standard; DNA; 15 BP. IGFBP3 oligonucleotide #2168. 30-MAR-2001 (first entry) AAF48748;

Antisense therapy, antiproliferative, antinflammatory, antipsoriatic; cytostatic, dermatological; cardiant, virucide, ophthalmological; kaloid; skin discorder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilatis; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keardosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition; the retina; ss.

WO200078341-A1 Homo sapiens

21-JUN-2000; 2000WO-AU000693

(MURD-) MURDOCH CHILDRENS RES INST. 99US-0140345P. 21-JUN-1999;

Edmondson SR; Werther GA, Wraight CJ,

Edmondson SR;

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or

Example 7; Page 58; 201pp; English.

The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [167]-1 receptor, 1GF binding protein [1GPBP]-2 or 1GPBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-C) rethipsis, pityriasis, ruba, pilaris, serborthoea, keloids, keratosis, inchthyosis, pityriasis, ruba, pilaris, serborthoea, keloids, keratosis, chethyosis, pityriasis, ruba, pilaris, serborthoea, keloids, keratosis, chyperneovascular condition such as a neovascular condition of the skin, a hyperneovascular condition such as a neovascular condition of the retina, chisans, kidney disease, hyperproliferation of the inside of blood disease, kidney disease, hyperproliferation of the inside of blood.

Gaps ö Query Match 1.2%; Score 12.4; DB 1; Length 15; Best Local Similarity 92.9%; Pred. No. 3.5e+02; Matches 13; Conservative 0; Mismatches 1; Indels

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Gaps 0

AAF48472 standard; DNA; 15 BP. AAF48472; RESULT 524 AAF48472/c

(first entry) 30-MAR-2001

IGFBP3 oligonucleotide #1892.

Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; stin disorder; insulin-like Growth Factor. I receptor; IGF-1; pityriasis; growth factor mediated cell proliferation; inframmation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition; hyperplasia; kidney disease;

28-DEC-2000.

WO200078341-A1.

21-JUN-2000; 2000WO-AU000693

99US-0140345P. 21-JUN-1999; (MURD-) MURDOCH CHILDRENS RES INST.

WPI; 2001-041421/05

inflammation.

Sequence 15 BP; 5 A; 1 C; 4 G; 5 T; 0 U; 0 Other;

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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an artisence oligomuclectide, (for Insulin-like Growth Factor [167]-1 receptor, 10F binding protein [167BP]-2 or 1GFBP3), which is capable inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligomuclectide which can be used to design the antisense oligomuclectides of the present invention (see AAF4151 and AAF45131-P45161). The method is useful for ameliorating the effects of psoriasis, inchthyosis, pityriasis, ruba, pliaris, sepborthoea, keloids, Keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a mediated malignancies other sclerotic brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperprovision of the inside of blood
                                                                                       Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
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1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels
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Edmondson SR;
                                                                                                                                                                                                                Example 7; Page 56; 201pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vessels or any other hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2248 AGTIGAAAATAAAG 2261
  Werther GA,
                                              WPI; 2001-041421/05.
                                                                                                                                                                         inflammation.
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  Wraight
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Gaps ö

14 AGATGAAAATAAAG 1

ABX03996 standard; DNA; 15 ABX03996; RESULT 525 **ABX**03996/

BP

(first entry) 09-JAN-2003

Resistance gene carb-4 DNA fragment.

therapy; Detection, probe, diagnosis, oral disease, paradontitis, caries, theral polymorphism, virulence factor, antibiotic resistance gene, prognosis, oral infection, detection, pathogen, coronary heart disease, diabetic symptom; ss

Unidentified.

DE20110013-U1

18-OCT-2001.

3-MAR-2001; 2001DE-02010013

13-MAR-2001; 2001DE-01012348 13-MAR-2001; 2001DE-02010013

(ROET/) ROETGER A.

MPI; 2001-657777/76

Oligonucleotide array, useful for diagnosing oral diseases, particularly paradontitis, carries human or microbial reference sequences.

The present invention provides the protein, cDNA and gene of human interleukin-4 (IL4). The coding sequences for this protein contain single nucleotide polymorphisms (SNPs) which may be associated with differences in susceptibility to atopy, inflammatory and immune diseases and different drug responses. They may also be used in applications such as forensic and parernity testing and studying population diversity and anthropological lineage. The IL4 gene is found on human chromosome 5q31.1

Sequence 15 BP; 3 A; 1 C; 4 G; 7 T; 0 U; 0 Other;

Polymucleotide comprising novel single nucleotide polymorphisms in human interleukin-4 gene for use in studying expression, function of interleukin-4, in developing drugs, diagnosis and treatment of immune

Claim 12; Page 16; 71pp; English.

disorders

Choi JY, Denton RR, Nandabalan K, Stephens JC

(GENA-) GENAISSANCE PHARM INC

WPI; 2001-316132/33.

Chew A,

Claim 10; Page 27; 58pp; German

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diagnosis of oral diseases, particularly paradontitis, but also caries, diagnosis of oral diseases, particularly paradontitis, but also caries, especially to identify genetic predisposition (as indicated by polymorphisms) to disease and to identify causative microorganisms or their associated virulence factors and antibiotic resistance genes, e.g. for selection of therapy and for prognosis. They are also useful for research into oral infections. The carriers allow simultaneous detection of both host and pathogen parameters, providing quickly and simply an individual's paradontitis profile, including detection of pathogens that are associated with increased risk of coronary heart diseases and/or aggravation of diabetic symptoms, and of opportunistic pathogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, interleukin-4; IL4; single nucleotide polymorphism; SNP; atopy; inflammatory disorder; immune disorder; population diversity; paternity test; forensic test; cytokine; chromosome 5q31.1; probe; PCR primer; ss.
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                                                                                                                                                                                                          Sequence 15 BP; 4 A; 3 C; 3 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human IL4 allele-specific primer SEQ ID NO: 47.
                                                                                                                                                                                                                                                                                                                                                                                               ВР.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0156825P.
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                                                                                                                                                                                                                                                                                             1275 TAGCACAAGTTATT 1288
                                                                                                                                                                                                                                                                                                                                                                                                AAH18788 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                      15 TAGCACAAGCTATT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                   of the invention
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ACD56418 standard; RNA; 15 BP

(first entry)

24-SEP-2003

ACD56418;

1 TITITITITITIT 15

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Gaps

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The invention discloses a method for identifying a candidate polymorphic repeat within a coding sequence (expressed sequence tag, EST), which comprises detecting tandem repeats in a target coding sequence, scoring the repeats for polymorphic probability and generating a dataset correlating the repeats with polymorphic probability to identify a candidate polymorphic repeat. The computational methods (polymorphic repeat. The computational methods (polymorphic repeats) and marker prediction of ubiquitous simple sequences, PoMPOUS, and Rep-X) are useful for identifying and detecting candidate polymorphic repeats in human genes, which can be used to understand, treat or eliminate genetic diseases linked to nucleotide repeats are Machado-Joseph, Haw River syndrome, Huntington's disease, fragile-X syndrome, Terdireich's ataxis, myotonic dystrophy, hyperandrogensemia, spinal and bulbar atrophy and spinocereballar ataxia. The sequences presented in ABX79676-ABX80022 are the polymorphic repeats identified for a search of human ESTS
                                                                                                                                                                                                                                                                                                                                                                                    EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat; polymorphic marker prediction of ubiquitous simple sequences; POMPOUS; Rep-X; human; genetic disease; drug-treatment; Machado-Joseph; Haw River syndrome; Huntington's disease; fragile-X syndrome; Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia; spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying a candidate polymorphic repeat within a coding sequence, i understanding or treating genetic disease, comprises detecting tandem repeats in a target coding sequence and scoring the repeats for polymorphic probability.
1.2%; Score 12.4; DB 1; Length 15; 92.9%; Pred. No. 3.5e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                               EST polymorphic DNA repeat polynucleotide #158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fondon JW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wren JD, Minna JD,
                                                                                                                                                                                                                          ABX79833 standard; cDNA; 15 BP
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                                                                                    2158 GGAAGCATTTGTTT 2171
                                                                                                                       Graagcarricarr 15
                                                                                                                                                                                                                                                                                                          (first entry)
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                                             13; Conservative
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                         Local Similarity
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    Query Match
                            Best Loca
Matches
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The present invention relates to nucleic acid molecules which modulate the synthesis, expression and/or stability of Hepatitis C virus (HCV) or Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense and enzymatic nucleic acids such as hammerhead ribozymes. DNAzymes, inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. DNAzymes, cranscriptase and/or HBV reverse transcriptase primer sequences, as well as oligomucleorides that specifically bind the Enhancer I region of HBV DNA. The nucleic acids may be used to modulate the expression of HBV of genes and HBV viral replication. Also disclosed is a method for screening compounds and/or preparation and/or replication of HCV. The compounds and method sof the invention are useful for the treatment of degenerative and methods of the invention are useful for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene expression such as cirrhosis, liver failure, and hepatocellular carcinoma. The present sequence represents a substrate for one of the HBV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus infection.
                                                                                                                     Nucleic acid molecule, Hepatitis C virus, HCV, Hepatitis B virus, HBV; RNA stability, RNA expression, RNA synthesis; antisense; enzymatic nucleic acid, hammerhead riboxyme; bNAzyme; inozyme; amberzyme; G-cleaver ribozyme; decoy molecule; aptemer; HBV reverse transcriptase; Enhancer I region, viral replication; degenerative; disease state; HBV infection; HCV infection; cirrhosis; liver failure; hepatcoclular carcinoma; hepatotropic; cytostatic; virucide; antiinflammatory; substrate; 8s.
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                                                                                                HBV enzymatic nucleic acid substrate sequence #143.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JUN-2001; 2001US-00877478.
08-JUN-2001; 2001US-0296876P.
24-OCT-2001; 2001US-0335059P.
05-DEC-2001; 2001US-03370559P.
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Roberts E;
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MACEJAK D.
MCSWIGGEN J.
MORRISSEY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-229207/22
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ROBERTS E.
                                                                                                                                                                                                                                                                                   Hepatitis B virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-2001;
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Draper K,
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(LEEP/)
(DRAP/)
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Local Similarity 86.7 tes 13; Conservative

Best Loca Matches

Query Match

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Gapa

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1.2%; Score 12.4; DB 1; Length 15; 86.7%; Pred. No. 3.5e+02; tive 0; Mismatches 2; Indels

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US2003190617-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders.
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8X88888888888X8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to nucleic acid molecules which modulate the synthesis, expression and/or stability of Hepatitis C virus (HCV) or Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes, incaymes, amberzymes, and G-cleaver ribozymes. Also disclosed are nucleic acid decoy molecules and aptamers that bind to HBV reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus
                                                                                                                                                                                                                                            Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV; RNA stability, RNA expression; RNA synthesis; antisense; enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; amberzyme; G-cleaver ribozyme; decoy molecule; aptamer; HBV reverse transcriptase; Enhancer I region; viral replication; degenerative; disease state; HBV infection; HCV infection; cirrhosis; liver failure; hepatocellular carcinoma; hepatotropic; cytostatic; virucide; antiinflammatory; substrate; ss.
                                                               Gaps
 enzymatic nucleic acid sequences disclosed in the present invention
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                                        Ouery Match 1.2%; Score 12.4; DB 1; Length 15; Best Local Similarity 92.9%; Pred. No. 3.5e+02; Matches 13; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                          HBV enzymatic nucleic acid substrate sequence #69.
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                      Seguence 15 BP; 2 A; 3 C; 4 G; 0 T; 6 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2001; 2001US-00817879.
08-UUN-2001; 2001US-00877478.
08-UUN-2001; 2001US-0296876P.
24-OCT-2001; 2001US-0337055P.
                                                                                                                                                             ACD56180 standard; RNA; 15 BP.
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                                                                                    2095 AATGAACAAATGGC 2108
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Roberts E;
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ROBERTS E.
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Draper K,
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(MCSW/) N
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as oligonucleotides that specifically bind the Enhancer I region of HBV MNA. The nucleic acids may be used to modulate the expression of HBV genes and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds that modulate the expression and/or replication of HCV. The compounds methods of the invention are useful for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene expression such as dirrhosis, liver failure, and hepatocellular carcinoma. The present sequence represents a substrate for one of the HBV enzymatic nucleic acid sequences disclosed in the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, optineurin; ds; ophthalmological; single nucleotide polymorphism; SNP; glaucoma; progressive ocular hypertensive disorder; glaucoma related disorder; motif; repeat element; regulatory region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15 BP; 2 A; 3 C; 3 G; 0 T; 7 U; 0 Other;
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ID ADE13970 standard; DNA; 15
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(RAYM/) RAYMOND V.
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Sequence 13 BP; 6 A; 1 C; 0 G; 6 T; 0 U; 0 Other;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPD at the printed specification, but the wipo.int/pub/published_pct_sequences
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in a sample containing DNA, determining the presence or increased discreptibility to glaucoma or to a progressive ocular hypertensive disorder resulting in loss of visual field in a patient (or the severity or progression of glaucoma in a patient, comprising providing manplification reaction primers that direct amplification of a selected nucleic acid region containing the variation within the optimeurin promoter and amplifying the DNA) and detecting a polymorphism (comprising obtaining a sample containing thus manned DNA), providing a nucleic acid detecting the polymorphism). The invention is used to diagnose and detecting the polymorphism). The invention is used to diagnose and prognose glaucoma and also to treat glaucoma related disorders. The present sequence is an optimeurin promoter motif, repeat element or putative regulatory region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                  Sequence 15 BP; 5 A; 3 C; 0 G; 7 T; 0 U; 0 Other;
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nes 13; Conservative
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Matches
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                                                                                                                                                                                                                                                                                                                    SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                                                                       Oligonucleotide SEQ ID NO 119128 for detecting SNP TSC0029746.
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100.0%; Pred. No. 3.5e+02;
ive 0; Mismatches 0; Indels
Score 12; DB 1; Length 13;
Pred. No. 3.5e+02;
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1.1%; Score 12; DB Local Similarity 100.0%; Pred. No. 3.5 les 12; Conservative 0; Mismatches
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     Query Match
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RESULT 533

ABC12932,

ABC12932/c

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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                         Oligonucleotide SEQ ID NO 12939 for detecting SNP TSC0003018.
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1.1%; Score 12; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels
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                  ABC12932 standard; DNA; 13 BP.
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ABF19130;

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RESULT 534 ABF19130/c

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cycosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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          typing, is
Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                     Claim 1; SEQ ID NO 119127; 29pp + Sequence Listing; German.
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The present invention describes a method for detecting the presence of polymorphisms associated with inflammatory bowel diseases such as ulcerative colitis and crohn's disease. The methods can be used to detect the presence of generic polymorphisms associated with inflammatory bowel disease and correlating their occurrence with disease states. They may be used in this way for phenotypic correlations, forensics, paternity testing, medicine and genetic analysis. The present sequence is a polymorphic site described in the exemplification of the invention
                                                                                                                                Seguence 19 BP; 9 A; 4 C; 0 G; 5 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                                                                      RESULT 537
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                                                                                                                  Detecting polymorphisms between 2 nucleic acid samples, esp. in microsatellite regions, comprises digesting the nucleic acid to generate fragments, ligating adaptor segments to their ends, amplifying them using primer directed amplification and comparing the prods. to detect differences. The primers used in the amplification comprise a primer consisting of a perfect cpd. simple sequence repeat (SSR), and am adaptor segment. The present sequence is an example of a compound SSR primer. Requence is a nexample of a compound SSR primer. The method represents a modified amplified fragment length polymorphism assay, which is partic. useful for genome fingerprinting, i.e. for genetic trait marking and germplasm comparisons
                                                  Modified amplified fragment length polymorphism assay - for detection of polymorphism esp. in micro:satellite regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, inflammatory bowel disease, Crohn's disease, ulcerative colitis, single nucleotide polymorphism; SNP; chromosome 19p13; paternity test; chromosome 5q31-33; forensic test; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Testing for the presence of polymorphisms associated with inflammatory bowel disease, using a hybridization assay.
                                                                                                                                                                                                                                                                                                                                           Gaps
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/note= "SNP, optional deletion at this position"
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                                                                                                                                                                                                                                                                                                              1.1%; Score 12; DB 1; Length 22; 75.0%; Pred. No. 4.4e+02; rative 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                        Sequence 22 BP; 11 A; 6 C; 0 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (WHED ) WHITEHEAD INST BIOMEDICAL RES. (BLLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       1813 TATATATATATATGTACA 1832
                                                                                              Disclosure; Fig 1c; 173pp; English
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                                                                                                                                                                                                                                                                                                                                             15; Conservative
  Vogel JM;
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                              WPI; 1996-277795/28.
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  Morgante M,
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNR) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99899, ABH00010-ABF9989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP, single nucleotide polymorphism, human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                   Gaps
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Query Match
1.1%; Score 11.6; DB 1; Length 19;
Best Local Similarity 73.7%; Fred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 5; Indels
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                                                                                                                                                              1813 TATATATATATATGTAC 1831
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1.1%; Score 11.4; DB 1; Length 13;

Fri Apr

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide SEQ ID NO 138747 for detecting SNP TSC0034761.

(first entry)

21-FEB-2002

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABF000010-ABF9989, ABF000010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                            1; Indels
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Pred. No. 4e+02;
0; Mismatches
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Best Local Similarity 92.3%;
Matches 12; Conservative
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Matches 12, Conservative
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Set of oligonucleotides, useful for diagnosis and cell typing, idealgned to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS

WPI; 2001-657177/75

06-APR-2001; 2001WO-IB000713. 37-APR-2000; 2000DE-01019173

WO200177384-A2 Homo sapiens.

18-OCT-2001,.

Claim 1; SEQ ID NO 138747; 29pp + Sequence Listing; German.

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1814 ATATATATATA 1826

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1 ATATATATATACA 13

ABF38750/c . ID ABF38750 standard; DNA; 13 XX AC ABF38750;

RESULT 539

06-APR-2001; 2001WO-IB000713.

18-OCT-2001

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but fire wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, aradiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989 and ABI00010-ABI82073
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                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide SEQ ID NO 138748 for detecting SNP TSC0034761.
                                                                                                                                                                                                                                                                          1.1%; Score 11.4; DB 1; Length 13; 92.3%; Pred. No. 4e+02; tive 0; Mismatches 1; Indels
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                                              Claim 1; SEQ ID NO 28605; 29pp + Sequence Listing; German
                                                                                                                                                                                                                                                   Sequence 13 BP; 6 A; 0 C; 1 G; 6 T; 0 U; 0 Other;
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Best Local Similarity 92.3
Matches 12; Conservative
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Sequence 20 BP; 8 A; 3 C; 5 G; 4 T; 0 U; 0 Other;

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The present invention relates to endothelial cell-specific molecule 4
(ECSM4), and the polynuclectide sequences encoding it. The ECSM4 proteins
are useful for imaging vascular endothelium in the body of an individual,
and for diagnosing and treating a proliferative disease or condition
involving the vascular endothelium (preferably, neovasculature) such as
cancer, psoriasis, diabetic retinopathy, atherosclerosis or menorrhagia.
The ECSM4 proteins are also useful in the manufacture of diagnostic or
prognostic agent for such conditions. The proteins are also useful for
detecting endothelial damage or activation, detecting a tumour or tumour
neovasculature, cardiac disease, or endometriosis by detecting the amount
of ECSM4 present in a sample. The polynucleotide sequences encoding ECSM4
are useful for medicaments for treating the above disease. The sequences
manufacture of medicaments for treating the above disease. The sequences
are useful for medulating anglogenesis in an individual. The present
sequence represents a RT-PCR primer for RNA encoding human connective
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, endothelial cell-specific molecule 4, ECSM4, necvasculature, imaging vascular endothelium; proliferative disease; cancer; psoriasis; diabetic retinopathy; atherosclerosis; menorrhagia; endothelial damage; tumour necvasculature; cardiac disease; endometriosis; hypoxic condition; angiogenesis; cytostatic; RT-PCR; connective tissue growth factor; reverse transcription-PCR; primer; ss.
represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fit, wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for imaging, diagnosing and treating a condition involving vascular endothelium e.g. cancer, cardiac disease, endometriosis, diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human connective tissue growth factor, RT-PCR primer #2.
                                                                                                  Sequence 13 BP; 7 A; 1 C; 0 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 165; 248pp; English.
                                                                                                                                                                                                                                                                                                                                                                       ABK87132 standard; DNA; 20 BP
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Best Local Similarity 92.3
Matches 12, Conservative
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ABK87132/c
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                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                               Oligonucleotide SEQ ID NO 89619 for detecting SNP TSC0022467.
Query Match 1.1%; Score 11.4; DB 1; Length 20; Best Local Similarity 92.3%; Pred. No. 4.8e+02; Matches 12; Conservative 0; Mismatches 1; Indels
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RESULT 545

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABR0010-ABF9989, ABH0010-ABH99999 and ABI0010-ABI82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Set of oligonuclectides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                   Oligonucleotide SEQ ID NO 89620 for detecting SNP TSC0022467.
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ftp.wipo.int/pub/published_pct_sequences
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ABC89603
ID ABC89603 standard; DNA; 13 BP.
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                                                                                             (first entry)
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                                                        ABC89603;
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Gaps

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1.0%; Score 11; DB 1; Length 13; 100.0%; Pred. No. 4.4e+02; tive 0; Mismatches 0; Indels

Search completed: April 2, 2004, 14:31:05 Job time: 9 secs

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3 ATATATATA 13

Best Local Similarity 100. Matches 11; Conservative

Query Match

			ACCESSION: ARI29716 ACCESSION: ARI29716 ACCESSION: ARI29716 ACCESSION: ARX238676 ACCESSION: ARX762730 ACCESSION: ARX71774 ACCESSION: ARX71774 ACCESSION: ARX71801 ACCESSION: ARX71801 ACCESSION: ARX71803 ACCESSION: ARX71803 ACCESSION: ARX242049 ACCESSION: ARX242049 ACCESSION: ARX258883 ACCESSION: ARX2588106 ACCESSION: ARX2588106 ACCESSION: ARX271804 ACCESSION: ARX271804 ACCESSION: ARX271804 ACCESSION: ARX71809 ACCESSION: ARX71806 ACCESSION: ARX71806 ACCESSION: ARX71809 ACCESSION: ARX71806
AX54776 1 131213 1 AX12780 1 AX11782 1 AX11783 1 A60454 1 AR0454		13153 7X040 1 AX040 1 AX126 1 AR126 1 BD0826 1 BD083 1 BX178 1 AR178 1 AR178 1 AR178 1 AR178 1 AR178 1 AR178 1 AR178 1 AR178 1 AR178	20 1 BC5497 20 1 AR129716 20 1 AR129716 17 1 AX39576 17 1 AX762730 18 1 AR771774 18 1 AR771774 18 1 AR771801 20 1 E36173 20 1 E36173 20 1 E36173 20 1 E36173 20 1 E36173 21 1 AX256883 22 1 AX256883 21 1 AX256883 21 1 AX771809 18 1 AR771804 18 1 AR771806 18 1 AR771806 18 1 AR771806 18 1 AR771806 18 1 AR771806 18 1 AR771806 19 1 E28534 19 1 E28534 10 1 E28534 11 1 AR771806 11 1 AR771806 12 1 AX241816 13 1 AR771806 14 1 AR771806 15 1 AR771806 16 1 AR771806 17 1 AR771806 18 1 AR771806 19 1 AR771806 10 1 AR771806 10 1 AR771806 11 1 AR771806 11 1 AR771806 12 1 AR771806 13 1 AR771806 14 1 AR771806 16 1 AR771806 17 1 AR771806 18 1 AR771806 19 1 AR771806 10 1 AR771806 10 1 AR771806 11 1 AR771806 11 1 AR771806 12 1 AR771806 13 1 AR771806 14 1 AR771806 16 1 AR771806 17 1 AR771806 18 1 AR771806 19 1 AR771806 10 1 AR771806 10 1 AR771806 11 AR771806 11 AR771806 12 1 AR771806 13 1 AR771806 14 1 AR771806 16 1 AR771806 17 1 AR771806 18 1 AR771806 18 1 AR771806 19 1 AR771806 10 1 AR771806 10 1 AR771806 11 AR771806
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	Title: Derfect score: 1049 Sequence: 1 ttgaactgattcacatctcagtgtatattttttctataaa 1049 Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 0.5 Searched: 296 seqs, 5242 residues	um DB seq length: 8 um DB seq length: 8 processing: Minimum Match 0% Maximum Match 100% Listing first 316 summaries ase : rge.seq:* Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pand is derived by analysis of the total score distribution. SUMMARIES * Cuery	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

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CESSION AR090280. RSION AR090280.1 GI:10017035 URCE Unknown. ORGANISM Unclassified. Unclassified. Unclassified. TITLE GENERALS (as and Bibilashvilli, R. AUTHORS Chenchik, A., Jokhadze, G. and Bibilashvilli, R. AUTHORS Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers // Organism="unknown" // Mol_Lype="unassigned DNA"	3.1%; Score 32; DB 1; Length 3 Local Similarity 100.0%; Pred. No. 2.5; Onservative 0; Mismatches 0; Indel 1732 CTTGTGGGAAGTGAATTTGCCTGTAACAAGCC 1763	SULT 2 19715/C CUS RA197315 RESIGN RESIGN RA197315 RA1973111 RA197315 RA1973111 RA197315 RA197315 RA197315 RA197315 RA197315 RA197311 RA19731 RA197311 RA197311 RA197311 RA197311 RA19731	<pre>L Patent: US 6352829-A 400 05 MAR-2002; Location/Qualifiers 1</pre>	υ Ζ Σ	Unclassified. Unclassified. AUTHORS Chenchik, A., Jokhadze, G. and Bibilashvilli, R. TITLE Methods of assaying differential expression JOURNAL Patent: US 6489455-A 400 03-DEC-2002; AUTHORS Location/Qualifiers 1. 32 /organism="unknown" /mol_type="genomic DNA"
ACCESSION:E3226 ACCESSION:138676 ACCESSION:138682 ACCESSION:138682 ACCESSION:138682 ACCESSION:138682 ACCESSION:14821692 ACCESSION:AR22462 ACCESSION:AR22462 ACCESSION:AR32672 ACCESSION:AR32648 ACCESSION:AR33448	ò a	8 K U D U S K U S	E 6 6	S S S S S S S S S S S S S S S S S S S	REFER AUT
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Query Match 3.1%; Score 32; DB 1; Length 32; Best Local Similarity 100.0%; Pred. No. 2.5;

RESULT 1
AR090280/c
LOCUS AR090280 32 bp DNA
DEFINITION Sequence 400 from patent US 5994076.

linear PAT 07-SEP-2000

В

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BD242/42 Connective tissue growth factor (CTGF) and methods of use.
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               AGIPI)/00, AGIP19/02, AGIP41/00, AGIP43/00, CO7K14/475, CO7K16/22, C12N1/15, C12N1/19, C12N1/12, C12N5/10, C12P21/02, C12Q1/68/AGIK35/74, PC
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artificial construct
artificial sequences.

E 1 (bases 1 to 25)
Schmidt, B.F., Allen, M.L., Sverdrup, F. and Carmichael, D.F.
Connective tissue growth factor (CTGF) and methods of use
L Patent: JP 2002529066-A 7 10-SEP-2002;
FIBROGEN INC
OS Artificial Sequence
PN 19 2002529066-A/7
PD 10-SEP-2002
PF 05-NOV-1999 JP 2000581045
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1 (bases 1 to 25)
Schmidt, B.Frederick., Allen, M.Leah., Sverdrup, F. and Carmidt, B.Frederick., Allen, M.Leah., Sverdrup, F. and Carmidel, D.F. Connective tissue growth factor (CTGF) and methods of use Patent: US 6358741-A 9 19-MAR-2002;
Location/Qualifiers
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/organism="synthetic construct"

/mol type="genomic DNA"

/db_xref="taxon:32630"
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     PC A61P1/00,A61P19/02,A61P41/00,A61P43/0
PC C12N1/15,
PC C12N1/15,
PC C12N1/19,C12N1/21,C12N5/10,C12P21/02,C
PC C12P21/08,C12N15/00,C12N5/00
PC Antisense CTGF Oligonucleotide
FH Rey Location/Qualifiers
FT source /organism='Artificial'
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Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 9 from patent US 6358741.
AR201291.1 GI:20252179
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JP 2002529066-A/7.
A61P13/12
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synthetic construct
artificial sequences.

E. 1 (bases 1 to 25)
Schmidt, B.F., Allen, M.L., Sverdrup, F. and Carmichael, D.F.
Connective tissue growth factor (CTGF) and methods, of use
patent: JP 2002529066-A 6 10-SEP-2002;
FIBROGEN INC
OS Artificial Sequence
PN JP 2002529066-A/6
PD 10-SEP-2002
PF 05-NOV-1999 JP 2000581045
PR 06-NOV-1999 JP 2000581045
PR 06-NOV-1999 US 09/187478, 14-APR-1999 US 09/292036 PI
BRIAN FREDERICK SCHMIDT, MARGARET LEAH ALLEN, FRAN SVERDRUP, PI
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"P52218.1 GI:13021838

"P7 2000060559-A/20.

Haliotis discus metavota; Maliotoidea; Haliotidae; Haliotidae; Haliotis.

E 1 (bases I to 30)

E 1 (bases I to 30)

E 1 (bases I to 30)

E 2 Hideaki,T. and Masashi,S.

Mathod isolating satellite sequence

D PATO 1807 D P 2000060559-A 20 29-FBB-2000;

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OS Haliotis discus dis
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                                                   1732 CTTGTGGCAAGTGAATTTGCCTGTAACAAGCC 1763
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     0; Mismatches
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Matches 27; Conservative
     Matches 32; Conservative
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Nucleic acid molecules and other molecules associated with soybean
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                                                                                                                                                                                                                                                                                               Query Match 2.2%; Score 23.4; DB 1; Length 27; Best Local Similarity 96.0%; Pred. No. 21; Matches 24; Conservative 0; Mismatches 1; Indels
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    24
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db xref="teaxon:32630"
        /note="primer"

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                       Cyst nemarcde resistance
Patent: WO 0151627-A 601 19-JUL-2001;
MONSANTO COMPANY (US)
Location/Qualifiers
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Sequence 1870 from Patent WO0129262.
AX116747. GI:14033689
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Sequence 87 from patent US 5955276.
AR074790 AR074790.1 GI:10001543
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PR 06-NOV-1998 US 09/187478,14-APR-1999 US 09/292036 PI BRIAN FREDERICK SCHMIDT, MARGARET LEAH ALLEN, FRAN SVERDRUP, PI DAVID F CARMICHAEL

PC CIZNI5/09,A61K31/711,A61K48/00,A61P1/16,A61P9/10, PC
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Glycine max
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Agnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
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Connective tissue growth factor (CTGF) and methods of use Patent: US 6358741.A 10 19-MAR-2002;
Location/Qualifiers
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1 (bases 1 to 25)
Schmidt, B.Frederick., Allen, M.Leah., Sverdrup, F. and
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/organism='Artificial Sequence'
Location/Qualifiers
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Sequence 10 from patent US 6358741.
AR201292.1 GI:20252180
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1. .27
//organism="Glycine max"
//mol type="unassigned DNA"
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//noEe="Seq ID: 240017_region_G3_11301_29_Forward_Primer"
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Unclassified.
1 (bases 1 to 24)
1 (bases 1 to 24)
Morgante,M. and Vogel,J.Marie.
Compound microsatellite primers for the detection of genetic polymorphisms
Patent: US 5955276-A 87 21-SEP-1999;
Location/Qualifiers
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Best Local Similarity
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Unknown.
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I baser, J. L.
Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same
method of using the same
Patent: US 5523979-A HG 10-DEC-1996;
Patent: US 5523979-A HG 10-DEC-1996;
                 JM Unknow...
Unclassified.
E 1 (bases 1 to 22)
(S Morgante,M. and Vogel,J.Marie.
Compound microsatellite primers for the detection of genetic compound microsatellite primers for the detection of genetic polymorphisms
Journal Patent: US 5955276-A 88 21-SEP-1999;
J. Coation/Qualifiers
Jurce /organism="unknown"
/mol_type="unassigned DNA"
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Gryaznov,S.M.
Convergent synthesis of branched and multiply connected macromolecular structures
Patent: US 5830558-A 23 03-NOV-1998;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 23;
Matches 22; Conservative 0; Mismatches 0; Indels
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Sequence 23 from patent US 5830658.
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AR051255.1 GI:5974619
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Sequence 146 from patent US 5
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AR051255/c
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Patent: US 5582979-A 143 10-DEC-1996;
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Therapeutically useful synthetic oligonucleotides
Patent: Wo 0144465-A S 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
Location/Qualifiers
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/organism="synthetic construct"
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Sequence 143 from patent US 5582979.
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Sequence 88 from patent US 5955276.
AR074791. GI:10001544
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Sequence 5 from Patent W00144465.
AX175241 GI:14598609
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131231.1 GI:1822022
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Best Local Similarity 88.99
Matches 24; Conservative
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1 (bases 1 to 27)
Weber, J.L.
       23; Conservative
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REFERENCE AUTHORS TITLE

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PAT 06-FEB-1997

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PAT 29-SEP-1999

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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

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RESULT 17 AR127802/c LOCUS

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2.1%; Score 21.8; DB 1; Length 27; 92.0%; Pred. No. 33; tive 0; Mismatches 2; Indels
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                                               Therapeutically useful synthetic oligonucleotides Therent: WO 0144465-A 1 2 UVIX-2001; Bioniche Life Sciences Inc. (CA) Location/Qualifiers
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Therapeutically useful synthetic oligonucleotides
Patent: Wo 0144465-A 66 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
Location/Qualifiers
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Hyaluronic acid in the treatment of cancer
Patent: WO 0147561-A 2 05-UUL-2001;
Bioniche Life Sciences Inc. (CA)
Location/Qualifiers
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Best Local Similarity 92.0%; Pred. No. 33;
Matches 23; Conservative 0; Mismatches
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Sequence 66 from Patent WO0144465.
AX175302
AX175302.1 GI:14598670
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Sequence 2 from Patent WO0147561
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                                  Phillips, N.C. and Filion, M.C.
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AX189457.1 GI:15142969
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AX175302
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Patent: US 5571677-A 23 05-NOV-1996;
Location/Qualifiers
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Synthesis of branched nucleic acids
Synthesis of B0777-A 23 30-JAN-2001,
Patent: Uccation/Qualiflers
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Sequence 23 from patent US 6180777.
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Sequence 1 from Patent W00144465.
AXI75237.1 GI:14598605
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AR127802.1 GI:14114397
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Gryaznov, S.M.
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         23; Conservative
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LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE

RESULT 18 128384/c ORGANISM

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PAT 08-AUG-2001

RESULT 19
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PAT 03-JUL-2001

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Immidostimulacory nucleic acids
Immidostimulacory nucleic acids
Patent: WO 0122972-A 1086 05-ABR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
                                                                                                                Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same Patent: US 5582979-A 445 10-DEC-1996;
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Best Local Similarity 95.7%; Pred. No. 31;
Matches 22; Conservative 0; Mismatches 1; Indels
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Therapeutically useful synthetic oligonucleotides
Patent: WO 0144465-A 21 21-UUN-2001;
Bioniche Life Sciences Inc. (CA)
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Best Local Similarity 95.7%; Pred. No. 31;
Matches 22; Conservative 0; Mismatches
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Sequence 1068 from Patent WO0122972.
AX104876
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Sequence 21 from Patent WO0144465.
AX175257 43175257.1 GI:14598625
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                 GI:1822324
                                                             Unknown.
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   Query Match 2.1%; Score 21.8; DB 1; Length 27; Best Local Similarity 92.0%; Pred. No. 33; Matches 23; Conservative 0; Mismatches 2; Indels
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Best Local Similarity 95.7%; Pred. No. 29;
Matches 22; Conservative 0; Mismatches 1;
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Orchid BioSciences, Inc. (US)
Location/Qualifiers
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Patent: WO 0129262-A 1099 26-APR-2001;
Orchid BioSciences, Inc. (US)
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Matches 22; Conservative 0; Mismatches 1;
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Sequence 2959 from Patent WO0129262.
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Sequence 1099 from Patent WO0129262.
AX115976.1 GI:14032918
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Therapeutically useful synthetic oligonucleotides
Patent: Wo 0144465.A 22.J.JUN-2001;
Bioniche Life Sciences Inc. (CA)
Location/Qualifiers
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ilarity 95.7%; Pred. No. 31;
Conservative 0; Mismatches 1;
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llarity 95.7%; Pred. No. 31;
Conservative 0; Mismatches 1;
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Sequence 22 from Patent WO0144465.
AX175258 4175258.1 GI:14598626
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PAT 16-MAY-2001
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Weber, J.L.
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Fatent: US 582979-A 125 10-DEC-1996;
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Inhibition of angiogenesis by nucleic acids
Patent: WO 02053141-A 907 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
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Seguence 125 from patent US 5582979.
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Sequence 907 from Patent WO02053141.
AX5477768.1 GI:25812912
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muinostimulatory nucleic acids
Patent: WO 0122972-A 907 05-ABF-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
                   Weber, J.L.
Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same method of using the same Patent: US 5582979-A 160 10-DEC-1996;
Location/Qualifiers
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Therapeutically useful synthetic oligonucleotides
Patent: WO 0144465-A 19 21-UUN-2001;
Bloniche Life Sciences Inc. (CA)
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Sequence 19 from Patent W00144465.
AX175255.
AX175255.1 GI:14598623
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RESULT 33 AX175255 LOCUS

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Scaggiante, B. and Quadrifoglio, F.
A CLASS OF OLIGONUCLEOTIDES, THERAPEUTICALLY USEFUL AS ANTITUMOURAL
AGENTS
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Unclassified.
1 (bases 1 to 20)
Morgante,M. and Vogel,J.Marie.
Compound microsatellite primers for the detection of genetic
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                              Query Match 2.0%; Score 21; DB 1; Length 25; Best Local Similarity 100.0%; Pred. No. 37; Matches 21; Conservative 0; Mismatches 0; Indels
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SAICOM S R L (IT)
Other publication IT MI952539 19970604
Other publication AU 1175497 19970627.
Location/Qualifiers
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Location/Qualifiers
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AR074792
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Sequence 11 from Patent W09720924.
A63570
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 /note="Primer"
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A63570
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2.0%; Score 21; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 0; Indels
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2.0%; Score 21; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 21; Conservative 0; Mismatches 0; Indels
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/mol_type="unassigned DNA"
    /db xref="taxon:32630"
    /noTe="Primer"

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                                                                           Horn,T.
Synthesis of branched nucleic acids
Synthesis of 5180777-A 22 30-JAN-2001;
Patent: US 6180777-A 22 30-JAN-2001;
Location/Qualifiers
1. 23
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AX117828.1 GI:14034779
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1 (bases 1 to 23)
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PAT 03-JUL-2001

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Linnik, M.D. and Monealy, P.A.
Methods of treating lupus based on antibody affinity and screening
methods and compositions for use thereof
Patent: WO 0141813.A I 14-UWN-2001;
LA JOLLA PHARMACEUTICAL COMPANY (CA)
Location/Qualifiers
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Methods of treating lupus based on antibody affinity and screening methods and compositions for use thereof Parent: WO 0141813-A 2 14-UM-2001;
LA JOLLA PHARMACEUTICAL COMPANY (CA)
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/organism="synthetic construct"
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Sequence 2 from Patent WO0141813
AX179299 GI:14598970
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Sequence 1 from Patent WO0141813
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Unclassified.
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Matson.K.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
Oligonucleotide repeat arrays
Patent: US 5981185-A 32 09-NOV-1999;
Localion/Qualifiers
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Unclassified.

E 1 (Dasse 1 to 20)

S Bruice,T.C. and Dev,A.P.

Deoxymaciaic alkyl thiourea compounds and uses thereof

AL Patent: US 6168176-A 5 02-JAN-2001;

SS Location/Qualifiers

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/ organism="unknown"
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E. 1 (bases 1 to 20)
AS McKay,R., Butler,M.M., Wyatt,J. and Cowsert,L.M.
Antisense modulation of pepck-cytosolic expression
AL Patent: US 6187545-A 88 13-FEB-2001;
Location/Qualifiers
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AR084543.1 GI:10011314
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 5 from patent US 6169176.
AR123339
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Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                      Unknown.
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AR123339/c
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AR129684/c
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RESULT 41
AR084543/c
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PAT 03-JUL-2001

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BD105781.

GD105781.

GD105782.

IS SYNTHETIC CONSTRUCT

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ALLI (bases 1 to 20)

RS Conrad, M.J. and Coutts, S.

CONTAG, M.J. and Coutts, S.

LA JOLLA PHARMACEUTICAL CO

OS Artificial Sequence

PN JP 2001345569-A/6

PD 25-DEC-2001

PF 04-APR-2001 JP 2001106534

PR 16-AN-1990 US 466138,13-MAR-1990 US 494118 PI

MICHAEL J CONRAD, STEPHEN COUTTS

PC AGAIX31/7088,ASIX47448,AGAP37/02,CO7K14/00,C12N15/00,C12N15/00

CC Synthetic Construct

FH Key Location/Qualifiers

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Location/Qualifiers
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                                                                         DB 1; Length 20; 35;
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Therapeutically useful synthetic oligonuclectides
Patent: Wo 0144465-A 20 2J-UUN-2001;
Bioniche Life Sciences Inc. (CA)
Location/Qualifiers
                                                                                                                                 0; Indels

    .20
    /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

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Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches
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Sequence 20 from Patent WO0144465.
AX175256 GI:14598624
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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AX175256
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DD016468.1 GI:22557644

JP 2001231567-A/9.

Synthetic construct

Synthetic construct

Synthetic construct

artificial sequences.

El (Bases it of 20)

D Cta, K. and Shibata, T.

Method for regulating telomeric length

D Patent: JP 2001231567-A 9 28-AUG-2001,

THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, JAPAN SCIENCE AND TECHNOLOGY CORP

OS Artificial Sequence

PN JP 2001231567-A/9

PP 28-AUG-2001

PP 18-PEB-2000 JP 2000041929

PP 18-PEB-2000 JP 2000041929

PP C12N15/09, A61X35/76, A61X38/00, A61X48/00, A61P35/00, A61P35/00, PC C07H21/4)95, CI2N15/09, A61X39/16, CI2N15/00, A61X37/02

CC Description of Artificial Sequence: Synthetic DNA FH Key
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artificial sequences.
I (bases 1 to 20)
Cta, K. and Shibata, T.
Method for regulating telomeric length
Batent: WO 0160996-A9 23-AUG-2001,
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, JAPAN SCIENCE AND
TECHNOLOGY CORP, KUNIHIRO OTA, TAKEHIKO SHIBATA
OS ARTIficial Sequence
NW 0160996-A/9
PP 14-FREB-2001 WO 2001JP0011024
PR 18-FEB-2000 UP 00P 41929
PI KUNIHIRO OTA, TAKEHIKO SHIBATA
PC C12N1S/09, AGIX35/76, AGIX38/00, AGIX48/00, AGIP35/00, AGIP33/00,
PC C07K14/395, C12N9/16
CC Description of Artificial Sequence: synthetic DNA FH Key
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JP 2001231567-A/9
28-Aug-2001
18-PEB-2000 JP 2000041929
KUNIKAZU CTA, TAKEHIKO SHIBATA
C12N15/09, A61K35/76, A61K38/00, A61K48/00, A61P35/00, A61P41/00,
C07K14/395, C12N9/16, C12N15/00, A61K37/02
Description of Artificial Sequence: synthetic DNA FH Key
Location/Qualifiers
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CO7K14/395,C12N9/16
Description of Artificial Sequence:synthetic DNA
Location/Qualifiers
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/organism='Artificial Sequence'
Location/Qualifiers
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    .20
    ^2organism="synthetic construct"
|mol_type="genomic DNA"
|db_xref="taxon:32630"

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/organism="synthetic construct"
                                                        DNA
length.
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                                                     BD016468 20 bp
Method for regulating telomeric
BD016468
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WO 0160996-A/9.
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BD097545
LOCUS
DEFINITION
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RESULT 46
BD016468
LOCUS
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                                                                                                                                                                     1 (bases 1 to 21)
Hoke, G.D., Bradley, M.O., Williams, T.J. and Lee, C.-H.,
Antisense oligonuclectides directed against human ICAM-I RNA
Patent: US 558089-A 10 03-DEC-1996;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 19)
Morgante, M. and Vogel, J.Marie.
Compound microsatellite primers for the detection of genetic
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                                                                                                                                                                                                                                                                                                                1.8%; Score 19.4; DB 1; Length 21; 95.2%; Pred. No. 44; tive 0; Mismatches 1; Indels
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                                            DNA
                                   21 bp 1
Sequence 10 from patent US 5580969.
130547
130547.1 GI:1821338
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Sequence 2153 from Patent WO0129262.
AX117030
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1.8%; Score 19.4; E
Best Local Similarity 95.2%; Pred. No. 53;
Matches 20; Conservative 0; Mismatches
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Sequence 74 from patent US 5955276.
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/mol_type="unassigned DNA"
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Matches 20; Conservative
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Unclassified.
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             RESULT 52
130547/c
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AR074777
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Best Local Similarity 100.0%; Pred. No. 38;
Matches 20; Conservative 0; Mismatches 0; Indels
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                                             Length 21;
                                                                          0; Indels
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/organism=synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
/note="Sequence prepared in Example 4"
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/organism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
/note="Sequence prepared in Example 4"
                                        Ouery Match 1.9%; Score 20; DB 1; Best Local Similarity 100.0%; Pred. No. 38; Matches 20; Conservative 0; Mismatches C
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Synthons for oligonucleotide synthesis
Patent: WO 0220543-A 2 14-MAR-2002;
Avecia Biotechnology, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                          Synthons for oligonucleotide synthesis
Synthons WO 0220543-A 114-MAR-2002;
Patent: WO 0220543-A 114-MAR-2002;
Avecia Biotechnology, Inc. (US)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Sequence 2 from Patent W00220543.
AX398277
AX398277.1 GI:21261078
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Sequence 1 from Patent WO0220543.
AX398276
                                                                                                       1794 GIGTGTGTGTGTGTGT 1813
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Best Local Similarity 100.
Matches 20; Conservative
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AX398277
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mcgarry191-19.rge

19 TGTGTGTGTGTGTGTGT 1

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PAT 16-MAY-2001
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Unclassified.
Unclassified.
1 (bases 1 to 21)
Ginzinger,D.G., Godfrey,T.E., Jensen,R.H. and Gray,J.W.
Quantitative PCR method to enumerate DNA copy number
Patent: US 6180349-A 1 30-JAN-2001;
Location/Qualifiers
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1.8%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                       linear
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Locked mucleic acid hybrids and methods of use
Patent: WO 0053365-A 8 26-OCT-2000;
Pangene Corporation (US)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
/note="Z-DNA"
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1.8%; Score 19; DB 1;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches
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Sequence 1 from patent US 6180349.
AR126570 GI:14113163
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Sequence 2 from patent US 6180349.
AR126571 GI:14113164
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Sequence 8 from Patent WO0063365.
AX040468
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AR126570
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AR126571
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AX040468
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Weber, J.L.
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Best Local Similarity 100.0%; Pred. No. 43;
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Best Local Similarity 100.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 0; Indels
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/db xref="taxon:32630"
/noTe="Z-DNA"
polymorphisms
Patent: US 5955276-A 74 21-SEP-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 442 from patent US 5582979.
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Sequence 7 from Patent W00063365.
AX040467
AX040467.1 GI:11230259
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artificial sequences.
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RESULT 56
AX040467/c
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Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H., Morohashi, A., Ohira, M., Nakagawara, A., Liu, S., Hoshi, M., Horii, A. and Soeda, E. A. A. A. A. A. A. A. A. S. S. C. Content map spanning a 35-Mb region of human
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Location/Qualifiers
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1.8%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 19; Conservative 0; Mismatches 0; Indels
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/organism="Haliotis discus discus"
/ordlrype="genomic DNA"
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                                                                                                                                                                                                                                                                                     /organism="synthetic construct"
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i. 721
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Method for isolating satellite sequence.
E32219
                                                                         chromosome 1p35-p36
Genomics 74 (1), 55-70 (2001)
21269192
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JP 2000060559-A/21.
Haliotis discus discus
Haliotis discus discus
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E32219/c
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JP 2001321190-A/1418
20-NOV-2001
12-MAR-2001
BIICHI SOEDA
C12NIS/09,C12NIS/09,C12NI/00,C12Q1/68,G01N33/53,G01N33/566,PC
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Patent: JP 2001321190-A 1418 20-NOV-2001,
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
GENOTECHS
OS ARTIficial Sequence
PD 20-NOV-2001
PP 12-NAR-2001
PP 12-NAR-2001
PP 21-ARA-2001
PP C12-NAS-2001
PP C12-NAS-2001
PP C12-NAS-2001
PP C12-NAS-2001
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         Ginzinger, D.G., Godfrey, T.E., Jensen, R.H. and Gray, J.W. Quantitative PCR method to enumerate DNA copy number Patent: US 6180349-A 2 30-JAN-2001;
Location/Qualifiers
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/organism='Artificial Sequence'
Location/Qualifiers
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llarity 100.0%; Pred. No. 49;
Conservative 0; Mismatches 0; Indels
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A method of arraying genome clone.
BD089174
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                                                                                                                                                                                                                                                                                                                                                                                                         /note="reverse primer for human STS sts-R12616F at 1p36 sts-R12616F obcained from clones B12616, B156A20, B141IM15, B137L6, B157A17, B157P23, Human BAC library RPCI-11"
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E 1 (bases 1 to 20)

S Hideaki, T. and Masahi, S.

Hideaki, T. and Masahi, S.

Method for isolating satellite sequence

In Patent: UP 200060559-A 21 29-FEB-2000;

NATL INST OF AGNOBIOLOGIGAL RESOUCES

OS Haliotis discus pp 29-FEB-2000

PP 18-AUG-1998 UP 1998222153

PR HIDBAKI TAKAHASHI, MAGASHI SEKINO

CC LINIS/09,C12Q1/68,C12N15/00

CC LONIS/09,C12Q1/68,C12N15/00

CC LONIS/09,C12Q1/68,C12N15/00

FF Source 1. .20

FT F Source 1. .20
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11374902
2 (bases 1 to 21)
2 (bases 1 to 21)
4 Horil.A.
Horil.A.
Direct Submission
Submitted (04-AUG-2001) Akira Horil, Tohoku University School
Submitted, Wolecular Pathology, 2-1 Selryomachi, Aoba-ku, Senda
Miyagi 980-8855, Japan (B-mail.horismail.cc.tohoku.ac.jp,
Tel:81-22-717-8042, Fax:81-22-717-8047)
Location/Qualifiers
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Gaps

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PAT 20-APR-2002
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Binding assay using binding agents with tail groups Patent: US 6316186-A 2 13-NOV-2001;
Location/Qualifiers
Binding assay using binding agents with tail groups Patent: US 6316186-A 1 13-NOV-2001; Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.7%; Score 18; DB 1; Length 18; ilarity 100.0%; Pred. No. 52; Conservative 0; Mismatches 0; Indels
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1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 18; Conservative 0; Mismatches 0; Indels
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Unclassified.
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Unclassified.
I (bases It to 18)
Head, S. R., Goelet, P., Karn, J. and Boyce-Jacino, M.
De novo or 'universal' sequencing array
Patent: US 6337188-A 28 08-JMN-2002;
Location/Qualifiers
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1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 18; Conservative 0; Mismatches 0; Indels
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/organism="unknown"
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Sequence 28 from patent US 6337188.
AR182079 GI:20224995

    .18
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AR182079
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AR178166
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Best Local Similarity 100.0%; Pred. No. 52;
Matches 18; Conservative 0; Mismatches 0; Indels
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Stoler,D., Basik,W. and Anderson,G.
Rapid means of quantitating genomic instability
Patent: US 5912147-A 5 15-JUN-1999,
Location/Qualifiers
                                                                                                                                                                                                                                     1 (bases 1 to 18)
Stoler, D., Basik, M. and Anderson, G.
Rapid means of quantitating genomic instability
Patent: US 5912147-A 4 15-JUN-1999;
Location/Qualifiers
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Sequence 5 from patent US 5912147.
AR071776 GI:7222664
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Sequence 4 from patent US 5912147.
AR071775
           1793 TGTGTGTGTGTGTGTGTG 1812
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1 (bases 1 to 18)
Ekins, R.Philip.
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AR178165/c
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AR071776/c
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AR071775/c
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1..18
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PACHEL: JP 1993244995-A 7 24-SEP-1993;
KYOWA HAKKO KOGYO CO LTD
OS Artificial gene
                                                               DB 1
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100.0%; Pred. No. 52;
ive 0; Mismatches
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JP 199324955-A7.
Synthetic construct
synthetic construct
artificial sequences.
I (bases 1 to 20)
Komatsu,Y. and Kikuchi,Y.
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E05497
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BD087486
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1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 18; Conservative 0; Mismatches 0; Indels
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Therapeutically useful synthetic oligonucleotides
Patent: Wo.0144465.A.17 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
Location/Qualifiers
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Therapeutcally useful sytthetic oligonucleotides
Patent: WO 0144465-A 18 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
               linear
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Head, S.R., Goelet, P., Karn, J. and Boyce-Jacino, M. De novo or 'universal' sequencing array
Patent: US 6322968-A 28 27-NOV-2001;
Location/Qualifiers
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/organism="synthetic construct"
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                DNA
         18 bp 1
Sequence 28 from patent US 6322968.
AR261503
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Sequence 17 from Patent WO0144465.

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Length polymorphisms in (dC-dA).sub.n.(dG-dI).sub.n sequences and method of using the same
Patent: US 5582979-A 448 10-DEC-1996;
Location/Qualifiers
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Query Match
Best Local Similarity 94.7%; Pred. No. 70;
Matches 18; Conservative 0; Mismatches 1; Indels
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1.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 17; Conservative 0; Mismatches 0; Indels
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Patent: WO 0164948-A 16 07-SEP-2001;
Dr. van Haeringen Laboracatorium B.V. (NL)
Location/Qualifiers
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                                                                                                                                                                131536 17 bp DNA Sequence 448 from patent US 5582979.
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Sequence 16 from Patent WO0164948.
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I31536.1 GI:1822327
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Unclassified.
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Bennett, C. Frank., Ackermann, E.J., Swayze, E.E. and Cowsert, L.M. Antisense modulation of survivin expression
Patent: US 333194-A 235 01-JAN-2002;
Location/Qualifiers
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MCKAy,R., Butler,M.M., Wyatt,J. and Cowsert,J.M.
Antisense modulation of pepck-cytosolic expression
Patent: US 6187545-A 120 13-FEB-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                     1.7%; Score 18; DB 1; Length 20; 100.0%; Pred. No. 60; or Indels ive 0; Mismatches 0; Indels
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Location/Qualifiers
1. .20
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/mol_type="genomic DNA"
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                                               24-SEP-1993
24-SEP-1993
24-SEP-1991 UP 1991243122
KOMATSU YUKI, KIXUCHI YASUHIRO
C12Q1/68, C12N15/11;
strandedness: Single;
topology: Linear;
hypothetical: No;
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Sequence 120 from patent US 6187545.
AR129716
AR129716.1 GI:14117613
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Best Local Similarity 94.7%; Pred. No. 70;
Matches 18; Conservative 0; Mismatches
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/organism="unknown"
/mol_type="unassigned DNA"

    .20
    /organism="unknown"
    /mol_type="unassigned DNA"

      Artificial sequence, Genes.
Zea maize
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E (Dases 1 to 18)

S Stoler,Do, Basik,M. and Anderson,G.

Rapid means of quantitating genomic instability

ML Patent: US 5912147-A 30 15-JUN-1999;

Location/Qualifiers
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                                             1.6%; Score 17; DB 1; Length 18; 100.0%; Pred. No. 68; 0; Indels tive 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 68;
Matches 17; Conservative 0; Mismatches 0; Indels
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1 (bases 1 to 18)
Stoler,D., Basik,M. and Anderson,G.
Rapid means of quantitating genomic instability
Patent: US 5912147-A 28 15-UUN-1999;
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1.6%; Score 17; DB 1;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 17; Conservative 0; Mismatches
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AR071801
AR071801.1 GI:7222689
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Sequence 31 from patent US 5912147.
AR071802
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                                                                                                                                                                                                                  18 bp
Sequence 28 from patent US 5912147.
AR071799
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="unassigned DNA"
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/organism="unknown"
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AR071799/c
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                                                                              Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                            Telerman, A., Amson, R. and Tuijnder, M. Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
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1 (bases 1 to 18)
Stoler,D., Basik,M. and Anderson,G.
Rapid means of quantitating genomic instability
A Patent: US 5912147-A 3 15-UW-1999;
Location/Qualifiers
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1 (bases 1 to 18)
Stoler,D., Basik,M. and Anderson,G.
Rapid means of quantitating genomic instability
Letent: US 5912147-A 1 15-UW-1999;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred: No. 68;
Matches 17; Conservative 0; Mismatches 0; Indels
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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    .17
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                      AX762730.1 GI:32257346
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                                                                    Homo sapiens
        AX762730
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AR071774/c
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AR071772/c
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E36173

Upstream regulatory sequence of melanocortin-1 receptor gene and utilization thereof.

E36173.

E36173.

E36173.

E36173.

E36173.1 GI:18626400

JP 2000166563-A/15.

Homo sapiens (human)

ISM Homo sapiens (human)

ENKARYOCA; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

EM Noro,O., Ifuku,O. and Ideta,T.

EM Dostream regulatory sequence of melanocortin-1 receptor gene and utilization thereof

EM Patent: JP 2000166563-A 15 20-JUN-2000; SHISEIDO CO LFD
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CIZNIS/09,CIZNS/10,C12Q1/66,C12Q1/68//C07K14/705,(C12N15/09,
C12R1:91),
                   OSAMU MORO, OJI IFUKU, TATSURO IDETA
CIZNIS/09, C12NS/10, C12Q1/66, C12Q1/68//C07K14/705, (C12N15/09,
C12R1:91),
C12N15/00, C12N5/00, (C12N15/00, C12R1:91)
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                                                                                                                                                                                                                                                                                                                                                                        Query Match
1.6%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 82;
Matches 18; Conservative 0; Mismatches 2; Indels
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/organism="Homo sapiens"
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JP 2000166563-A/15
20-JUN-2000
04-DEC-1998 JP 1998345881
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Moro,O., Ifuku,O. and Ideta,T.

Upstream regulatory sequence of melanocortin-1 receptor gene and utilization thereof
Patent: JP 200166563-A 15 20-JUN-2000,
SHISEIDO CO LID
OS Homo sapiens (human)
PN JP 200166563-A/15
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1.6%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                          Unclassified.
Unclassified.
1 (bases 1 to 18)
Scoler,D., Basik,M. and Anderson,G.
Rapid means of quantitating genomic instability
Patent: US 5912147-A 31 15-UUN-1999;
Location/Qualifiers
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Stoler, D., Basik, M. and Anderson, G.
Rapid means of quantitating genomic instability
Patent: US 5912147-A 32 15-UW-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                             1. .18
/organism="unknown"
/mol_type="unassigned DNA"
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/organism="unknown"
/mol_type="unassigned DNA"
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  AR071802.1 GI:7222690
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Homo sapiens (human)
Homo sapiens
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AR071803/c
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PAT 18-FEB-2000
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Juclassified.
E 1 (bases 1 to 24)
(S Morgante,M. and Vogel,J.Marie.
Compound microsatellite primers for the detection of genetic Compound microsatellite primers for the detection of genetic polymorphisms
[AL Patent: US 5955276-A 87 21-SEP-1999;
Location/Qualifiers
J. 24
ource //organism="unknown"
/mol_type="unassigned DNA"
- " A R DB 1; Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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               /mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
                                                                                                                                                                                                                                                                                                                 note="LNA-T (Locked Nucleic Acid)"
mod_base=OTHER
                                                                                                                                                                                                                                                                      note="LNA-T (Locked Nucleic Acid)"
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/mod_base=OTHER
                                                                                                                           note="LNA-T (Locked Nucleic Acid)"
"mod_base=OTHER
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"mod_base=OTHER
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   organism="synthetic construct"
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Sequence 7 from patent US 5912147.
AR071778 GI:7222666
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Matches 18; Conservative
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AR071778/c
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AR074790
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                                                                                                               1 (bases 1 to 20)
Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
Polymorphic repeats in human genes
Patent: 18 6472154-A 337 29-OCT-2002;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vicari,A.P., Caux,C. and Laface,D.
Chemokines as adjuvants of immune response
Patent: WO 02058723-A 10 01-AUG-2002;
Schering Corporation (US)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_kref="taxon:32630"
 Sequence 337 from patent US 6472154.
AR242049
AR242049.1 GI:27287861
                                                                                                                                                                                                                                                             1.6%; Score 16.8; Ilarity 90.0%; Pred. No. 82; Conservative 0; Mismatches
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Best Local Similarity 90.0%; Pred. No. 88;
Matches 18; Conservative 0; Mismatches
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Sequence 10 from Patent WO02058723.
AX556883
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Sequence 4 from Patent WO03072818.
AX825106
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/organism="unknown"
/mol_type="genomic DNA"
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B (bases 1 to 18)
(S Stoler, D., Basik, M. and Anderson, G.
Rapid means of quantitating genomic instability
(AL Patent: US 5912147-A 35 15-JUN-1999;
Location/Qualifiers
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1 (bases 1 to 18)
Stoler,D., Basik,M. and Anderson,G.
Rapid means of quantitating genomic instability
Patent: US 5912447-A 37 15-UUN-1999;
Location/Qualifiers
                                                                                                                                                                                                                         instability
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1 (bases 1 to 18)

Stoller,D., Basik,M. and Anderson,G.
Rapid means of quantitating genomic:
Patent: US 5912147-A 33 15-JUN-1999;
Location/Qualifiers
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1.6%; Score 16.4; Esst Local Similarity 94.4%; Pred. No. 79; Matches 17; Conservative 0; Mismatches
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Sequence 37 from patent US 5912147.
AR071808.1 GI:7222696
                                                                                                                                                                                                                                                                          1. .18
/organism="unknown"
/wol_type="unassigned DNA"
                                                           Sequence 33 from patent US 5912147.
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AR071806
AR071806.1 GI:7222694
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AR071806/c
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AR071804/c
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Unclassified.

1 (baces 1 to 18)

$\frac{1}{2}$ (baces 1 to 18)
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1 (bases 1 to 18)

Stoler, D., Basikh, and Anderson, G.

Rapid means of quantitating genomic instability

Patent: US 5912147-A 8 15-JUN-1999;

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 18)
Stoler,D., Basik,M. and Anderson,G.
Rapid means of quantitating genomic instability
Patent: US 5912147-A 29 15-JUN-1999;
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1.6%; Score 16.4; D
Best Local Similarity 94.4%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches
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/mol_type="unassigned DNA"
                                                                                                                 /organism="unknown"
/mol_type="unassigned DNA"

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    /organism="unknown"
    /mol_type="unassigned DNA"

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Sequence 29 from patent US 5912147.
AR071800
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Sequence 8 from patent US 5912147.
AR071779
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AR071800/c
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AR071779/c
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E28534 18-JUN-2001 Method for labeling oligonucleotide and utilization thereof. E28534
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PN JP 1999075880-A/1
PD 23-MAR-1999
PF 10-JUL-1998 JP 1998195719
PR KENICHI HANDAKI, HIROSHI YOSHIKURA, MASAHIDE NOZAKI PC C12N15/09, C12Q1/68, G01N33/58, C12N15/00
CC Strandedness: Single,
CC Topology: Linear;
FH Key
Location/Qualifiers
FT source /organism='Unidentified'.
                                                                                                                                                                                                                                                                                                                      Kenichi,H., Hiroshi,Y. and Masahide,N.
Kenichi,H., Hiroshi,Y. and Masahide,N.
Kenich for labeling oligonucleotide and utilization thereof
Method for 1999975880-A 1 23-MAR-1999;
CHEMO SERO THERAPEUT RES INST
OS Unidentified
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Unclassified.
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1 (bases it to 18)
Garner, H.S., Wren, J.D., Minna, J.D. and Fondon, J.W. III.
Garner, H.S., Wren, J.D., Minna genes
Polymorphic repeats in human genes
Patent: US 6472154-A 104 29-OCT-2002;
Location/Qualifiers
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        Score 16.4; DB 1; Length 18;
Pred. No. 79;
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Sequence 104 from patent US 6472154.
AR241816.
AR241816.1 GI:27287628
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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/organism="unknown"
/mol_type="genomic DNA"
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JP 1999075880-A/1.
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Best Local Similarity 94.4%;
Matches 17; Conservative
          Query Match
Best Local Similarity 94.43
Matches 17, Conservative
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E28534/c
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S. Kenichi, H. Hiroshi, Y. and Masahide, N. Method for labeling oligomuclectide and utilization thereof.

D. Patent: UP 1999075880-A1 23-MAR-1999;
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CHEADO SERO THERAPEUT RES INST.

PP UP 1999075880-A/1

PP NOTUL-1998 UP 1998195719

PR KENICHI HANAKI, HIROSHI YOSHIKURA, MASAHIDE NOZAKI PC CLIVALS/09, CLIVALS (S. GAIN33/58, CLIVALS/09)

CC Strandedness: Single;

CC Topology: Linear;
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E 1 (bases 1 to 18)
& Stoler,Do., Basik,M. and Anderson,G.
Rapid means of quantitating genomic instability
(AL Patent: US 5912147-A 38 15-UN-1999;
Location/Qualifiers
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/organism='Unidentified'
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Best Local Similarity 94.4%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches
                                                            Query Match
1.6%; Score 16.4; EBest Local Similarity 94.4%; Pred. No. 79; Matches 17; Conservative 0; Mismatches
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Sequence 38 from patent US 5912147.
AR071809
AR071809.1 GI:7222697

    .18
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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JP 1999075880-A/1.
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E28534
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BD084130.1
BD08130.2
BD0825663-A/18
BD08200.2
BD08200.2
BD08200.2
BD08200.3

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synthetic construct
artificial sequences.
1 (bases 1 to 16)
Epplen, 7.
Process for the detection of restriction fragment length
polymorphisms in eukaryotic genomes
Patent: EP 0266787-A 13 11-MAY-1988;
Max-planck-Gesellschaft zur Poerderung der Wissenschaften
Location/Qualifiers
                                                                                                                                                                                                                                                20 bp DNA linear PA. Polymorphisms and new genes in the region of the human hemochromatosis gene.
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94.4%; Pred. No. 91;
tive 0; Mismatches

    .20
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Oligonucleotide.
A12053
A12053.1 GI:491255
     Best Local Similarity 94.4
Matches 17; Conservative
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A12053
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BD084130/c
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BN JP 2001525663-A/18

BD J1-DEC-2001

PP 10-CT-1996 US 08/724394,07-MAY-1997 US 08/852495 PI

MINSTON J THOMAS, ZENTA TSUCHIHASHI, ROGER K WOLFF PC
CO7H21/04, C12Q1/68, C12M25,63, C12M15/85, C12P21/02 CC

BH Key

Location/Qualifiers

FT source

() organism='Home sapiens (human)'.
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I (Dases I to 20)
Feder, J.N., Krommal, G.S., Lauer, P.M., Ruddy, D.A., Thomas, W.J.,
Tsuchihashi, Z. and Wolff, R.K.
Polymorphisms and new genes in the region of the human
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Unclassified.

I (bases 1 to 18)

Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
Polymorphic repeats in human genes
Patent: US 6472154-A 104 29-OCT-2002;
Location/Qualifiers
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Polymorphisms and new genes in the region of the human
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Location/Qualifiers
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Patent: JP 2001525663-A 18 11-DEC-2001;
PROGENTIOR INC
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AR241816
           0; Mismatches
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JP 2001525663-A/18.
Homo sapiens (human)
Homo sapiens
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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PAT 09-DEC-1993

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AX239677
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DP 2000660559-A/26.
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Patent: BP 0266787-A 14 11-MAY-1988;
Max-Planck-Gesellschaft zur Foerderung der Wissenschaften Location/Oualifiers
1. 16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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                                                                             Length 16;
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    /organism="Haliotis discus discus"

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Best Local Similarity 100.0%; Pred. No. 75;
Matches 16; Conservative 0; Mismatches
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C12N15/09, C12Q1/68, C12N15/00
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Al2054.1 GI:489449
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E32224/c
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Unclassified.
I (bases 1 to 16)
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Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Rethod and reagent for the treatment of diseases or conditions
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
related to levels of vascular endothelial growth factor receptor
Patent: US 656127-A 6069 20-MAY-2003;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 75;
Matches 16; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 75;
Matches 16; Conservative 0; Mismatches 0; Indels
DB 1; Length 16; 75;
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Sequence 439 from patent US 5582979.
I31527.
I31527.1 GI:1822318
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Query Match
1.5%; Score 16; DB
Best Local Similarity 100.0%; Pred. No. 75;
Matches 16; Conservative 0; Mismatches
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Patent: WO 0164948-A 19 07-SEP-2001;
Dr. van Haeringen Laboratorium B.V. (NL)
Location/Qualifiers
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AX239681
AX239681.1 GI:15797346
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Sequence 20 from Patent WO0164948.
AX239680
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                                                                                                                                            van Haeringen, W.A. and van Haeringen, H. Universal variable fragments
Patent: Wo 0164948-A.17.07-SEP-2001;
Dr. van Haeringen Laboratorium B.V. (NL)
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Universal variable fragments
 17 bp
Sequence 17 from Patent WO0164948.
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Sequence 19 from Patent WO0164948.
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Sequence 18 from Patent WO0164948.
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1.5%; Score 16; DB 1; Length 17;
100.0%; Pred. No. 81;
tive 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 81;
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Matches

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 113 AR071773/c LOCUS

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Location/Qualifiers
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Unclassified.
Unclassified.
S 1 (Dases 1 to 18)
S Stoler,Do. Basik,M. and Anderson,G.
Sapid means of quantiteting genomic instability
AL Patent: US 5912147-A 36 15-JUN-1999;
Location/Qualifiers

Location/Qualifiers
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1 (bases 1 to 18)
Stoler,D., Basik,M. and Anderson,G.
Rapid means of quantitating genomic instability
Patent: US 5912147-A 34 15-UUN-1999;
Location/Qualifiers
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/noTe="Primer"
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1.5%; Score 16; DB 1;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 16; Conservative 0; Mismatches
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AXII5187
AXII5187.1 GI:14032129
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Best Local Similarity 100.0
Matches 16; Conservative
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AR071807/c
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1 (December 1 to 18)

S Stoler, D., Basik, M. and Anderson, G.
Rapid means of quantitething genomic instability

A Patent: US 5912147-A 2 15-UN-1999;

Location/Qualifiers
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1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 16; Conservative 0; Mismatches 0; Indels
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Stoler D., Basik M. and Anderson, G.
Rapid means of quantitating genomic instability
Patent: US 5912147.A 6 15-UW-1999,
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 88;
Matches 16; Conservative 0; Mismatches
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 34 from patent US 5912147.
      Mismatches
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Sequence 6 from patent US 5912147.
AR071777.1 GI:7222665
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Sequence 2 from patent US 5912147.
AR071773
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AR071805/c
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source

AUTHORS TITLE JOURNAL FEATURES

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SOURCE ORGANISM

RESULT 114 AR071777/c LOCUS DEFINITION

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REFERENCE AUTHORS TITLE

JOURNAL

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Unknown.
Unknown:
Unclassified.

1 (bases 1 to 15)

1 (bases 1 to 15)

Morgante, M. and Vogel, J.Marie.

Compound microsatellite primers for the detection of genetic polymorphisms

Polymorphisms

Location/Qualifiers

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unclassified.
1 (Dases 1 to 15)
Morgante, M. and Vogel, J.Marie.
Compound microsatellite primers for the detection of genetic
                                                                                                                   (bases 1 to 15)
Morgante, M. and Vogel, J.Marie.
Compound microsatellite primers for the detection of genetic
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1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 89; "
Matches 15; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 89;
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Location/Qualifiers
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Patent: US 5955276-A 8 21-SEP-1999;
Location/Qualifiers
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Sequence 9 from patent US 5955276.
AR074712.1 GI:10001465
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Sequence 8 from patent US 5955276.
AR074711
Sequence 7 from patent US 5955276.
AR074710
AR074710.1 GI:10001463
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Matches 15; Conservative
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AR074711/c
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backbone"
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backbone"
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Best Local Similarity 94.1%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 94.1%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels
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UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
Location/Qualifiers
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Sequence 85 from Patent WO0197843.
AX355057
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Sequence 85 from Patent WO0197843.
AX355057
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artificial sequences.
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AX355057/c
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AR074710/c
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PAT 28-AUG-2000

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PAT 28-AUG-2000

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PAT 13-MAY-1997
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Unclassified.
1 (bases 1 to 16)
Cook,P.D. and Sanghvi,Y.S.
Nuclease resistant, pyrimidine modified oligonucleotides that
Nuclease resistant, pyrimidine profession
detect and modulate gene expression
Patent: US 5614611-A 2 25-MAR-1997,
Location/Qualifiers
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                                      Unknown.
Unknown.
Unclassified.
Unclassified.
Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
Gene expression profiles in normal and cancer cells
Patent: US 6331352-A 733 25-DEC-2001;
Location/Qualifiers
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Therapeutically useful synthetic oligonucleotides
Patent: Wo 0144455-A 16 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
Location/Qualifiers
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    15
    Organism="synthetic construct"
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/db_xref="taxon:32630"

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cive 0; Mismatches
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Sequence 2 from patent US 5614617.
138642.
138642.1 GI:2084696
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/mol_type="unassigned DNA"
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Sequence 16 from Patent WO0144465.
AX175252
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 AR180665.1 GI:20222698
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138642
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                                                                                                                                                                                                                                                                                          Unclassified.
1 (bases 1 to 15)
Morgante,M. and Vogel,J.Marie.
Compound microsatellite primers for the detection of genetic polymorphisms
Patent: US 5955276-A 10 21-SEP-1999;
Location/Qualifiers
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1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 15; Conservative 0; Mismatches 0; Indele
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100.0%; Pred. No. 89;
trive 0; Mismatches
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Patent: US 6180777-A.24 30-JAN-2001;
Location/Qualifiers
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Seguence 733 from patent US 6333152.
AR180665
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AR074713
AR074713.1 GI:10001466
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Sequence 24 from patent US 6180777,
AR127803
AR127803.1 GI:14114398

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/organism="unknown"
/wol_type="unassigned DNA"
/mol_type="unassigned DNA"
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1 (bases 1 to 15)
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AR180665
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AR074713
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AR127803/c
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PAT 14-FEB-2003

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Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,B.,
Lewin,A., Lipscher,E., Maler,S., Model,F., Mueller,V., Otto,T.,
Pelet,C. and Ziebarth,H.
                                                   Unclassified.

1 (bases 1 to 16)

Pavoo, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J. McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J. McHod and reagent for the treatment of diseases or conditions related to levels of vaccular endothelial growth factor receptor Patent: US 6566127-A 6070 20-MAY-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berlin, K., Braun, A., Distler, J., Guetig, D., Howe, A., Mueller, J., Olek, A., Piepenbrock, C., Adorjan, P., Grabs, G., Lesche, R., Leu, E., Lewin, A., Lipscher, E., Maier, S., Model, F., Mueller, V., Otto, T., Pelet, C. and Ziebarth, H.
Methods and mucleic acids for the analysis of hematopoietic cell proliferative disorders
Prent: WO 02077272-A 650 03-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .18 /organism="synthetic construct" /organism="synthetic construct" /mol_type="unassigned DNA" /db xref="texon:32630" /noTe="Detection oligonucleotide for ELK1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.4%; Score 15; DB 1; Length 18;
ilarity 100.0%; Pred. No. 1.1e+02;
Conservative 0; Mismatches 0; Indels
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97;
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Sequence 650 from Patent WO02077272.
AX599310
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/organism="unknown"
/mol_type="unassigned RNA"
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Location/Qualifiers
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AX599310
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1 (bases 1 to 16)

Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
McHod and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 6068 20-MAY-2003;
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Cook, P.D. and Sanghvi, Y.S.
Nuclease resistant, pyrimidine modified oligonucleotides that detect and modulate expression
Patent: US 5614617-A 2 25-WAR-1997;
Location/Qualifiers
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1.4%; Score 15; DB 1; Length 16; 100.0%; Pred. No. 97; tive 0; Mismatches 0; Indels
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1.4%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 15; Conservative 0; Mismatches 0; Indels
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/mol_type="unassigned DNA"

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    /organism="unknown"
    /mol_type="unassigned RNA"

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Sequence 2 from patent US 5614617.
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Sequence 6070 from patent US
AR328668
AR328668.1 GI:33714476
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                   Best Local Similarity 100. Matches 15; Conservative
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Unclassified.
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AR328668
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AR328666
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/mol_type="unassigned_DNA"
/db_xref="taxon:32630"
/noTe="Detection_oligonucleotide_for_EDK1"
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1.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                M Unknown.
Unclassified.
2 1 (bases 1 to 32)
3 1 (bases 1 to 32)
5 Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
8 Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
Methods of assaying differential expression
AL Patent: US 59940'6-A 400 30-NOV-1999;
Location/Qualifiers
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Unclassified.

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E 1 (bases i to 32)

S Chenchik,A., Joshadze,G. and Bibilashvilli,R.

Methods of assaying differential expression

AL Patent: US 6352829-A 400 05-MAR-2002;

Location/Qualifiers
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Sequence 400 from patent US 6352829.
AR197315.1 GI:20247164
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Method and nucleic acids for the analysis of a lung cell proliferative disorder
Patent: WO 30122135-A 507 26-JUN-2003;
Epigenomics AG (DE)
Location/Qualifiers
   Methods and nucleic acids for the analysis of hematopoietic cell
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Method and nucleic acids for the analysis of a lymphoid cell proliferative disorder.

Batent: WO 03044226-A 374 30-MAY-2003;

Epigenomics AG (DE)
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1. 18
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//col_type="unassigned DNA"
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//noTe="Detection oligonucleotide for ELK1"
                                                                                                                                                                                           1.4%; Score 15; DB 1; Length 18; 100.0%; Pred. No. 1.1e+02; tive 0; Mismatches 0; Indels
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1.4%; Score 15; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0;
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                      proliferative disorders
Patent: WO 2027/22-A 1242 03-0CT-2002;
Epigenomics AG (DE)
Location/Qualifiers
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Sequence 374 from Patent WO03044226.
AX767726
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Best Local Similarity 100.6
Matches 15; Conservative
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Unclassified.
1 (bases 1 to 16)
West,M.D., Shay,J., Wright,W., Blackburn,E.H. and McBachern,M.J.
West,M.D., cardyJ., Wright,W., disgnosing pathogenic infections
Telomerase activity assays for diagnosing pathogenic infections
Patent: US 5695932-A 57 09-DEC-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                               Unclassified.

1 (Dases 1 to 16)

1 (Dases 1 to 16)

Wright, W.E., Harley, C.B., Strahl, C.M., McEachern, M.J., Shay, J., Wright, W.E., Blackburn, B.H. and Vaziri, H.
Therapy and diagnosis of conditions related to telomere length and/or telomerase activity and/or telomerase activity batent: US 5645986-A 58 08-UUL-1997;

Location/Qualifiers
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Matches 15; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 93.8%; Pred. No. 1.18+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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Sequence 58 from patent US 5645986.
1151790 17:2472991

    .16
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Unclassified.
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I bases 1 to 16)
West,M.D., Shay,J. and Wright,W.E.
Wethod for screening for agents which increase telomerase activity
in a cell
in a cell
Patent: US 5830644-A 58 03-NOV-1998;
Incation/Qualifiers
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PLORIGENE LIMITED (AU); BRUGLIERA FILIPPA (AU); HOLTON TIMOTHY
ALBERT (AU); MICHAEL MICHAEL ZENON (AU)
Location/Qualifiers
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1.4%; Score 15; DB 1; Length 32;
Best Local Similarity 67.7%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 10; Indels
                                                              .M Unknown.
Unclassified.

Unclassified.

E 1 (bases 1 to 32)

S Chenchik, A., Jokhadze, G. and Bibilashvilli, R.

Methods of assaying differential expression

AL Patent: US 6489455-A 400 03-DEC-2002;

Location/Qualifiers
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Sequence 27 from Patent WO9732023.
AX028843
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       AR259469.1 GI:27309980
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PAT 29-SEP-1999
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                                                                                                                                                                                                                                                                                                                                       Unclassified.

(Dases 1 to 17)

Paoletti,E. Perkus,M.E., Taylor,J., Tartaglia,J., Norton,E.K.,
Paoletti,E., Perkus,M.E., Limbach,K.J., Johnson,G.P., Pincus,S.E.,
Riviere,M., de Taisne,C., Limbach,K.J., Johnson,G.P., Pincus,S.E.,
Cox,M.I., Audonnet,J.-C.Francis. and Gettig,R.Robert.

Modified recombinant vaccinia virus and expression vectors thereof
Patent: Uscation/Qualifiers
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Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T. C-myb ribozymes having 2'-5'-linked adenylate residues Patent: US 5817796-A 1058 06-OCT-1998;
Location/Qualifiers
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1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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                                            Length 16;
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Best Local Similarity 93.8%; Pred. No. 1.18+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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Sequence 235 from patent US 5762938.
AR011362.1 GI:3969352
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/organism="unknown"
/mol_type="unassigned RNA"
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Best Local Similarity 93.8
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Unclassified.
1 (bases I to 16)
1 (bases I to 16)
Nest,M.D., Harley,C.B., Weinrich,S.L., Strahl,C.M., McEachern,M.J.,
Shay,J., Wright,W.E., Blackburn,E.H., Kim,N.W. and Vaziri,H.
Diagnostic methods for conditions associated with elevated cellular
levels of telomerase activity
Patent: US 6551774-A 80 22-APR-2003;
Patent: US 6551774-A 80 22-APR-2003;
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     PAT 20-JUN-2002
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1 (bases 1 to 16)

Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.

Rethod and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 6071 20-MAY-2003;
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1 (bases | Lo 16)
West, M.D., Shay, J., Wright, W. and Blackburn, E.H.
Screening methods to identify inhibitors of telomerase activity
Patent: US 6368789-A 57 09-APR-2002;
Location/Qualifiers
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1.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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6566127.
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Sequence 80 from patent US 6551774.
AR307317.1 GI:31697844
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/organism="unknown"
/mol_type="unassigned DNA"
     16 bp 1
Sequence 57 from patent US 6368789.
AR204607.1 GI:21501976
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Sequence 6071 from patent US
AR328669
AR328669.1 GI:33714477
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Best Local Similarity 93.8<sup>§</sup>
Matches 15; Conservative
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AR328669
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/mol_type="unassigned DNA"

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Unclassified.
Unclassified.
Unclassified.
Unclassified.
I (bases 1 to 17)
Pavco, P. McSwiggen, J., Stinchcomb, D. and Escobedo, J.
Pavco, P. McSwiggen, J. C. the treatment of diseases or conditions
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
related to 18 634638-A 4159 12-FEB-2002;
Location/Qualifiers
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Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
                        Ouery Match 1.4%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 1.2e+02; Matches 15; Conservative 0; Mismatches 1; Indels
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Unclassified.
B. I. (bases 1 to 17)
S. Gut, 1.G., Beelin, K., Lechner, D. and Lehrach, H.
Mutation analysis using mass spectrometry
AL Patent: US 6503110-A 13 07-JAN-2003;
Location/Qualifiers
                                                                                                                                                                                                  Sequence 4159 from patent US 6346398.
AR188671
AR188671.1 GI:20234636
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Sequence 13 from patent US 6503710.
AR271518
AR271518.1 GI:29702938
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/organism="unknown"
/mol_type="genomic DNA"
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AR324524
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AR271518/c
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AR188671
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                                                                                                           1 (bases 1 to 17)
Paoletti, E. and Maki, J.
Alvac poxvirus-rabies compositions and combination compositions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unclassified.

1 (bases 1 to 17)
Robleti,E., Perkus,M.E., Taylor,J., Tartaglia,J., Norton,E.K.,
Raviere,M., de Taisne,C., Limbach,K.J., Johnson,G.P., Pincus,S.E.,
Cox,W.I., Audonnet,J.-C.F. and Gettig,R.R.
NYVAC vaccinia virus recombinants comprising heterologous inserts
Patent: US 5494807-A 27-FEB-1996;
Location/Qualifiers
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Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
C-myb targeted riboaymes
Patent: US 5646042-A 1058 08-JUL-1997;
Locatlon/Qualifiers
1..17
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1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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Sequence 1058 from patent US 5646042.
153317
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Patent: US 5843456-A 52 01-DEC-1998;
Location/Qualifiers
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/organism="unknown"
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 Sequence 52 from patent US 5843456.
AR061027
AR061027.1 GI:5988718
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PAT 27-SEP-2002
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Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Randi, A.M.
Method and reagent for the inhibition of erg
Patent: WO 1088124-A 706 22-NOV-2201;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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Human testis expressed patched like protein
Patent: EP 1229046-A 4088 07-AUG-2002;
Acomica, Inc. (US)
Location/Qualifiers
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                                                                                                                                                                                                                                                           AX422370
Sequence 706 from Patent WO0188124.
AX422370
AX422370.1 GI:21525752
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/db_xref="taxon:9606"
/db_xref="taxon:32630"
/note="oligonucleotide"
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Homo sapiens
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AX422370/c
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Live recombined vaccines injected with adjuvant
Patent: WO 9944633-A 22 10-88P-1999;
MINKE JULES MAARTEN (FR); MERIAL SAS (FR); AUDONNET JEAN CHRISTOPHE
FRANC (FR)
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                                                   Unknown.
Unknown.
Unclassified.
1 (bases 1 to 17)
1 (bases 1 to 17)
Pavob'P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Pavob'P., McSwiggen for the treatment of diseases or conditions
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 666127-A 1926 20-MAY-2003;
Location/Qualifiers
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Unclassified.
I (bases 1 to 17)
I (bases 1 to 17)
Pavco, P., McGwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Pavco, P., McGwiggen, for the treatment of diseases or conditions
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US.656127-A 6656 20-MAY-2003;
Location/Qualifiers
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    .17
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/mol_type="unassigned DNA"

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Sequence 6656 from patent US 6566127.
AR329254
AR329254.1 GI:33715062
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Sequence 22 from Patent WO9944633.
AX018733
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     GI:33710332
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synthetic construct
artificial sequences.
     AR324524.1
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Unknown
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AR329254
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PAT 08-MAY-2003

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SOURCE
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REFERENCE AUTHORS TITLE JOURNAL

FEATURES

RESULT 157 AX502782

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Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Telerman, A., Amson, R. and Tuijnder, M. Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as
                                                                                                    Telerman, A., Amson, R. and Tuijnder, M. Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as
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Sequences involved in phenomena of tumour suppression, tumour
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Molecular Engines Laboratories (FR)
Location/Qualifiers
                                                                                                                                                                    medicines
Patent: WO 03025176-A 1343 27-WAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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Sequence 3832 from Patent W003025175.
AX732198
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Homo sapiens
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Best Local Similarity 93.8
Matches 15; Conservative
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AX736543/c
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AX732198/c
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria, Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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Human testis expressed patched like protein
Patent: EP 1229046-A 4089 07-AUG-2002;
Aeomica, Inc. (US)
Location/Qualifiers
                                                                               17 bp DNA
Sequence 4089 from Patent EP1229046.
AX502782
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Sequence 1343 from Patent WO03025176.
AX722656
AX723656.1 GI:30502999
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Sequence 73 from Patent WO03004526.
AX671628
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Homo sapiens
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Homo sapiens
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DEFINITION ACCESSION VERSION KEYWORDS

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AX723656 LOCUS

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Bynthetic construct
synthetic construct
synthetic construct
artificial sequences.

1 (bases 1 to 18)
Inoko, H., Kagiya, T., Ichihara, T., Matsumura, Y., Moriya, S. and
Nishida, M.
Kit and method for determining HLA type
Patent: WO 0192572-A 1015 06-DEC-2001;
NISSHINBO INDUSTRIES INC, SYSTEM RESEARCH INC, HIDETOSHI INOKO, TAEKO
KAGIYA, TAISUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO
NISHIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAT 27-AUG-2002
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W0 0192572-A/1015
W0 0192572-A/1015
06-DEC-2001
01-JUN-2001 WO 2001JP004662
01-JUN-2000 JP 00P 164798
HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI
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                                                                          1.4%; Score 14.4; DB 1; Length 17; ilarity 93.8%; Pred. No. 1.2e+02; Conservative 0; Mismatches 1; Indels
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C12Q1/68,C12M1/00,C12N15/09,G01N33/53
Description of Artificial Sequence:capture
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/mol_type="unassigned DNA"
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                                                                                                                                                                                                                                                                                                                                                                                         18 bp
Sequence 36 from Patent WO0077250.
AX058584
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WO 0192572-A/1015.
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Best Local Similarity 93.8
Matches 15; Conservative
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PF 01-JU
PR 01-JU
PI HIDET
MATSUMURA,
PI SHOGO
PC C12Q1
CC Descr
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JOURNAL
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VERSION
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
Patent: WO 03025177-A 2133 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
Patent: WO 03040369-A 5321 15-WAY-2003;
Molecular Engines Laboratories (FR)
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1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1;
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Sequence 4252 from Patent WO03040369.
AX760931

    .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Homo sapiens
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AX760931/c
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Unknown.
Unclassified.
1 (bases 1 to 14)
1 (bases 1 to 14)
Gomi,Y., Sunamachi,H., Takahashi,M. and Yamanishi,K.
Method for quality control of an attenuated vericella live vaccine
Patent: US 6653069-A 27 25-NOV-2003;
Patent: US 6653069-A 27 25-NOV-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same Patent: US 5582979-A 436 10-DEC-1996; Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels
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                      1. .14
/organism="Haliotis discus discus"
/orl_type="genomic DNA"
/sub_species="discus"
/db_xref="taxon:91233"
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1.3%; Score 14; DB 1; Lk
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 0;
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Sequence 436 from patent US 5582979.
I31524.
I31524.1 GI:1822315
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1.3%; Score 14; DB
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Matches 14; Conservative 0; Mismatches
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Sequence 27 from patent US 6653069.
AR431517.1 GI:40193621
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/organism="unknown"
/mol_type="unassigned DNA"
location/Qualifiers
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1 (bases 1 to 14)
Weber, J.L.
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Vetigastropoda; Haliotoidea, Haliotidae; Haliotis.

Kideaki, T. and Masahi, S.

Kideaki, T. and Masahi, S.

Method for isolating satellite sequence

L. Patent: JP 2000060559-A, 4 29-FEB-2000;

NATL INST OF AGROSIOLOGICAL RESOUCES

OS Haliotis discus discu
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Bennett, C. Frank., Ackermann, E.J., Swayze, E.E. and Cowsert, L.M. Antisense modulation of survivin expression
Patent: US 6335194-A 235 01-JAN-2002;
Location/Qualifiers
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                      ce 1..18 /organism='Artificial Sequence'.
Location/Qualifiers
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1.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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1.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
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                                                                                                      1..18
/organism="synthetic construct"
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/db_xref="taxon:32630"
     Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
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E32202/c
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OS THOMOS SEQUENCE (human)

No SED-1997 JP 1998516815

PD 11-DEC-2001

PF 30-SEP-1997 JP 1998516815

PF 01-COT-1996 US 08/74334,07-MAY-1997 US 08/852495 PI

MINSTON J THOMAS, ZENTA TSUCHIHASHI, RCGER K WOLFF PC

C07121/04,01201/68,012N15/53,012N15/65,012P21/02 CC

POLY (1201/68,012N15/53,012N15/68,012P21/02 CC

Location/Qualifiers
Polymorphisms and new genes in the region of the human hemochromatosis gene Patent: JP 2001525663-A 13 11-DEC-2001; PROGENTIOR INC
                                                                                                                                                                                                                                        ce 1. .14
/organism='Homo sapiens (human)'.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                         1.3%; Score 14; DB 1; Length 14; 100.0%; Pred. No. 1.1e+02; tive 0; Mismatches 0; Indels
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/organism="Homo sapiens"
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    .14
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

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Best Local Similarity 100.0%
Matches 14; Conservative
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                                         PAT 18-DEC-2003
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Gomi.Y., Sunamachi,H., Takahashi,M. and Yamanishi,K.
Method for quality control of an attenuated vericella live vaccine
Patent: US 6653069-A.7 25-NOV-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa, Chordata, Craniata, Vertebrata; Suteleostomi,
Mammalia; Sutheria, Primates; Catarrhini; Hominidae; Homo.
I (bases I to 14)
Feder,J.N., Krommal,G.S., Lauer,P.M., Ruddy,D.A., Thomas,W.J.,
Tsuchihashi,Z. and Wolff,R.K.
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                                                                                                                                                                                                                                                                                                                                   Length 14;
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Therapeutically useful synthetic cligonuclectides
Patent: Wo 0144465.A 15 ZJ-JUN-2001;
Bioniche Life Sciences Inc. (CA)
Location/Qualifiers
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100.0%; Pred. No. 1.1e+02;
iive 0; Mismatches 0;
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                                     14 bp Sequence 27 from patent US 6653069. AR431517 GI:40193621
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Sequence 15 from Patent WO0144465.
AX175251
AX175251.1 GI:14598619
                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA
                                                                                                                                                                                                                                                               1. .14
/organism="unknown"
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BD084125
BD084125.
JP 200152563-A/13.
Homo sapiens (human)
Homo sapiens
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synthetic construct
artificial sequences.
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AR431517/c
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BD044125.

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BD04125.

Homo sapiens (human)

SM Homo sapiens (human)

SM Homo sapiens (human)

SM Homo sapiens (human)

SM Homo sapiens (human)

SM Homo sapiens (human)

SM Homo sapiens and new genes in the region of the human

BR069NTJOR INC

CHARLE SECTION (human)

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14 bp DNA linear PAI Polymorphisms and new genes in the region of the human hemochromatosis gene.
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1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels
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Gaps

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Query Match 1.3%; Score 14; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 1.46+02; Matches 14; Conservative 0; Mismatches 0; Indels
JOURNAL Patent: US 5817796-A 1855 06-OCT-1998; FEATURES Location/Qualifiers
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/organism="unknown"
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AR047066
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AR047068
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Unclassified.
Unclassified.
1 (bases 1 to 17)
Stinchcomb.D.T., Draper,K., McSwiggen,J. and Jarvis,T.
C-myb ribosymes having 2'-5'-linked adenylate residues
Patent: US 5817796-A 1060 06-OCT-1998;
Location/Qualifiers
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Stinchcomb, D.T., Draper, K., 'McSwiggen, J. and Jarvis, T. C-myb ribozymes having 2'-5'-linked adenylate residues
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                                                                                                                                                                                         Unclassified.

1 (bases 1 to 16)

2 ckstein,F., Ludwig,J. and Beigelman,L.

Nucleic acid catalysts with endonuclease activity

Patent: US 656731-A 336 02-DEC-2003;

Location/Qualifiers
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                                                                                  AR436077 16 bp RNA
Sequence 336 from patent US 6656731.
AR436077
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       14 TATATATATATA
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AR046267/c
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Unclassified.
Unclassified.
1 (bases 1 to 17)
Stinchcomb.D.T., Draper,K., McSwiggen,J. and Jarvis,T.
C-myb ribozymes having 2'-5'-linked adenylate residues
Patent: US 5817796-A 1857 06-OCT-1998;
Location/Qualifiers
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1 (bases 1 to 17)

Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.
C-myb ribozymes having 2'-5'-linked adenylate residues
Patent: US 5817796-A 1859 06-OCT-1998;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.46+02;
Matches 14; Conservative 0; Mismatches 0; Indels
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1.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels
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  AR047064 17 bp DNA Sequence 1857 from patent US 5817796. AR047064.1 GI:5968529
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REFERENCE AUTHORS TITLE JOURNAL FEATURES

RESULT 180 AR074719/c LOCUS

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AUTHORS TITLE JOURNAL FEATURES

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PAT 07-0CT-1997
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1 (bases 1 to 17)
Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.
C-myb targeted ribozymes
Patent: US 5646042-A 1855 08-JUL-1997;
Location/Qualifiers
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Unclassified.
1 (bases 1 to 17)
Stinchcomb.D.T., Draper,K., McSwiggen,J. and Jarvis,T.
C-myb targeted ribozymes
Patent: US 5646042-A 1857 08-JUL-1997;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.46+02;
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Matches 14; Conservative 0; Mismatches 0;
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Sequence 1859 from patent US 5646042.
154118 GI:2475321
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I54118
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I54116
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 PAT 29-SEP-1999
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Unclassified.

E 1 (bases 1 to 17)

S Morgante,M. and Vogel,J.Marie.
Compound microsatellite primers for the detection of genetic polymorphisms
Location/Qualifiers

1. 17

/mol_type="unassigned DNA"
/mol_type="unassigned DNA"
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Unclassified.
1 (bases 1 to 17)
2 stinchcomb.D.T. Draper,K., McSwiggen,J. and Jarvis,T.
C-myb targeted ribozymes
Patent: US 5646042-A 1060 08-JUL-1997;
Location/Qualifiers
                                                                                                                      (bases 1 to 17)
Stinchcomb.D.T., Draper.K., McSwiggen,J. and Jarvis,T. C-myb ribozymes having 2'-5'-linked adenylate residues Patent: 18 5817796-A 1861 06-OCT-1998,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.3%; Score 14; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 14; Conservative 0; Mismatches 0; Indels
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   linear
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100.0%; Pred. No. 1.4e+02;
tive 0; Mismatches 0;
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153319
153319.1 GI:2474522
 AR047068 17 bp DNA Sequence 1861 from patent US 5817796. AR047068
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 16 from patent US 5955276.
AR074719
                                                                                                                                                                                                                               /mol_type="unassigned DNA"
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/organism="unknown"
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                                            AR047068.1 GI:5968533
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Best Local Similarity 100.0
Matches 14; Conservative
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Unclassified.
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153319/c
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PAT 29-SEP-1999
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synthetic construct
artificial sequences.

1 (bases 1 to 17)
Holton, T.A., Cornish, B.C., Kovacic, F., Tanaka, Y. and Lester, D.R.
Genetic sequences encoding flavonoid pathway enzymes and uses
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1 (bases 1 to 17)

2tinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.

C-myb ribozymes having 2-5'linked adenylate residues

Patent: US 5817796-A 874 06-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.3%; Score 13.8; DB 1; Length 17; Best Local Similarity 88.2%; Pred. No. 1.4e+02; Matches 15; Conservative 0; Mismatches 2; Indels
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Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
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Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels
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INTERNATIONAL FLOWER DEVELOPMENTS Pty. Ltd
Location/Qualifiers
                                                                                                                                                                                         A28997 17 bp DNA primer sequence 4 from patent EP0522880. A28997

    1. 17
    forganism="synthetic construct"
|mol type="unassigned DNA"
|db_xref="taxon:32630"

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Sequence 874 from patent US 5817796.
AR046081
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AR057784/c
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A28997
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
C-myb targeted ribozymes
Patent: US S646042-A 1861 08-JUL-1997;
Location/Qualifiers
                      Unknown.
Unclassified.
Unclassified.
1 (bases 1 to 17)
Stinchcomb.D.T., Draper,K., McSwiggen,J. and Jarvis,T.
C-myb targeted ribozymes
Patent: US 5646042-A 1859 08-JUL-1997;
Location/Qualifiers
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1.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Sequence 5823 from Patent W003040369.
AX762502
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/organism="unknown"
/wol_type="unassigned DNA"

    .17
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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Homo sapiens
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IS4120.1 GI:2475323
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AX762502
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I54120
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Methods and products related to genotyping and DNA analysis.
BD241082 BB241082.1 GI:33050852
UP 2002525127-A/29.
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Unknown.
Unclassified.
1 (bases I to 17)
1 (bases I to 17)
Manoharan, M. and Maier,M.A.
Compounds, processes and intermediates for synthesis of mixed backbone oligomeric compounds
backbone oligomeric compounds
backbone oligomeric compounds
backbone oligomeric - 27-MAR-2001,
Iocation/Qualifiers
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Matches 15; Conservative 0; Mismatches 2; Indels
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Length 17;
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                              2; Indels
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Unknown.

Unclassified.

E (bases 1 to 17)

S Cech, T.R. and Nakamura, T.

Telomerase 6309867-A 132 30-OCT-2001;

AL Patent: US Location/Qualifiers

Location/Qualifiers

17
Query Match
1.3%; Score 13.8; DB 1;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2;
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Sequence 132 from patent US 6309867.
AR175846
AR175846.1 GI:17917145
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/mol_type="unassigned DNA"
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Sequence 5 from patent US 6207819.
AR141074. GI:14483570
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BD241082/c
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AR141074
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1 (bases 1 to 17)

Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
Draper,K.G.
Ribozyme treatment of diseases or conditions related to levels of
intercellular adhesion molecule-1 (ICAM-1)
Patent: US 6132567-A 1988 17-OCT-2000;
Location/Qualifiers
                                                                                                                                                                                                                                                          Gaps
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                                                 Unknown.
Unclassifted.
1 (bases 1 to 17)
Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
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                                                                                                      Draper K.G.
Intercellular adhesion molecule-1 (ICAM-1) ribozymes
Patent: US 5837542-A 1988 17-NOV-1998;
Location/Qualifiers
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1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
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1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
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1 (bass 1 to 17)

2 cech, T.R. and Lingner, J.

Telomerase
Patent: US 6093809-A 132 25-JUL-2000;

Location/Qualifiers
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Sequence 132 from patent US 6093809.
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/mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
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/organism="unknown"
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       AR057784.1 GI:5983361
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Methods and products related to genotyping and DNA analysis.
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Homo sapiens (human)
Homo sapiens
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1 (bases 1 to 17)
1 anders, J.E., Jordan, B., Housman, D.E. and Charest, A. Methods and products related to genotyping and DNA analysis Patent: JP 2002255127-A 564 13-AUG-2002;

NASSACHUSETTS INSTITUTE OF TECHNOLOGY
OS Homo sapiens (human)

PN JP 200255127-A/564

PN JP 2002525127-A/564

PR 25-SEP-1999 UP 2000572407

PR 25-SEP-1999 US 60/101757
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F 24-SEP-1999 JP 2000572407
R 25-SEP-1999 US 60/101757
I JOGIN E LANDERS, BARBARA JORDAN, DAVID E HOUSMAN, ALAIN CHAREST P
CIENTS/09, CI2Q1/68, GOIN33/53, GOIN33/566, GOIN33/56, GOIN33/58, GOIN37/00, PC
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Best Local Similarity 88.2%; Pred. No. 1.46+02;
Matches 15; Conservative 0; Mismatches 2; Indels
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/organism="Homo sapiens"
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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (basea 1 to 17)

2 Landers, J.E., Jordan, B., Housman, D.E. and Charest, A.

2 Methods and products related to genotyping and DNA analysis

2 Methods and products related to genotyping and DNA analysis

3 Homo sapiens (human)

3 Homo sapiens (human)

4 P 2002525127-A38

5 Homo sapiens (human)

5 P 24-SEP-1999 JP 200572407

7 PR 25-SEP-1999 US 60/101757

8 JOHN B LANDERS, BARBARA JORDAN, DAVID E HOUSMAN, ALAIN CHAREST PC
   Homo sapiens (human)

Mino sapiens

Eukaryorata, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;

Eukaryorata, Metazoa, Chordata, Catarrhini; Hominidae, Homo.

El (bases 1 to 17)

I (bases 1 to 17
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Methods and products related to genotyping and DNA analysis FH
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Matches 15; Conservative 0; Mismatches 2; Indels
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    .17
    /organism="Homo sapiens"
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JP 2002525127-A/38.

Homo sapiens (human)

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PI JOHN E LANDERS, BARBARA JORDAN, DAVID E HOUSMAN, ALAIN CHAREST PC C12N15/09, C12Q1/68, G01N33/53, G01N33/566, G01N33/58, G01N37/00, PC
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A61X37/02,
(C12NS/00,C12R1:91)
Regulation of repressor genes using nucleic acid molecules FH
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PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MCHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC C12P21/02,
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1 (bases 1 to 17)
Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Pequlation of repressor genes using nucleic acid molecules Patent: JP 2002541795-A 2340 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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Regulation of repressor genes using nucleic acid molecules.
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forganism="Homo sapiens"
forganism="Homo sapiens"
fmol type="genomic DNA"
fb_xref="texon:9606"
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Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
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1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
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    .17
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10-DEC-2002
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BD255193 17-JUL-2003
Regulation of repressor genes using nucleic acid molecules.
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PR 12-ARR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61B43/00,C12NS/10, PC
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1 (bases 1 to 17)

1 bases 1 to 17)

1 bases 1 to 17)

1 class 1 to 17)

1 class 2 delty.u., Zwick,M., Pavco,P. and Mcswiggen,J.

1 class 2 delty.u., Zwick,M., Pavco,P. and Mcswiggen,J.

1 class 2 delty.genessor genes using nucleic acid molecules patent: JP 2002541795-A 2986 10-DEC-2002;

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2 class 2 delty.genessor genes using nucleic acid molecules patent: JP 2002541795-A/2986

2 class 2 delty.genessor genessor g
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Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T. C-myb targeted ribozymes
Patent: 18 5646642-A 874 08-JUL-1997;
Location/Qualifiers
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/wol_type="unassigned DNA"
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/organism="unidentified"
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/db_xref="taxon:32644"
                                                                                                 BD255193
BD255193.1 GI:33064963
JP 2002541795-A/2986.
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IS3133.1 GI:2474336
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1 (bases I to 17)
1 (bases I to 17)
Manoharan,M. and Maier,M.A.
Compounds, processes and intermediates for synthesis of mixed backbone oligomeric compounds
backbone oligomeric compounds
backbone 16 462184.A. 5 08-OCT-2002;
Patent: Uscation/Qualifiers
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                                                                                                   Query Match 1.3%; Score 13.8; DB 1; Length 17; Best Local Similarity .88.2%; Pred. No. 1.46+02; Matches 15; Conservative 0; Mismatches 2; Indels
Patent: US 6346398-A 6049 12-FEB-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                             Unclassified.

1 (bases 1 to 17)

Kurz, M., Lobse, P. and Wagner, R.
Peptide acceptor ligation methods
Patent: US 6429300-A 23 06-AUG-2002;

Location/Qualifiers
                                    1. .17
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                      17 bp | Sequence 23 from patent US 6429300.
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AR236087
AR236087.1 GI:27279786
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(CE I (bases 1 to 17)

DRS Parco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.

DRS Parco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.

Enthod and reagent for the treatment of diseases or conditions

Enthod and reagent for the treatment of diseases or conditions

Telated to levels of vascular endothelial growth factor receptor

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RNAL Patent: US 6346398-A 647

Location/Qualifiers

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1 (bases 1 to 17)

Pavoo, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.

Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
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Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.

Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6346598-A 2550 12-FEB-2002;

Location/Qualifiers
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Best Local Similarity 89.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
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Sequence 6047 from patent US 6346398.
AR190559
AR190559.1 GI:20236524
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Sequence 6049 from patent US 6346398.
AR190561 GI:20236526
                                                       AR187062
Sequence 2550 from patent US 6346398.
AR187062
AR187062.1 GI:20233027

    17 / organism="unknown"
/mol_type="unassigned DNA"

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1 CTTTTTTTTTTTTTTT 17
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S Gu,Y. and Shannon,M.E.

RAI Discorns of human pregnancy-associated protein-E

Tosforms of human pregnancy-associated protein-E

Location/Qualifiers

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AR433962 GI:40196805
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Sequence 384 from patent US 6656700.
AR433961.1 GI:40196804
1. .17
/organism="unknown"
/mol_type="unassigned RNA"
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1 (bases 1 to 17)
2 (bases 1 to 17)
Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
Pavco,P., McSwiggen, or the treatment of diseases or conditions
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 1074 20-MAY-2003;
Location/Qualifiers
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Unclassified.
1 (bases 1 to 17)
Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
Method and reagent for the treatment of diseases or conditions
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 2884 20-MAY-2003;
Location/Qualifiers
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1 (bases 1 to 17)

1 (bases 1 to 17)

Parco.P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.

Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 2886 20-MAY-2003;

Location/Qualifiers
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                  17 bp RNA
AR223672
AR323672 GI:33709480
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Sequence 2884 from patent US 6566127.
AR325482
AR325482.1 GI:33711290
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/organism="unknown"
/wol_type="unassigned RNA"
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AR325482
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Indels
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Gu, Y. and Shannon, M.E.
Isoforms of human pregnancy-associated protein-E
Patent: US 6656700-A 389 02-DEC-2003;
Location/Qualifiers
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Sequence 389 from patent US 6656700.
AR433966.1 GI:40196809
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
 Mismatches
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Sequence 60 from Patent WO0211674.
AX578222
AX578222.1 GI:27647424
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/organism="unknown"
/mol_type="genomic DNA"
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                                1798 GTGTGTGTGTGTA 1814
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AX578222/c
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AR433966
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llarity 88.2%; Pred. No. 1.4e+02;
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Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
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1 (bases 1 to 17)

10, Y. and Shannon, M.E.

1soforms of human pregnancy-associated protein-E

Patent: US 6656700-A 388 02-DEC-2003;

Location/Qualifiers
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Gu,Y. and Shannon,M.E.

Isoforms of human pregnancy-associated protein-E
Patent: US 6656706-A 387 02-DEC-2003;

Location/Qualifiers
                                                                                            1 (bases 1 to 17)

Gu, Y. and Shannon, M.E.
Isoforms of human pregnancy-associated protein-E
Patent: US 6656700-A 386 02-DEC-2003;
Location/Qualifiers
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AR433965.
AR433965.1 GI:40196808
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/mol_type="genomic DNA"
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/mol_type="genomic DNA"
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/mol_type="genomic DNA"
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      AR433963.1 GI:40196806
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AR433964
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PAT 29-SEP-1999
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1 (bases 1 to 15)

1 (bases 1 to 15)

Shay, J. and Wright, W.E. Method for screening for agents which increase telomerase activity in a cell
            Shannon,M., Gu,Y. and Nguyen,C.T.
Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Telerman, A., Amson, R. and Tuijnder, M.
Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
Patent: WO 03025177-A 1096 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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Homo sapiens
Eukaryots metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
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AX735506.1 GI:30514783
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Patent: EP 1281758-A 5257 05-FEB-2003;
Acomica, Inc. (US)
Location/Qualifiers
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Location/Qualifiers
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/db_xref="taxon:9606"
                                                                                                                                          organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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AX735506
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                                                                                                                        Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)
Patent: WO 0211674-A 60 14-FEB-2002;
RIBOZYME PHARMACENTGALS, INC. (US); Syntex (U.S.A.) LLC (US);
Thompson, James (US)
Location/Qualifiers
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Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stinchcomb, D.T., Dudycz, L.W., Chowrira, B., Grimm, S., Direnzo, A., Karpeisky, A., Draper, K.G., Kisich, K., Matulic-Adamic, J., Mcswiggen, J.A., Modak, A., Pavco, P., Beigelman, L., Sullivan, S.M., Sweedler, D., Thompson, J.D., Tracz, D., Usman, N., Wincott, F.E. and Woolf, T.
                                                                                       Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.B.
and Grupe,A.
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Sequence 1962 from Patent EP1260586.
AX634823
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RIBOZYME PHARMACEUTICALS, INC. (US)
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/mol_type="unassigned RNA"
/db_xref="taxon:32644"
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1 (bases 1 to 15)
West,M.D., Harley,C.B., Weinrich,S.L., Strahl,C.M., McEachern,M.J.,
Nest,M.D., Harley,C.B., Weinrich,S.L., Kim,N.W. and Vaziri,H.
Shay,J., Wright,W.B., Blackburn,E.H., Kim,N.W. and Vaziri,H.
Diagnostic methods for conditions associated with elevated cellular
levels of telomerase activity
Patent: US 6551774-A 79 22-APR-2003;
Patent: US 6551774-A 79 22-APR-2003;
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                                                                                  1 (bases 1 to 15)
West, M.D., Shay, J., Wright, W. and Blackburn, E.H.
Screening methods to identify inhibitors of telomerase activity
Patent: US 6368789 - 51 09-APR-2002;
Location/Qualifiers
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I (bases 1 to 15)
Garner, H. R., Wren, J. D., Minna, J. D. and Fondon, J. W. III.
Polymorphic repeats in human genes
Patent: US 6472154-A 83 29-OCT-2002;
Location/Qualifiers
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1.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
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Sequence 83 from patent US 6472154.
AR241795.
AR241795.1 GI:27287607
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Sequence 79 from patent US 6551774.
AR307316
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/mol_type="genomic DNA"

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/organism="unknown"
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/organism="unknown"
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West, M.D., Shay, J., Wright, W., Blackburn, E.H. and McEachern, M.J.
Telomerase activity assays for diagnosing pathogenic infections
Patent: US 5695932-A 51 09-DEC-1997;
Location/Qualifiers
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West,M.D., Harley,C.B., Strahl,C.M., McEachern,M.J., Shay,J.,
Wright,W.E., Blackburn,E.H. and Vaziri,H.
Therapy and diagnosis of conditions related to telomere length
and/or telomerase activity
Patent: US 5645986-A 52 08-UUL-1997;
Location/Qualifiers
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1.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
                  Query Match 1.3%; Score 13.4; DB 1; Length 15; Best Local Similarity 93.3%; Pred. No. 1.3e+02; Matches 14; Conservative 0; Mismatches 1; Indels
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Sequence 51 from patent US 6368789.
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Sequence 51 from patent US 5695932.
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/mol_type="unassigned DNA"
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IS1784
IS1784.1 GI:2472985
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Unclassified.
1 (bases 1 to 17)
Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.
Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.
C-myb ribozymes having 2'-5'-linked adenylate residues
Patent: US 5817796-A 1060 06-OCT-1998;
Location/Qualifiers
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Unclassified.
Unclassified.
1 (bases 1 to 17)
Stinchocomb.D.T., Draper,K., McSwiggen,J. and Jarvis,T.
C-myb targeted ribozymes
Patent: US 5646042-A 1060 08-JUL-1997;
Location/Qualifiers
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                                        Unknown.
Unclassified.
E 1 (bases 1 to 16)
& Schetein,F., Ludwig,J. and Beigelman,L.

Nucleic acid catalysts with endonuclease activity
(AL Patent: US 6656731-A 185 02-DEC-2003;
Location/Qualifiers
                                                                                                                                                                                                                            1.3%; Score 13.4; DB 1; Length 16; ilarity 93.3%; Pred. No. 1.5e+02; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
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/organism="unknown"
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 GI:40199010
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Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J. McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J. McWinggen, For the treatment of diseases or conditions related to levels of vascular endochelial growth factor receptor Patent: US 656127-A 6067 20-MAY-2003;
Location/Qualifiers
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                   Indels
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Method for detecting gram-positive bacteria
Patent: WO 02097126-A 37 05-DEC-2002;
Hain Lifeschience GmbH (DE)
Location/Qualifiers
   Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1;
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/organism="synthetic construct"
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Sequence 6067 from patent US 6566127.
AR328665
AR328665.1 GI:33714473
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Sequence 185 from patent US 6656731.
AR435926
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Sequence 37 from Patent W002097126.
AX663411
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synthetic construct
artificial sequences.
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AR435926/c
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AX663411
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RESULT 231
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PAT 20-DEC-2002
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1 (bases 1 to 15)
Garner, H.R., Wren, J.D., Minna, J.D. and Fondon, J.W. III.
Polymorphic repeats in human genes
Patent: US 6472154-A 83 29-OCT-2002;
Location/Qualifiers
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1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels
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1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels
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Unknown.
Unclassified.
3 1 (bases 1 to 13)
S. Schroth,G.P., Bruice,T.W. and Suh,Y.J.
Nucleic acid ligand interaction assays
An Patent: US 6420109-A 41 16-JUL-2002;
Location/Qualifiers
              Chroth, G.P., Bruice, T. Mayne, and Suh, Y.J.
Schroth, G.P., Bruice, T. Mayne, and Suh, Y.J.
Nucleic acid ligand interaction assays
Patent: US 6355428-A 41 12-MAR-2002;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 0;
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Sequence 41 from patent US 6420109.
AR218382 AR218382.1 GI:23319079
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1 (Dases I to 13)

Morgante, M. and Vogel, J.Marie.
Compound microsatellite primers for the detection of genetic polymorphisms
Polymorphisms
Patent: US 5955276-A 15 21-SEP-1999,
Location/Qualifiers
                                                                                                                                                                                                                                                                               1 (bases 1 to 13)
Morgante, M. and Vogel, J.Marie.
Compound microsatellite primers for the detection of genetic
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1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels
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Patent: US 5955276-A 13 21-SEP-1999;
Location/Qualifiers
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Sequence 41 from patent US 6355428.
AR199332.1 GI:20249406
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Sequence 13 from patent US 5955276.
AR074716
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                        1813 TATATATATATAT 1827
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REFERENCE AUTHORS TITLE

RESULT 232 AR074718 LOCUS

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heterogeneous mixtures of oligonucleotide probes
Patent: US 6309824-A 2 30-OCT-2001;
Location/Qualifiers
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                                                       /organism="unknown"
/mol_type="unassigned DNA"
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AR175436/c
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Unclassified.

I (bases I to 15)

Drmanac, R. T., Drmanac, S., Hou, A. and Hauser, B.

Methods for sequencing repetitive sequences and for determining the order of sequence subfragments

Patent: US 6297006-A 1 02-00T-2001,

Location/Qualifiers
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Drmanac, R.T., Drmanac, S., Hou, A. and Hauser, B.
Methods for sequencing repetitive sequences and for determining the order of sequence subfragents
Patent: US 6297006-A 2 02-0CT-2001;
Location/Qualifiers
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Drmanack.T.
Methods for analyzing a target nucleic acid using immobilized
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1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels
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    /mol_type="unassigned DNA"

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Sequence 2 from patent US 6297006.
AR170920.
AR170920.1 GI:17909870
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Sequence 1 from patent US 6297006.
AR170919
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AR175435
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Unclassified.
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1 (bases 1 to 15)

Drmanac,R.T.
Methods for analyzing a target nucleic acid using immobilized heterogeneous mixtures of ollgonucleotide probes
Patent: US 6309824-R. 3 30-OCT-2001;

Location/Qualifiers
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1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.56+02;
Matches 13; Conservative 0; Mismatches 1; Indels
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Query Match
1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels
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1 (bases 1 to 15)
Stinchromb,D.T., Draper,K.G. and McSwiggen,J.
Rel a targeted ribozymes
Patent: US 5558780-A 121 19-AUG-1997;
Location/Qualifiers
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Method and reagent for inhibiting the expression of disease related
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Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
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Unclassified.

Unclassified.

Inclassified.

S. Ford, J. and Yeung, G. Chemokine receptor obtained from a cDNA library of fetal liver-spleam in 19.00 fetal live
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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 92.9%; Pred. No. 1.5e+02;
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RIBOZYME PHARMACEUTICALS, INC. (US)
: Location/Qualifiers
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Sequence 3025 from Patent EP1260586.
AX635886

    .15
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

                                                                                                                                                                                                                                                                                                             Sequence 10 from patent US 6472173.
/organism="unknown"
/wol_type="genomic DNA"
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Ford, J. and Yeung, G.
Chemokine receptor obtained from a cDNA library of fetal liver-spleen
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Unclassified.
3 1 (bases 1 to 15)
5 1 (nonboomb, D.T., Draper, K.G. and McSwiggen, J.
5 Stinchcomb, D.T., Draper, K.G. and McSwiggen, J.
Rel a targeted ribozymes
Rel a targeted ribozymes
Location/Qualifiers
Location/Qualifiers
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Stinchcomb, D.T., Draper, K.G. and McSwiggen, J.
Rel a targeted ribozymes
Patent: US 5658780-A 194 19-AUG-1997;
Location/Qualifiers
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100.0%; Pred. No. 1.5e+02;
tive 0; Mismatches 0;
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Sequence 310 from patent US 5658780.
161756.
161756.1 GI:2479704
                                                         15 bp DNA Sequence 194 from patent US 5658780.
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/mol_type="unassigned DNA"
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Location/Qualifiers
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Sequence 9 from patent US 6472173.
AR242246
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I61640.1 GI:2479588
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1 (bases 1 to 16)

Kutyavin,I.v., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.

Covalently linked oligonucleotide minor grove binder conjugates

Patent: US 5801155-A 2 01-SEP-1998;
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Unclassified.
1 (bases 1 to 16)
Bazile,D., Emile,C., Helene,C. and Spenlehauer,G.
Bazile,D., Emile,C., Helene,C. and Spenlehauer,G.
Nucleic acid-containing composition, its preparation and use
Patent: US 5856435-A 15 05-JAN-1999;
Location/Qualifiers
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1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
                                     linear
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                                                                                                                                                         Unclassified.
Unclassified.
(Dases 1 to 16)
Eckstein,F., Ludwig,J. and Beigelman,L.
Nucleic acid catalysts with endonuclease activity
Patent: Ug 6656731-A 117 02. DEC-2003;
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                                       RNA
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Sequence 117 from patent US 6656731.
AR435658
AR435858.1 GI:40198942
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 15 from patent US 5856435.
                                                                                                                                                                                                                                                                                                        /mol_type="unassigned RNA"
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Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stinchcomb, D.T., Dudycz, L.W., Chowrira, B., Grimm, S., Direnzo, A., Karpelsky, A., Draper, K.G., Kisch, K., Matulic-Adamic, J., Moswiggen, J.A., Modak, A., Pavco, P., Beigelman, L., Sullivan, S.W., Sweedler, D., Thompson, J.D., Tracz, D., Usman, N., Wincotc, F.E. and
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RIBOZYME PHARMACEUTICALS, INC. (US)
                                                                                    AX636032 15 bp RN
Sequence 3171 from Patent EP1260586.
AX636032
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1.2%; Score 1s; us Sest Local Similarity 100.0%; Pred. No. 1.5% Matches 13; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="unidentified"
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AX636075/c
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/organism="unknown"

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RESULT 251
AR104584/c
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Unknown.
Unknown.
Unclassified.
1 (bases 1 to 16)
Cook, P.D. and Sanghvi, Y.S.
Nuclease resistant, pyrimidine modified oligonucleotides that detect and modulate gene expression detect and modulate gene expression
Patent: US 5614617-A 36 25-MR-1997,
Location/Qualifiers
JP 2000060559-A/28.
Haliotis discus discus
Haliotis discus Haliotoidea; Haliotidae; Haliotis.
Verigastropoda; Haliotoidea; Haliotidae; Haliotis.

I (Lases I to 16)
Haleaki, T. and Massahi, S.
Hadeaki, T. and Massahi, S.
Hadeaki, T. and Massahi, S.
Hadeaki, T. and Massahi, S.
Method for isolating satellite sequence
Patch of 2000060559-A 28 29-FEB-2000;
NATL INST P AGRONOLOGICAL RESOUCES
NATL INST P AGRONOLOGICAL RESOUCES
NATL INST P AGRONOCOSS9-A/28
PD 29-FEB-2000
PP 18-AUG-1998 JP 1998232153
                                                                                                                                                                                                                                                                                                                                         ce 1.16 / Organism='Haliotis discus discus'.
Location/Qualifiers
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1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
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/organism="Haliotis discus discus"
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11arity 87.5%; Pred. No. 1.7e+02;
Conservative 0; Mismatches 2;
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C12N15/09, C12Q1/68, C12N15/00
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Sequence 36 from patent US 5614617.
138676
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138682
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Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2;
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1.2%; Score 12.8; DB 1;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2;
                                               Query Match
1.2%; Score 12.8; DB 1;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2;
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Patent: US 6309867-A 131 30-OCT-2001;
Location/Qualifiers
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Telomerase
Patent: US 6093809-A 131 25-JUL-2000;
Location/Qualifiers
1. 16
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/organism="unknown"
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           /mol_type="unassigned DNA"
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1 (bases 1 to 16)
Cech, T.R. and Nakamura, T.
                                                                                                                                                                                                                                                                                                                                                                                     Unclassified.
1 (bases 1 to 16),
Cech, T.R. and Lingher, J.
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RESULT 252
AR175845/c
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PAT 13-MAY-1997

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PAT 13-MAY-1997

RESULT 253 B32226/c LOCUS DEFINITION ACCESSION VERSION

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PAT 17-AUG-2003
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Best Local Similarity 97.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
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1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
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Sequence 6072 from patent US 6566127.
AR328670
AR328670.1 GI:33714478
                                                                                                                                                                                                                                                                                                      / Unknown.
Unclassified.
1 (bases 1 to 16)
2 I (bases 1 to 16)
S Kurz, M. Lonse, P. and Wagner, R.
Peptide acceptor ligation methods
AL Patent: US 6429300-A 22 06-AUG-2002;
Location/Qualifiers
                                                                                                                                                                        16 bp |
Sequence 22 from patent US 6429300.
AR222462
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Sequence 2 from patent US 6486308.
AR257437
AR257437.1 GI:27307448
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            1865 TTTTTTTTTTTT 1880
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1 (bases 1 to 16)
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AR328670
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AR257437
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Kutyavin, I.V., Lukhtanov, E.A., Gamper, H.B. and Meyer, R.B. Jr.
Covalently linked oligonucleotide minor groove binder conjugates
Patent: US 6426408-A 2 30-JUL-2002;
Location/Qualifiers
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1 (bases 1 to 16)
Cook, P.D. and Sanghvi, Y.S.
Cook, P.D. and Sanghvi, Y.S.
Nuclease resistent, pyrindine modified oligonucleotides that detect and modulate gene expression
Patent: US 5614617-A 42 25-MAR-1997;
Location/Qualifiers
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Cook, P.D. and Sanghvi, Y.S.
Nuclease resistant, pyrimidine modified oligonucleotides that detect and modulate gene expression
Patent: uS 5614617-A 60 25-MAR-1997;
Location/Qualifiers
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1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
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/mol_type="unassigned DNA"
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/mol_type="genomic DNA"
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Nucleoside derivatives with photo-unstable protective groups
Patent: WO 0061594-A 2 19-OCT-2000,
DEUTSCHES KREBSFORSCH (DE) ; BEIER MARKUS (DE) ; HOHEISEL JOERG (DE)
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Personal gene library
Parsonal gene library
Patent: EP 1113080-A 5 04-JUL-2001;
Wang, Xiao Bing (US); Morisawa, Shinkatsu (JP)
Wang, Location/Qualifiers
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87.5%; Pred. No. 1.7e+02;
tive 0; Mismatches 2;
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    16
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    /db xref="taxon:32630"
    /noTe="Oligonuclectid"

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Sequence 9 from Patent WO0163282.
AX235176
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Sequence 5 from Patent EP1113080.
AX135448 GI:14271796
                                                                16 bp
Sequence 2 from Patent WO0061594,
AX039049
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AX135448/c
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AX039049/c
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Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 6072 20-MAY-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unclassified.

1 (bases 1 to 16)
Pavco.P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
Pavco.P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 6074 20-MAY-2003;
Location/Qualifiers
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B 1 (Dases 1 to 16)
S Eckstein,F., Ludwig,J. and Beigelman,L.
Nucleic actalysts with endonuclease activity
Nucleic actalysts with endonuclease activity
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Location/Qualifiers
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Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
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Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
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Sequence 6074 from patent US 6566127.
AR328672
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6656731.
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    /organism="unknown"
    /mol_type="unassigned RNA"

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Sequence 522 from patent US 6
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/organism="unknown"
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AR436263.1 GI:40199347
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BD167414.1 GI:27873226
JP 2002211954-A/2.
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No Up 2001186882-A/5

PN JP 2001186882-A/5

PD 10-JUL-2001

PF 17-NOV-2000 JP 2000350702

PR 01-DEC-1999 US 60/168297,09-NOV-2000 US 09/708493 PI

XIAOBING WANG

PC C12N1S/09,C12N1S/09,C12M1/00,C12Q1/68,C12N1S/00,C12N1S/00 CC

Strandedness: Single;

CC Personal gene library

FH Key Location/Qualifiers

FT Source Location/Qualifiers

FT FOURCE LOCATION CONTINIENTY

PT SOURCE LOCATION CONTINIENTY
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                                                                                   Cuzin,M., Peltie,P., Fontecave,M., Decout,J.L. and Dueymes,C. Analysis of biological targets using a biochip comprising a flucrescent marker Patent: WO GIVES A 90-AUG-2001; COMMISSARIAT A L'ENERGIE ATOMIQUE (FR)
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Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
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Patent: JP 2001166882-A 5 10-JUL-2001;
AIAOBING WANG, SHINKATSU MORISAWA
OS Unidentified
PN JP 2001186882-A/5
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PP 10-NOV-2000 JP
PR 01-DEC-1999 US 60/168297,09-NOV-2000 US
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Location/Qualifiers
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BD167413/c
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VERSION
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BD016420/c
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            ORGANISM
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unclassified.

unclassified.

loases 1 to 16)

Schamtza H., Tanga, M., Cba, M., Yamakawa, K. and Takagi, K.

Surface-roughened slide glass and method of analyzing biological
substance using the same

L. Patent: JP 2002211954-A 2 31-JUL-2002;

TOYO KOHAN CO LID

OS Artificial Sequence
PN JP 2002211954-A/2
PP 31-JUL-2002
PP 31-JUL-2002
PP 30-OCT-2001 JP 2001332778
PI HIROSHI OKAMURA, MICHIFUMI TANGA, MITSUVOSHI OBA, KAORU YAWAKAWA,

PI KENICHI TAKAGI

PC CO3C15/00, CO3C17/245, C12M1/00, C12N11/14, C12N15/09,
BD167413.1 GI:27873225

Unidentified

unidentified

unidentified

unclassified.

Is (bacer in the series of the se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OS Artificial Sequence
DN JP 2002211954-A/1
PD 31-UTU-2002
PF 31-UTU-2002
PF HIROSHI OKAMURA,MICHIFUMI TANGA,MITSUYOSHI OBA,KAORU YAMAKAWA,
PI HIROSHI DAKAGI
PC C03C15/00,C03C17/245,C12M1/00,C12N11/14,C12N15/09,C12N15/09,CC C12Q1/68,C12N13/53,G01N37/00,C12N15/00,C12N15/00,CC Surface-roughened Slide glass and method of analyzing CC biological substance
CC using the same
CC using the same
FH Key
FH Source
FT Source
FT Source
FT
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Surface-roughened slide glass and method of analyzing biological
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PC 030215/00,C03C17/245,C12M1/00,C12N11/14,C12N15/09,(0)

PC 010201/60,C03C17/245,C12M1/00,C12N15/00,C12N15/00

Surface-roughened slide glass and method of analyzing biological substance

C using the same Location/Qualifiers

FH Key Location/Qualifiers

FT source /organism='Artificial Sequence'.
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1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity. 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels

    .16
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/db_xref="taxon:32644"
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Query Match
1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels

1865 TITITATITITE 1880

16 TTTTTTTTTTTTT 1

1. .16 /organism="unidentified" /mol_type="genomic DNA" /db_xref="taxon:32644"

Location/Qualifiers

source

FEATURES

linear

AR046265 17 bp DNA Sequence 1058 from patent US 5817796. AR046265 GISSOF
DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 269 AR046265 LOCUS

Unclassified. Unknown.

REFERENCE AUTHORS TITLE JOURNAL FEATURES

source

/mol_type="unassigned DNA"

1811 TGTATATATATATA 1826

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2 TITATATATATACA 17

/organism="unknown"

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                                                                                                                                                              Thompson, J., Mcswiggen, J., Mckenzie, T., Ayers, D., Szymkowski, D.E. and Grupe, A.
Method and treagent for the inhibition of calcium activated chloride channel 1 (clca.1)
Patent: WO 0211674-A 60 14-FEB-2002;
RIBOZYME PHARMAGENTICALS, INC. (US); Syntex (U.S.A.) LLC (US);
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Unclassified.
1 (Dases 1 to 14)
West, M.D., Shay, J. and Wright, W.E.
Method for screening for agents which increase telomerase activity
PAT 10-JAN-2003
                                                                                    Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Unclassified.
1 (bases 1 to 14)
West,M.D., Harley,C.B., Strahl,C.M., McBachern,M.J., Shay,J.,
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Best Local Similarity 87.5%; Pred. No. 1.88+02;
Matches 14; Conservative 0; Mismatches 2; Indels
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1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels
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Patent: US 5830644-A 57 03-NOV-1998;
Location/Qualifiers
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Sequence 57 from patent US 5645986.
IS1789
IS1789.1 GI:2472990
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Sequence 57 from patent US 5830644.
AROSO988.1 GI:5974352
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/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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 17 bp
Sequence 60 from Patent WO0211674.
AX578222
                                                                                                                                                                                                                                                                      Thompson, James (US)
Location/Qualifiers
1. .17
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1807 TGTGTGTATATATA 1822
                                                  AX578222.1 GI:27647424
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AR050988
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Unclassified.
1 (bases 1 to 17)
Stinchcomb.D.T., Draper,K., McSwiggen,J. and Jarvis,T.
C-myb targeted ribozymes
Patent: US 5646042-A 1058 08-JUL-1997;
Location/Qualifiers
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StinchComb, D.T., Draper, K., McSwiggen, J. and Jarvis, T. C-myb ribozynes having 2'-5'-linked adenylate residues Patent: 18 5817796-A 1058 06-OCT-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.2%; Score 12.8; DB 1; Length 17; Best Local Similarity 87.5%; Pred. No. 1.8e+02; Matches 14; Conservative 0; Mismatches 2; Indels
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linear

17 bp DNA Sequence 1058 from patent US 5646042. 153317

I53317.1 GI:2474520

RESULT 270 153317 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOUNCE ORGANISM

Unknown

2; Indels

Query Match
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2;

1811 TGTATATATATATA 1826

2 TTTATATATATACA 17

RESULT 271 AX578222

1. .17 /organism="unknown" /mol_type="unassigned DNA"

source

REFERENCE AUTHORS TITLE JOURNAL FEATURES

PAT 12-JUN-2003

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Unclassified.

(Dases I to 14)

(Dases I to 14)

Wellrich,S.L., Strahl,C.M., McEachern,M.J.,

West,M.D., Harley,C.B., Welnrich,S.L., Kim,N.W. and Vaziri,H.

Diagnostic methods for conditions associated with elevated cellular

levels of telomerase activity

Patent: US 6551774-A 78 22-APR-2003;

Location/Qualifiers
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Analysys of double stranded nucleic acid using scanning probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C1201/68,C12N15/09,G01N13/16,G01N33/483,G01N33/50,C12N15/00 Analysys of double stranded nucleic acid using scanning probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Analysys of double stranded nucleic acid using scanning probe patent: JP 2002360300-A 1 17-DEC-2002;
OLYMPUS OPTICAL CO LTD
OS Artificial Sequence
PD 17-DEC-2002
PD 17-DEC-2002
PF 06-UUN-2001
PI MINORU TAREUCHI
PC C12Q1/68,C12N15/09.G01N12/15
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/organism='Artificial Sequence'
Location/Qualiflers
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92.9%; Pred. No. 1.6e+02;
tive 0; Mismatches 1;
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                                            DNA
                                     14 bp 1
Sequence 78 from patent US 6551774.
AR307315
AR307315.1 GI:31697842
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/mol_type="genomic DNA"
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PP 2002356300-A/1.
synthetic construct
synthetic construct
artificial sequences.
I (bases 1 to 14)
Takeuchi,M.
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BD185612
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BD185612
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                RESULT 276
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Unclassified.
1 (bases 1 to 14)
West, M.D., Shay, J., Wright, W. and Blackburn, E.H.
Screening methods to identify inhibitors of telomerase activity
Patent: US 6368789-A 56 09-APR-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                          Unknown.
Unclassified.
Unclassified.
1 (Sases 1 to 14)
West,M.D., Shay,J., Wright,W., Blackburn,E.H. and McEachern,M.J.
Telomerase activity assays for diagnosing pathogenic infections
Patent: US 5695932-A 56 09-DEC-1997;
Location/Qualifiers
Wright, W.E., Blackburn, E.H. and Vaziri, H.
Therapy and diagnosis of conditions related to telomere length
and/or telomerase activity
Patent: US 564596-A 57 08-UUL-1997;
Location/Qualifiers
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1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels
                                                                                                                                                 ch 1.2%; Score 12.4; DB 1; Length 14; I Similarity 92.9%; Pred. No. 1.6e+02; 13; Conservative 0; Mismatches 1; Indels
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Sequence 56 from patent US 6368789.
AR204606.
AR204606.1 GI:21501975
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Sequence 56 from patent US 5695932.
184398
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AR204606
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REFERENCE AUTHORS TITLE JOURNAL

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RESULT 278 BD185613/c

linear PAT 16-MAY-2001

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Draper, K.G.
Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
Patent: US 6132967-A 331 17-OCT-2000;
Location/Qualifiers
                                                                                                                   Unknown.
Unclassified.
1 (Dases 1 to 15)
Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
                                                                                                                                                                                                                                                                                                                                                       Query Match 1.2%; Score 12.4; DB 1; Length 15; Best Local Similarity 92.9%; Pred. No. 1.7e+02; Matches 13; Conservative 0; Mismatches 1; Indels
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1 (bases 1 to 15)

1 (bases 1 to 15)

Soreg.H. and Zakut.H.

Method of screening for genetic predisposition to anticholinesterase therapy
Patent: US 6236139-A 1 04-DEC-2001;

Location/Qualifiers
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         DNA
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1 (bases 1 to 15)
Chien, D.Y.
NAMBU diagnostics and vaccines
Patent: US 6150087-A 203 21-NOV-2000;
Location/Qualifiers
15 bp DN Sequence 331 from patent US 6132967. AR113885 AR113885.1 GI:14094207
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Sequence 1 from patent US 6326139.
AR179058.1 GI:20220613
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Analysys of double stranded nucleic acid using scanning probe
Patent: JP 2002360300-A 2 17-DEC-2002;
Daypus OPTICAL CO LID
OS Artificial Sequence
PN JP 2002360300-A/2
PN JP 2002360300-A/2
PP 0-UNN-2001 JP 2001171590
PP 06-UNN-2001 JP 2001171590
PP 06-UNN-2001 JP 2001171590
PP 07-2002 Analysys of double stranded nucleic acid using scanning probe CC
Analysys of double stranded nucleic acid using scanning probe CC
                                           BD185613 14-JUN-2003
Apalysys of double stranded nucleic acid using scanning probe
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Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
Intercellular adhesion molecule-1 (ICAM-1) ribozymes Patent: US 5837542-A 331 17-NOV-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism='Artificial Sequence'. Location/Qualifiers
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1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Prad. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels
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BD185613.1 GT:31877813
JP 200236300-A2.
SYNThetic construct
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artificial sequences.
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RESULT 279 AR056127

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PAT 16-MAY-2001

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PAT 20-APR-2002

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RESULT 280 AR113885

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linear PAT 13-MAY-1997
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                                                           Unclassified.

In (bases I to IS)

1 (bases I to IS)

Sallivan, S., Draper, K.G., McSwiggen, J. and Stinchcomb, D.T.

IL-5 targeted thosymes

Patent: US 5616488-A 474 01-APR-1997;

Location/Qualifiers
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1 (bases 1 to 15)
Sullivan, S., Draper, K.G., McSwiggen, J. and Stinchcomb, D.T.
IL-5 targeted tabozymes
Patent: US 5616488-A 491 01-APR-1997;
Location/Qualifiers
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Best Local Similarity 92.9%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels
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MCSwiggen,J., Draper,K., Pavco,P. and Woolf,T.
Respiratory syncytial virus ribozymes
Patent: US 569532-A 335 02-DEC-1997;
Location/Qualifiers
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Sequence 335 from patent US 5693532.
177628.
177628.1 GI:3013782
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Sequence 491 from patent US 5616488.
139453
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   I39436.1 GI:2083916
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Best Local Similarity 92.9%; Pred, No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels
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Unknown.

Unclassified.

3 1 (bases 1 to 15)

S Houghton M. (Choo, Q.-L. and Kuo, G.
Nanbv diagnostics and vaccines
AL Patent: EP 0318316-Al 25 31-MAY-1989;
Location/Qualifiers
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Houghton, W. Choo, O.-L. and Kuo, G.
Nanbv diagnostics and vaccines
Patent: EP 0318216-A1 36 31-MAY-1989;
Location/Qualifiers
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Sequence 474 from patent US 5616488.
139436
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Sequence 25 from Patent EP 0318216.
106405
106405.1 GI:590295
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Sequence 36 from Patent EP 0318216.
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Method and reagent for inhibiting the expression of disease related
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                                      Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
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                                                                                                                                                               Patent: EP 1260586-A 373 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers

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Nucleotide carrier for diagnosing and treating oral diseases
Patent: WO 02072883-A 120 19-SEP-2002;
ROETGER, Antje (DE)
Location/Qualifiers
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Unclassified.
Unclassified.
1 (bases 1 to 15)
Garner, H.K. Wren, J.D., Minna, J.D. and Fondon, J.W. III.
Garner, H.K. Wren, J.B., D., Minna, J.D. and Fondon, J.W. III.
Polymorphic repeats in human genes
Patent: US 6472154-A 158 29-OCT-2002;
Location/Qualifiers
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Sequence 373 from Patent BP1260586.
AX633234
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Sequence 158 from patent US 6472154.
AR241870.1 GI:27287682
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Sequence 120 from Patent W002072883.
AX587098

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Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0;
JOURNAL Patent: US 5582979-A 433 10-DEC-1996;
FEATURES Location/Qualifiers
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Sequence 21 from patent US 6383747.
AR208365.1 GI:21509500
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Sequence 2 from patent US 6322971.
AR261535 GI:28072603
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                                                                            Woolf, \mathbf{r}. Method and reagent for inhibiting the expression of disease related
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Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and
method of using the same
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   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A., Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J., Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
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Sequence 5043 from Patent BP1260586.
AX637904
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Patent: EP 1260586-A 2894 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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PAT 20-JUN-2002
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1 (bases 1 to 12)
2 (bases 1 to 12)
3 wkins, R.Letts. and Abraham, L.Joseph.
Method for determining ancestral haplotypes using haplospecific geometric elements within the major histocompatibility complex multigene cluster. 42 07-MAY-2002;
Patent: US 6383747- A 21 07-MAY-2002;
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1 (bases 1 to 12)
1 (bases 1 to 12)
Chevverin, A.B. and Kramer, F.R.
Oligonucleotide arrays and their use for sorting, isolating, sequencing, and manipulating nucleic acids
Patent: Uscation/Qualifiers
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Matches 12; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0;
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Dace, G.T., Kmmerly, W.J., Goff, S.A. and Celler, P.
In vitro capture of nucleic acids via modified oligonucleotides and
magnetic Deads
Patent: WO 02101088-A 2 19-DEC-2002;
Syngente Participations AG (CH)
Location/Qualifiers
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In vitro capture of nucleic acids via modified oligonucleotides and magnetic bacds
Patent: WO 02101088-A I 19-DEC-2002;
Syngenta Participations AG (CH)
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Best Local Similarity 100.0%; Pred. No. 1.46+02;
Matches 12; Conservative 0; Mismatches 0;
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Universal variable fragments
Patent: WO Offs4948-A 1 07-SEP-2001;
Dr. van Haeringen Laboratorium B.V. (NL)
Location/Qualifiers
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AX644020 GI:28610172
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Sequence 2 from Patent W002101088.
AX644021
AX644021.1 GI:28610173
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Therapeutically useful synthetic oligonucleotides
Patent: WO 0144465-A 13 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
Location/Qualifiers
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Therapeutically useful synthetic oligonucleotides
Patent: Wo 0144465-A 14 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0;
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                                                   Sequence 13 from Patent WO0144465. AXI75249
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25 degreence 14 from Patent WO0144465.

AX175250

AX175250.1 GI:14598618
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Sequence 1 from Patent W00164948.
AX239661.1 GI:15797326
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/db_xref="taxon:32644"

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urphy, B.R., Collins, P.L., Durbin, A.P., Skiadopoulos, M.H. and Ta,T.

synthetic construct
artificial sequence.

I (bases 1 to 12)

Rurphy, B.R., Collins, P.L., Durbin, A.P., Skiadopoulos, M.H. and Ta,T.

production of attenmated parainfluenza virus vaccines from cloned
nucleotide sequence

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Whuman poliovirus 3

Viruees, seRNA positive-strand viruses, no DNA stage;

Viruees; seRNA positive-strand viruses, no DNA stage;

Picornaviridae; Enterovirus.

I (bases 1 to 13)

Minor, P.D., Evans, D.M.A., Schild, G.C., Almond, J.W. and Ferguson, M. Peptides useful in vaccination against enteroviruses

Patent: EP 0197772.A 1 15-0CT-1996;

NATIONAL RESEARCH DEVELOPMENT CORPORATION

Location/Qualifiers
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          Query Match
Best Local Similarity 100.0%; Pred. No. 1.40+02;
Matches 12; Conservative 0; Mismatches 0; Indels
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BD106556.1 GI:23201374
JP 2002502241-A/50.
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BD106556/c
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Nishigaki, K., Takasawa, T. and Hamano, K.
Nishigaki, K., Takasawa, T. and Hamano, K.
Nishigaki, K., Takasawa, T. and Hamano, K.
Patent: JP 2001299398-A 11 30-OCT-2001;
D JP 2001299398-A/11
DD 30-OCT-2001
DD 30-OCT-2000 JP 2000123755
PF 25-APR-2000 JP 2000123755
PT XOLCHI NISHIGAKI, TSUTOWU TAKASAWA, KEIICHI HAMANO PC
C1201/68,C12N15/09,G01N21/64,G01N27/447,G01N33/50 CC
FH Key
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PF 25-ARR-2000 JP 2000123755
PF 25-ARR-2000 JP 2010123755
C1201/69, C12N15/99, G1N21/64, G1N27/447, G01N27/447, G01N33/50 CC
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Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels
Query Match 1.1%; Score 12; DB 1; Length 12; Best Local Similarity 100.0%; Pred. No. 1.46+02; Matches 0; Mismatches 0; Indels
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Method for identifying organism by genotype.
BD062286
BD062286.1 GI:22607891
UP 2001299398-A/11.
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unclassified.
1 (bases I to 12)
Nishigaki K., Takasawa, T. and Hamano, K.
Method for identifying organism by genotype
Patent: JP 2001299398-A 11 30-OCT-2001,
TIE TECH KK
OS Unknown
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BD062286.1 GI:22607891
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PAT 03-APR-1998
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Unclassified.
Unclassified.
1 (bases 1 to 15)
Sonemberg, N., Katze, M.G., Roy, S., Koromilas, A.E. and Barber, G.H.
Anti-tumor agent assay using PKR
Anti-tumor agent assay using PKR
Patent: US 5670330-A 16 23-SEP-1997;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.98+02;
Matches 12; Conservative 0; Mismatches 0; Indels
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Unclassified.
E. (bases 1 to 15)
S. McSwigen. J., Draper, K., Pavco, P. and Woolf, T.
Respiratory syncytial virus ribozymes
AL Patent: US 563352-A 32 02-DEC-1997;
Location/Qualifiers
                                      M Unknown.
Unclassified.
E 1 (bases 1 to 15)
S Stinchcomb, D.T., Draper, K.G. and McSwiggen, J.
Rel a targeted ribozymes
AL Patent: US 5658780-A 309 19-AUG-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                15 bp DNA
Sequence 16 from patent US 5670330.
166357.
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Sequence 32 from patent US 5693532.
177325 173325.1 GI:3013479
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 GI:2479703
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E 1 (bases 1 to 15)
E 3 (bases 1 to 15)
S Sinchcomb, D. T., Draper, K.G. and McSwiggen, J.
AL Patent: US $558780-A 193 19-AUG-1997;
AL Patent: US $658780-A 193 193 1, Length
                                                                                                                                                                                                                                                                                                                                          Unclassified.

1 (bases 1 to 15)
Stinchoomb, D.T., Draper, K.G. and McSwiggen, J. Stinchoomb, D.T., Draper, K.G. and Lasyeted ribozymes
Patent: US 5658780-A 120 19-AUG-1997;
Location/Qualifiers
                                                                                                                                                                                                                       15 bp DNA
Sequence 120 from patent US 5658780.
161566
161566.1 GI:2479514
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161639
161639.1 GI:2479587
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Sequence 309 from patent US 5658780.
161755
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RESULT 311 177326/c LOCUS

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Stinchcomb, D.T., Dudycz, L.W., Chowrira, B., Grimm, S., Direnzo, A., Karpeisky, A., Draper, K.G., Kisich, K., Matulic-Adamic, J., Mcswiggen, J.A., Modak, A., Pavco, P., Beigelman, L., Sullivan, S.M., Sweedler, D., Thompson, J.D., Tracz, D., Usman, N., Wincott, F.E. and Woolf, T.
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tive 0; Mismatches 0; Indels
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Sequence 3212 from Patent EP1260586.
AX636073
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RIBOZYME PHARMACEUTICALS, INC. (US)
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  AX636030.1 GI:28471644
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Best Local Similarity 100.
Matches 12; Conservative
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AX638069/c
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Method and reagent for inhibiting the expression of disease related
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Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
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1.1%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 0; Indels
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McSwiggen, J., Draper, K., Pavco, P. and Woolf, T. Respiratory syrcytial virus ribozymes
Patent: US 5693532-A 33 02-DEC-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 bp RNA
Sequence 3023 from Patent EP1260586.
AX635884
AX635884.1 GI:28471498
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Patent: EP 1260586-A 3023 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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Sequence 33 from patent US 5693532.
177326
177326.1 GI:3013480
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AX636030/c
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RESULT 312 AX635884/c LOCUS

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PAT 21-FEB-2003
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                                                                               Stinchcomb, D.T., Dudycz, L.W., Chowrira, B., Grimm, S., Direnzo, A., Karpelsky, A., Draper, K.G., Kiekch, K., Matulic-Adanic, J., Moswiggen, J.A., Modek, A., Pavco, P., Beigelman, L., Sullivan, S.W., Sweedler, D., Thompson, J.D., Tracz, D., Usman, N., Wincott, F.E. and
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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 0; Indels
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Sequence 5210 from Patent EP1260586.
AX638071
                                                                                                                                                                                                              genes
Patent: EP 1260586-A 5208 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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Search completed: April 2, 2004, 14:35:26 Job time: 6 secs

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Best Local Similarity 100.0 Matches 12; Conservative

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n 5.1.6 Compugen Ltd. Search time 3 Seconds (without alignments)	tgtatattttttctataaa 1049 338	chance to have result being stribution. Descript:	ACCESSION: NACES ACCESSION: AZA 612 ACCESSION: AZA 613 ACCESSION: AZA 613 ACCESSION: AZA 64361 ACCESSION: AZA 64361 ACCESSION: AZA 6429 ACCESSION: AZA 6426 ACCESSION: AZA 64479
GenCore version pyright (c) 1993 - 2004 search, using sw model 1 2, 2004, 14:41:23 ;	s-10-006-191-19 ttgaactgattcacatctcag DENTITY_NUC apop 10.0 , Gapext 0.5 69 seqs, 3566 residues its satisfying chosen parameters ngth: 8	h: 50 imum Match 01 imum Match 10 iting first 1: .seq:* the number of the number of than or equal than or equal by analysis 'y in Length DB	3.5 3.7 1 K06912 2.2 28 1 AZ781130 2.2 28 1 AZ781130 2.2 28 1 AZ49521 2.2 28 1 AZ44521 2.3 24 1 AZ44521 2.1 25 1 AZ44529 2.1 25 1 AZ745201 2.1 25 1 AZ74520 2.1 27 1 AZ345426 2.1 27 1 AZ345426 2.1 27 1 AZ38238 2.1 27 1 AZ38238 2.1 26 1 AZ3928 2.1 26 1 AZ39286 2.1 26 1 AZ39288 2.1 27 1 AZ49453 2.1 27 1 AZ898874 2.1 27 1 AZ88874 2.1 27 1 AZ88874 2.1 27 1 AZ88874
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RESULT 1 R06912/C LOCUS R06912 37 bp mRNA linear EST 05-APR-1995 DEFINITION Yf12905.81 Soares fetal liver spleen 1NFLS Homo sapiens CDNA clone IMAGE:126680 3' similar to gb:M92934 CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR (HUMAN);, mRNA sequence. ACCESSION R06912.1 GI:758835	S . ISM CE RS AL	#444 Forest Park Parkway, Box 8501, St. Louis, MO 63108. Tel: 314 286 1800 Fax: 314 286 1810 Fax: 314 286 1810 Email: est@watson.wustl.edu Insert 51ze: 1597 High qality sequence starts: I High qality sequence stops: 1 Source: IMAGE Consortium, LLNL This clone is available royalty-free through Linl.; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Insert Length: 1597 Std Error: 0.00 Seq primer: -21m13 High quality sequence stop: 1. FEATURES I37 /organism="Homo sapiens" //mol_type="mrRNA"		Ouery Match 3.5%; Score 37; DB 1; Length 37; Best Local Similarity 100.0%; Pred. No. 1.6; Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 2008 CCGTCAAACGATTGTTTCCAAAGGGGAGCATCAG 2044
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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2M0019A07F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                           Email: est@watson.wustl.edu
High quality sequence startes: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This olone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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IMAGE:270507 5' similar to gb:M92934 CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR (HUMAN);, mRNA sequence.
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                                                                                                                                                                                                                      Wilson,R.
The Washu-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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3.0%; Score 31; DB 1; Length 35;
Best Local Similarity, 91.2%; Pred. No. 5.6;
Matches 31; Conservative 0; Mismatches 3; Indels
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/Grone="Ouccamouspan" (Jab hose="Uncamouspan") / Grone="Uncamouspan" (Jab hose="Uncamouspan") / Grone="Uncamouspan" (John plasmid UnGCIM library" / Grone="Neales" (John plasmid UnGCIM library" / Grone="Neales" (John Parany Purified genomic DNA from M. musculus CS7BL/GJ (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oilgonicleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi[4732114]gb]AF12972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xillo-Gold (Stratagene) cells and selected for ampicillin resistance."
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 26)

S Dunn, D., Aoyagai,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Menen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah
RM. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT
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28 bp DNA linear GSS 03-OCT-2000
1M0173N21R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0173N21 R, genomic survey sequence.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

5

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musculus C57BL/60 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligomuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarces gel
electrophoresis. Vector DNA was prepared from a derivative
of pw042 (gi/4732114/gb/AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptores complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chamically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mue.
1 (bases 1 to 28)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Ungublished (2000)

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
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Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@genet
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84112, US
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Contact: Robert B. Weiss
University of Urah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 28)
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1M0238N03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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/note=""vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/60 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
  1 (bases 1 to 28)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
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                                                                                                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0173 row: N column: 21
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sex="Male"
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Best Local Similarity 89.34
Matches 25; Conservative
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RESULT 5 AZ443611

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodnamically sheared by repeated passage through a was hydrodnamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMAD42 (gil #4732114 [gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, adaptored mouse DNA was annealed cochemically-competent E. ooli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus
Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
1 (bases 1 to 24)
1 (bases 1, barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., Von
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/60"
/db_xref="taxon:10090"
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/clone lib="Wouse lobb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/60 (male) was obtained from the Jackson
                                                                                                                                                                                                                                            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
Reilly,W., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunm@genetics.utah.edu
Email: ddunm@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0513 row: C column: 13
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers
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                                                                                                       plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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AZ446429
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                                                                                 TITLE
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/clone_lib="Wouse 10kb plasmid UUGCIM library"
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musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/Interp. Jackson
(http://www.jack.org/resources/documents/Anares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarcse gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederbrauserri, A., and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae; Musinae; Lo 27)

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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0518 row: A column: 05
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Class: plasmid ends
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Best Local Similarity 89.3%; Pred. No. 24;
Matches 25; Conservative 0; Mismatches
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Location/Qualifiers
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/clone="UUGC1M0518A05"
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GSS.
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Fax: 801 585 7177
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

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RESULT 7 AZ646963 LOCUS

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Mouse whole genome scaffolding with paired end reads from 10kb
                                      plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGClM library"
/note="Tweetor: PMD4Znv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources
/nttp://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose ger
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|qf|qf|22114|gf|AR129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1M0556K17R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0556K17 R, genomic survey sequence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Railm, M., Longacres, S., Mahmoud, M., Menen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
        Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
Jasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA.
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                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Ext Error: 0.00
Plate: 0242 row: A column: 24
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Class: plasmid ends
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/db xref="taxon:10090"
/clone="UUGGIM0242A24"
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Location/Qualifiers
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AZ762101.1 GI:12871750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sex="Male"
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Matches 23; Conserv
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Dunn,D., Aoyaqi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Nederhausern,A. and Wright,D., Weise,R., Tingey,A., von Niederhausern,A. and Wright,D., Weise,R.
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              SLC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .25
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AZ435344 1M0222X17F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0222X17F, genomic survey sequence.
  Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 8td Error: 0.00
Plate: 0080 row: A column: 09
Seg primer: CGTTGTAAACGACGAGT
Class: plasmid ends
High quality sequence stop: 28.
Location/Qualifiers
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Mus musculus
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Unpublished (2000)
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Matches 23; Conserv
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AZ435344
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/note="Twetor: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources (Jackson Laboratory Mouse DNA Resources (Jackson Laboratory Mouse DNA Resources (Jackson Laboratory Mouse DNA Resources (Jackson Laboratory Mouse DNA Resources (Jackson Laboratory Mouse DNA Resources (Jackson Laboratory Mouse DNA Was hydrodynamically sheared by repeated by Resared DNA was blunt end repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gfrom a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XI10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0080A09F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0080A09 F, genomic survey sequence.
    plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blommedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
RM. 308, SLOMA
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Mus musculus
Mus maculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butaleostomi,
Bukaryota, Adazoa, Chordata, Craniata, Vertebrata, Butalaese,
I (bases 1 to 28)
Unun, D., Advagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Musderhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0017 row: J column: 19
Seq primer: CACACAGGAPACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.
                                                                                                                                                                                                                                                                                                                                                                              1. .25
/organism≂"Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITIGLE GIGIGIGIGIGI 2
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AZ345426.1 GI:10424663
                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
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Matches 23; Conserv
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Gaps ö Ē

COMMENT

FEATURES

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/clone_lib="wouse lokb plasmid UUGCIM library"
/note="vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWMP42 (gil 1732114|gib] AR129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
84112, USA
Tel: 801 S85 5107
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0498 row: H column: 05
Seq primer: GTTGTAAAAGGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 27.
High quality sequence stop: 27.
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2M0262D23F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0262D23 F, genomic survey sequence.
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2 (bases 2 to 27)

3 (bases 2 to 27)

4 (bases 2 to 27)

5 (bases 2 to 27)

5 (bases 2 to 27)

6 (bases 2 to 27)

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2.1%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 29;
Matches 24; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mol_type="genomic DNA"
strain="C57BL/6J"
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Mus musculus
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AZ981811/c
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[Aboratory Mouse DNR Resource
[Attp://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil 4732114] gb]AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah
Rm. 308; Iyo of Utah
Rm. 308; Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tell 801 585 5107
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0222 row: K column: 17
Seq primer: CGTTGTAAAACGACGGCAGT
Class: plasmid ends
Class: plasmid ends
High quality sequence stop: 27.
High quality sequence
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Mus musculus
Mus musculus
Mus musculus
Muscardis, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 27)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rose, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Mright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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1M0498H05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0498H05 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Male"
/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0222K17"
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Unpublished (2000)
Contact: Robert B. Weiss
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Matches 24; Conserv
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BX563211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch crifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWAP42 (gql 4732114 [gb] AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0004D22R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0004D22 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
musculus C57BL/6J (female) was obtained from M.
musculus C57BL/6J (female) was obtained from the Jackson
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Mus musculus
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
University of Utah
Rm. 308. Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112. USA
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                                                           Halls, USA
Tel: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0262 row: D column: 23
Seg primer: CGTTCTAAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 27.
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                                                                                                                                                                                                                                                                                                                                'organism="Mus musculus"
"mol type="genomic DNA"
strain="C57BL/6J"
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University of Utah Genome Center
University of Utah
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clone="UUGC2M0262D23"
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muscular Cylause DNR Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
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10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AF12972.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chamically-competent E. coli XII0-GG04 (Stratagene) cells
and selected for ampicillin resistance."
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BX563211
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Glossina morsitans morsitans
Glossina morsitans morsitans
Glossina morsitans
Glossina morsitans

Neoptera; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Hippoboscoidea; Glossinidae; Glossina.

(bases 1 to 25)
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
Hamilton, J., Soarse, M.B., Bonaldow, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the testse fly Glossina
morsitans morsitans and expression analysis of putative immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="B. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UGCIM library."
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
                      Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                                                                                                                                                   Std Error: 0.00
                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.0
Plate: 0004 row: D column: 22
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic_DNA"
/strain="c5/BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0004D22"
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Genome Biol. 4 (10), R63 (2003)
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Pathogen Sequencing Unit
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                              Rm. 308, Biomedical
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Unpublished (2000)

L Unpublished (2000)

L Contact: Robert B. Weiss
University of Utah Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                          'note="country: Zimbabwe; EST from adult gut infected with
The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix qlc are reverse primer reads starting at 5'
end of the CDNA all plc reads are from
the 3' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ339866 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0071H01R clone UUGCIM0071H01 R, genomic survey sequence.
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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High quality sequence stop: 25.
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// Alab-hosts E. Coll strain Xill-Gold (Treasivent, P. )

// Alab-hosts E. Coll strain Xill-Gold (Treasivent, P. )

// Alab-hosts E. Coll strain Xill-Gold (Treasivent, P. )

// Alab-hosts E. Cyber, (4) (1916) | Ass obtained from the Jackson instances of hosts of the Cyber, (4) (1916) | Ass obtained from the Jackson (thetp://www.jax.org/resources/documents/darse/). The DNA was prepared by the Sange through a coll of the Dinnie ends of the Cyber of the Dinnie ends of the Cyber of the Dinnie ends in high moir excess The alaber of the Dinnie ends in high moir excess The index the Cyber of the Dinnie ends in high moir excess The index the Cyber of the Dinnie ends in high moir excess The index the Cyber of the Dinnie ends in high moir excess The index the Cyber of the Dinnie ends in high moir excess The index the Cyber of the Dinnie ends in high moir excess The index the Cyber of the Dinnie ends in high moir excess The index the Cyber of the Dinnie ends the Cyber of the Cyber of the Dinnie ends the Cyber of the Dinnie ends the Cyber of the Dinnie ends the Cyber of ```

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 Inductory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 k range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|R129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 26)
Dunn, D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Physical end reads from 10kb plasmid inserts
 AZ307889 29-SEP-2000 1M0010L18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0010L18 F, genomic survey sequence.
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T.brucei"
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 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
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 Email: ddunn@genetics.utah.edu
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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 2 rérérérérérérérérérerer 26
 Mus musculus (house mouse)
Mus musculus
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 sex="Male
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
 VERSION
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COMMENT

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musculus CS7BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
/ Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage itrough a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114 [gb]/RI29072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
 Unpublished (2000)
Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Warsity of Utah
Wars. 308, Balla, Usah
Balla, Usah
 AZ345505 1000 26 bp DNA linear GSS 29-SEP-2000 1000800010F Mcuse 10kb plasmid UUGCIM library Mus musculus genomic cone UUGCIM0080001 F, genomic survey sequence.
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adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. L. (bases 1 to 26)

Dunn, D., Aoyagi, S.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niderhausern, A. and Wright, D., Weiss, R., Tingey, A., von

Mouse whole genome scaffolding with paired end reads from 10kb
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 Length 26;
 2; Indels
 DB 1;
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: H column: 01
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 Mus musculus (house mouse)
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and selected for ampicillin resistance."

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musculus C57BL/6J (male) was obtained from the Jackson
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(http://www.jax.org/resource/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
was blunt end-repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gdl
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AP129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
 Rm. 309, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 AZ494537 26 bp DNA linear GSS 05-OCT-2000 1M0329D24R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0329D24 R, genomic survey sequence.
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. L. (baes I to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von Mouse whole genome scaffolding with paired end reads from 10kb blasmid inscris
chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
 Gaps
 DB 1; Length 26;
 2; Indels
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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University of Utah Genome Center
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 Mus musculus (house mouse)
Mus musculus
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligomuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose Gsl electrophoresis. Vector DNA was prepared from a derivative of pwb042 (gil49p|AR129072.1); a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll Xillo-Gold (Stratagene) cells and selected for ampicillin resistance."
 Mus musculus (house mouse)

Mus musculus

Bukaryota; Matazoa, Chordata; Craniata; Vertebrata; Euteleostomi;

Musmalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 26)

2 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

1 Islam, H., Longacre, S., Mahmoud, M., Menen, B., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weise, R.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah Genome Center
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1MO343F01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0343F01 R, genomic survey sequence.
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 DB 1; Length 26;
 Indels
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 84112, u.s.
Fal: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Query Match 2.1%; Score 21.8; Est Local Similarity 92.0%; Pred. No. 30; Matches 23; Conservative. 0; Mismatches
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84112, USA
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AZ795803 LOCUS DEFINITION

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 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Bukaryota, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 26)

I (bases 1 to 26)

St (bases 1 to 26)

St Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederbauserri, A. and Wright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

University of Utah Genome Center
University of Utah Genome Center
 AZBOGOO4 1000 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCZMOO67H16 R, genomic survey sequence.
 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
 2.1%; Score 21.8; DB 1; Length 26;
DB 1; Length 26;
 2; Indels
 Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Brror: 0.00

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/db xref="taxon:1000"
/clone="UUGC2M0067H16"
 1793 TGTGTGTGTGTGTGTGTATAT 1817
 25
 1 rererererererererererer
 Mus musculus (house mouse)
Mus musculus
 AZ806004.1 GI:12966815
 Query Match 2.15
Best Local Similarity 92.05
Matches 23; Conservative
 Rm. 308, Bi
84112, USA
 RESULT 24
AZ806004
LOCUS
DEFINITION
 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 REFERENCE
AUTHORS
 JOURNAL
 FEATURES
 TITLE
 COMMENT
 Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CE 1 (bases 1 to 26)

Bunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Urah Genome Center

University of Urah Genome Center

University of Utah Genome Center

University of Utah

Rm. 308 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

#4112, USA
 muscular C./Buryon (marter) was Occarned from the Darken. Laboratory Mouse DNR Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymorlectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|RR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 AZ795803 26 bp DNA linear GSS 16-FEB-2001 2M0051P11F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0051P11 F, genomic survey sequence.
 ô
 /sex="male" | feet | fe
 Gaps
 ö
 DB 1; Length 26;
 2; Indels
 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0051 row: P column: 11
Seg primer: cGTTGTAAAACGACGGCCAGT
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Best Local Similarity 92.0%; Pred. No. 30;
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/db_xref="taxon:10090"
/clone="UUGC2M0051P11"
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 High quality sequence stop: 26.
Location/Qualifiers
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 AZ795803
AZ795803.1 GI:12943205
 Tel: 801 585 5606
Fax: 801 585 7177
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5

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Gaps

.. 0

Indels

..

GSS 29-SEP-2000

RESULT 25 AZ975568/c

ò d DEFINITION ACCESSION

LOCUS

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

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AZ129433
1M0053X11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0053X11 R, genomic survey sequence.
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 27)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Uingey, A., von Dlasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC 84112, USA
 Tel: 801 585 5606
Fax: 801 585 7177
Famil: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0053 row: K column: 11
Seg primer: CACACAGGAAACAGCTAATGACC
Class: plasmid ends
High quality sequence stop: 27.
0; Mismatches
 1793 TGTGTGTGTGTGTGTGTATAT 1817
 25 rererererererererererer
 AZ329433.1 GI:10390140 GSS.
Mus musculus (house mouse)
Mus musculus
 Query Match
Best Local Similarity 92.0
Matches 23; Conservative
 Matches 23; Conservative
 source
 VERSION
KEYWORDS
SOURCE
ORGANISM
 DEFINITION
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AZ329433
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 REFERENCE
 AUTHORS
 JOURNAL
 FEATURES
 TITLE
 COMMENT
 ò
 ద
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//sex="Female"
//lab host="E. coli strain XLIO-Gold, Tl-resistant, F-"
//clone lib="Mouse lokb plasmid UUGCZM library"
//clone lib="Mouse lokb plasmid UUGCZM library"
//note="Vector: PWD4ZNY; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05% inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligoniclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarces gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1) a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XiiO-Gold (Stratagene) cells
and selected for ampicillin resistance."
 Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 26)

2 Dunn, D., Ayagai, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid innerts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

University of Utah
 26 bp DNA linear GSS 27-APR-2001 ZM0250L12R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0250L12 R, genomic survey sequence. AZ975568 AZ975568 GSS.
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 ö
 Gaps
 ô
 2.1%; Score 21.8; DB 1; Length 26; 92.0%; Pred. No. 30;
 ..
7
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0250 row: L column: 12
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
 92.0%; Pred. No. 30; cive 0; Mismatches
 1. .26
/organism="Mus musculus"
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/strain="C57BL/69"
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 1793 TGTGTGTGTGTGTGTGTATAT 1817
 High quality sequence stop: 26.
Location/Qualifiers
 2 rGrGrGrGrGrGrGrGrGrGrGrGr 26
 23; Conservative
 Query Match
Best Local Similarity
Best Local Similarity
Matches 23; Conserv
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PEATURES

Б

S. 2030 E., SLC,

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ö
 Gaps
 ö
2.1%; Score 21.8; DB 1; Length 27; 92.0%; Pred. No. 31; ive 0; Mismatches 2; Indels
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AZ342492 LOCUS DEFINITION

RESULT 27

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE

JOURNAL COMMENT

TITLE

```
(http://www.jax.org/resources/documents/dnares/). The DNA (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligomuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwDA2 (gi/4732114/gbl/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XII0-Gold (Stratagene) cells and selected for ampicillin resistance."
 GSS.

Mus musculus (house mouse)

Mus musculus (house mouse)

Mus musculus

Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Musmalia; Eutheria; Rodenia; Sciurognathi; Muridae; Murinae; Musmalia; Eutheria; Rodenia; Sciurognathi; Muridae; Murinae; Musmalia; Eutheria; Rodenia; Sciurognathi; Muridae; Musinae; Musmalia; Eutheria; Rodenia; Sciurognathi; Muscae, Musca
 AZ404479

1M0172F18R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0172F18 R, genomic survey sequence.
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42zyr, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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 Query Match 2.1%; Score 21.8; DB 1; Length 27; Best Local Similarity 92.0%; Pred. No. 31; Matches 23; Conservative 0; Mismatches 2; Indels
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/mol type="genomic DNA"
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/clone="fugGC1M0172F18"
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1793 TGTGTGTGTGTGTGTGTATAT 1817
 2 rereferencerencerene 26
 AZ404479
AZ404479.1 GI:10528408
 source
 VERSION
KEYWORDS
SOURCE
ORGANISM
 DEFINITION
 AUTHORS
 JOURNAL
 RESULT 28
AZ404479
 ACCESSION
 REFERENCE
 FEATURES
 TITLE
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 g
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 27)

RS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Reilly,M., Rose,M., Mennoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Wense,R., Tingey,A., von Niederhausern,A. and Wridgh,D., Weiss,R., Tingey,A., von Conse whole genome scaffolding with paired end reads from 10kb plasmid finserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT #4112.005
 / GEACE—"MAILE"

[Jab hose="B. Coli strain XIIO-Gold, Tl-resistant, F-"

[Jab hose="B. Coli strain XIIO-Gold, Tl-resistant, F-"

[Jone 11b="Mouse 10kb plasmid UUGCIM library"

[Actom 11b="Mouse 10kb plasmid UUGCIM library"]

[Actom 11b="Mouse 10kb plasmid UUGCIM library"]

[Actom 11b="Mouse DIA Resource of trom the Jackson Laboratory Mouse DIA Resource of the Jackson Laboratory The sheared DIA was blunt end-repaired with T4 DIA polymerase and T4 polymuclectide kinase. Adaptor oligonaclectides ware ligated to the blunt ends in high molar excess. The adaptored using preparative agarose galelectrophoresis. Vector DIA was prepared from a derivative of pwD42 (gi | 4732114 | gb | AF129072.1) a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DIA was annealed to adaptored vector DIA, and transformed into chemically-competent E. coli XIIO-Gold (Stratagene) cells and selected for ampicillin resistance."
 ö
 AZ342492 27 bp DNA linear GSS 29-SEP-2000 1M0075004R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0075004 R, genomic survey sequence.
 Gaps
 ö
 Score 21.8; DB 1; Length 27;
Pred. No. 31;
0; Mismatches 2; Indels
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0075 row: 0 column: 04
Seg primer: CACAAGGAAACAGCTATGAC
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/strain="C57BL/O"
/db xref="taxon:1000"
/clone="UUGCIM0075004"
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 Mus musculus (house mouse)
Mus musculus
 AZ342492
AZ342492.1 GI:10419783
 Query Match 2.1%;
Best Local Similarity 92.0%;
Matches 23; Conservative 0
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source

FEATURES

5

ö

Gaps

2 TGTGTGTGTGTGTGTGTGTGT 26

```
Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gir a electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|q132114|gb|RF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 AZEB3081
1M0376L16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0376L16 R, genomic survey sequence.
 Б
 Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 27)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longares, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
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 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
 Tel: 801 585 5606
Fax: 801 585 777
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0376 row: L column: 16
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Class: plasmid ends
High quality sequence stop: 27.
 'organism="Mus musculus"
 mol type="genomic DNA"
strain="C57BL/6J"
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clone="UUGC1M0376L16"
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 sex="Male"
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Unpublished (2000)
 AZ583081
 VERSION
KEYWORDS
SOURCE
ORGANISM
 DEFINITION
 RESULT 29
AZ583081
 REFERENCE
AUTHORS
 ACCESSION
 JOURNAL
 FEATURES
 TITLE
 COMMENT
```

à ö Gaps .. 0 2.1%; Score 21.8; DB 1; Length 27; ilarity 92.0%; Pred. No. 31; Conservative 0; Mismatches 2; Indels 1793 TGTGTGTGTGTGTGTGTATAT 1817 Best Local Similarity Matches 23; Conserv Query Match

1793 TGTGTGTGTGTGTGTGTATAT 1817

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```
/ lab_host="E." Coli strain XLI0-Gold, Tl-resistant, F-"
/ lab_host="E." Coli strain XLI0-Gold, Tl-resistant, F-"
/ clone lib="Mouse 10kb plasmid UUGCIM library"
/ clone="Weetor: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligomuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarces get of a 9.5 to
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|q732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XLL0-Gold (Stratagene) cells
and selected for ampicillin resistance."
 ö
 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Am. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
 27 bp DNA linear GSS 16-FEB-2001
1M0550G18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0550G18 F, genomic survey sequence.
 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 27)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von Muse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
 Gaps
 .<u>`</u>
 Score 21.8; DB 1; Length 27; Pred. No. 31; 0; Mismatches 2; Indels
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunmegenetics.utah.edu
Insert Length: 10000 Std Brror: 0.
Plate: 0550 row: G column: 18
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Class: plasmid ends
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High quality sequence
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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 Mus musculus (house mouse)
Mus musculus
 AZ758321
AZ758321.1 GI:12863998
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Best Local Similarity 92.0%;
Matches 23; Conservative C
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AZ758321
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 AUTHORS
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GSS 16-FEB-2001

```
AZ801217 27 bp DNA linear GSS 16-FEB-200
2M0059P03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0059P03 R, genomic survey sequence.
 Mus musculus (house mouse)
Mus musculus
 AZ801217.1 GI:12953540
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ORGANISM
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COMMENT
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AUTHORS
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AZ801217
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/stane="UDCZMOUSENDED"
/lab_host="Coli strain XL10-Gold, Tl-resistant, F-"
/slobe="Mouse 10kb plasmid UNGCIM library.
/slobe="Weactor: PWNADIN: Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114 gip Ala123072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
 SM Mus musculus
Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
B 1 (bases 1 to 27)
S Dunn, D., Aoyaqi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,M., Stose,M., Sto
 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
12, USA
 AZ788874 100 27 bp DNA linear GSS 16-FEB-2001 2M0036H16F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0036H16 F, genomic survey sequence.
 chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
 Query Match 2.1%; Score 21.8; DB 1; Length 27; Best Local Similarity 92.0%; Pred. No. 31; Matches 23; Conservative 0; Mismatches 2; Indels
 Email: ddurn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0036 row: H column: 16
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
 organism="Mus musculus"
 mol_type="genomic_DNA"
strain="C57BL/6J"
 db_xref="taxon:10090"
clone="UUGC2M0036H16"
 High quality sequence stop: 27. Location/Qualifiers
 Mus musculus (house mouse)
 AZ788874.1 GI:12929113
 Tel: 801 585 5606
Fax: 801 585 7177
 source
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VERSION
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AZ788874
 JOURNAL
COMMENT
 REFERENCE
AUTHORS
 FEATURES
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Weetor: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt enderrepaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ende in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gil glo |AF129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli Xil10-Gold (Stratagene) cells
and selected for ampicillin resistance."
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 566 Fex: 801 585 7177 Eax: 801 585 7177 Exa: Roll secure country of Email: ddunn@genetics.utah.edu
 ö
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 27)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Railly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
 Gaps
 .
0
 Query Match 2.1%; Score 21.8; DB 1; Length 27; Best Local Similarity 92.0%; Pred. No. 31; Matches 23; Conservative 0; Mismatches 2; Indels
 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0059 row: P column: 03
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/mol_type="genomic DNA"
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/db_xref="taxon:10090"
/dlone="UUGC2M0059P03"
 1793 TGTGTGTGTGTGTGTGTATAT 1817
 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
 High quality sequence stop: 27.
Location/Qualifiers
 3 referererererererererer
 /sex="Male
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0; Gaps

1793 TGTGTGTGTGTGTGTGTGTATAT 1817

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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/motes="Vector: PWD42nv; Purificad genomic DNA from M.
musculus G75BL/6J (male) was obtained from the Jackson
Labozatory Mouse DNR Resources
/nttp://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwnyal (gil 4722114 gpl A712972.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
 AZ637290 23 bp DNA linear GSS 13-DEC-2000 IMO696005R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0496005 R, genomic survey sequence.
 5
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I Chases 1 to 23.

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Nedelly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
 SLC,
Mouse whole genome scaffolding with paired end reads from 10kb
 Gaps
 ö
 plaemid inserts
Unpublished (2000)
Unpublished (2000)
University of Utah Genome Center
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030
84112, USA
The: 801 585 506
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
 Query Match
2.0%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 30;
Matches 22; Conservative 0; Mismatches 1; Indels
 Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0309 row: C column: 01
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
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 mol type="genomic DNA"
|strain="C57BL/6J"
 db_xref="taxon:10090"
 clone="UUGC1M0309C01"
 1793 TGTGTGTGTGTGTGTGTAT 1815
 Mus musculus (house mouse)
 AZ637290.1 GI:11759480
 RESULT 35
AZ637290/c
 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 source
 LOCUS
 REFERENCE
AUTHORS
 JOURNAL
COMMENT
 TITLE
 FEATURES
 TITLE
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 d
 AZ483624
1M0309C01R Mouse 10kb plasmid UUGCIM library Mus musculus genomic close UUGCIM0309C01 R, genomic survey sequence.
 \bar{J} note="country: Zimbabwe, BST from adult gut infected with T.brucei"
 ô
 BX557786 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse34f11_plc, mRNA sequence.
 Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
 All clones with suffix qlc are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.
 Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota, morsitans morsitans
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Hippoboscoidea, Glossinidae, Glossina.

(bases 1 to 23)
Lehane,M.J., Assoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Iehane,M.J., Soarse,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the testse fly Glossina
morsitans morsitans and expression analysis of putative immune
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/db_xref="teaxon:37546"
/clone="19e34f11_plc"
/tissue_type="adult_infected_gut"
/clone_lib="Glossina morsitans morsitans adult_infected
 Gaps
 ô
 Contact: Hall N
Pathogen Sequencing Unit
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
 Query Match
2.0%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 30;
Matches 22; Conservative 0; Mismatches 1; Indels
 organism="Glossina morsitans morsitans"
 response genes
Genome Biol. 4 (10), R63 (2003)
 1793 TGTGTGTGTGTGTGTGTAT 1815
 Location/Qualifiers
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GSS.
 BX557786.1 GI:33428961
 AZ483624
 BX557786
 VERSION
KEYWORDS
SOURCE
ORGANISM
 DEFINITION
 VERSION
KEYWORDS
SOURCE
ORGANISM
 REFERENCE
AUTHORS
 RESULT 34
AZ483624
 DEFINITION
 ACCESSION
 JOURNAL
MEDLINE
PUBMED
COMMENT
 REFERENCE
AUTHORS
 RESULT 33
BX557786
 ACCESSION
 FEATURES
 TITLE
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mcgarry191-19.rst

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/lab hose="E" Coli strain XL10-Gold, T1-resistant, F-"
/lone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/mote="Vestor: PMD42nv; Purified ganomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/Accuments/Anares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|q732114|gb|AF129072.1); a copy-unmber
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed inco
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
 2M0106M12R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCZM0106M12 R, genomic survey sequence.
 Mus musculus (house mouse)

Mus musculus

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Eukaryota, Metazoa, Chordata, Sciurognathi, Muridae, Murinae;

Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;

1 (bases 1 to 23)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Elam, M., Longacres, S., Mahmoud, M., Menen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R.,

Niederhausern, A. and Wright, D., Weiss, R.

Niederhausern, A. and Wright, D., Weiss, R.

Nouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)
Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA.
 ·
0
 Query Match 2.0%; Score 21.4; DB 1; Length 23; Best Local Similarity 95.7%; Pred. No. 30; Matches 22; Conservative 0; Mismatches 1; Indels
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Class: plasmid ends
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| db xref="taxon:1009"
| clone="UUGC2M0038G13"
 1793 TGTGTGTGTGTGTGTGTAT 1815
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 AZ829195.1 GI:12999103
 /sex="Male"
 RESULT 37
AZ829195/c
 LOCUS
DEFINITION
 ORGANISM
 REFERENCE
AUTHORS
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 VERSION
KEYWORDS
SOURCE
 JOURNAL
 JOURNAL
COMMENT
 FEATURES
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 g
 Laboratory Mouse Down Resource (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt enderepaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|RR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xilo-Gold (stratagene) cells and selected for ampicillin resistance."
 AZ789907 2M0038G13F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0038G13 F, genomic survey sequence.
 Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weise, R.
Plasmid inserts
 plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 300, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 /sex="Male"
/lab host="E. Coli strain XLIO-Gold, TI-resistant, F-"
/clone lib="Mouse lobb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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 2.0%; Score 21.4; DB 1; Length 23; llarity 95.7%; Pred. No. 30; Conservative 0; Mismatches 1; Indels
 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0496 row: O column: 05
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
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 /mol_type="genomic DNA"
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 23 TGTGTGTGTGTGTGTGTGTGTGT 1
 AZ789907
AZ789907.1 GI:12931412
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
 Best Local Similarity
Matches 22; Conserv
 Query Match
 AZ789907/c
LOCUS
DEFINITION
 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 REFERENCE
 AUTHORS
 RESULT 36
 JOURNAL
 TITLE
 FEATURES
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COMMENT

FEATURES

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Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT
Contact: Hall N
Pathogen Sequencing Unit
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CBIO 18A, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix dic are reverse primer reads starting at 5'
end of the CDNA all plc reads are from
the 3' end.
 /note="country: Zimbabwe; BST from adult gut infected with
T.brucei"
 Mus musculus (house mouse)
Mus musculus
Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
Loases 1 to 24)
Dunn, D., Aoyagi, S., Mahmoud, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederinausern, A. and Wright, D., Weiss, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
 AZ419602
1M0196L12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0196L12 F, genomic survey sequence.
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/tiseue_type="adult infected gut"
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Best Local Similarity 95.7%; Pred. No. 31;
Matches 22; Conservative 0; Mismatches 1; Indels
 1. .24
/organism="Glossina morsitans"
 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0196 row: L column: 12
Stag primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifers

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 organism="Mus musculus"

 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
 /mol_type="genomic DNA"
/strain="C57BL/6J"
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Fax: 801 585 7177
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SOURCE
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 DEFINITION
 RESULT 39
AZ419602
 JOURNAL
 REFERENCE
AUTHORS
 ACCESSION
 PUBMED
COMMENT
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 BX559963
BX559963 Glossina morsitans morsitans adult infected gut Glossina morsitans adult infected gut Glossina BX559963
BX559963
 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length 10000 Std Error: 0.00
Plate: 0106 row: M column: 12
Seq primer: CACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
High quality sequence stop: 23.
 ö
 ₽.
 Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the testse fly Glossina morsitans morsitans and expression analysis of putative immune
 Glossina morsitans morsitans
Glossina morsitans morsitans
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
 Gaps
 ö
 2.0%; Score 21.4; DB 1; Length 23; ilarity 95.7%; Pred. No. 30; Conservative 0; Mismatches 1; Indels
 response genes
Genome Biol. 4 (10), R63 (2003)
22881942
 1793 TGTGTGTGTGTGTGTGTAT 1815
 23 TGTGTGTGTGTGTGTGTGTGT 1
 BX559963.1 GI:33367923
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Best Local Similarity
Matches 22; Conserv
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

ACCESSION

JOURNAL MEDLINE

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mcgarry191-19.rst

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 USA
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 ACCESSION
VERSION
 REFERENCE
AUTHORS
 RESULT 41
AZ807762
 JOURNAL
 KEYWORDS
 FEATURES
 TITLE
 COMMENT
 ਨੇ
 쉱
 Mus musculus (house mouse)

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae; Lo 24)

Islam, H., Longaoree,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von

Niederhausert and Wright,D.,Weiss,R., Tingey,A., von

Contact: Robert B. Weiss

Unpublished (2000)

Lontact: Robert B. Weiss

University of Utah Genome Center

University of Utah Genome Center

University of Utah

RM. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 muscular Lylanou (marie debratory Mass Ducained Libratory Mouse DNR Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 GSS 13-DEC-2000
 AZ621455
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 Gaps
 ö
 Query Match 2.0%; Score 21.4; DB 1; Length 24; Best Local Similarity 95.7%; Pred. No. 31; Matches 22; Conservative 0; Mismatches 1; Indels
 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0454 row: K column: 11
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
 organism="Mus musculus"
 /mol type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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 AZ621455.1 GI:11743645
 Tel: 801 585 5606
Fax: 801 585 7177
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 LOCUS
 ORGANISM
 RESULT 40
AZ621455
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KEYWORDS
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/lab_host="E. Coli strain XLI0-Gold, TI-resistant, F-"
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/clone="Woster: PWD42nr, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by respected passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was butnt end-repaired with T4 DNA polymerses and T4
polymuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwnfal (4172114) gp|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coll XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
 Б
 GSS 20-FEB-2001
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 24)
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1 (bases 1 to 24)
1 (bases 1 to 24)
1 (bases 2 to 24)
1 (bases 3 to 24)
1 (bases 3 to 24)
1 (bases 4 to 24)
1 (bases 4 to 24)
1 (bases 5 to 24)
1 (bases 6 to 24)
1 (bases 6 to 24)
1 (bases 7 to 24)
1 (ba
 AZ807762 20-FEB-200 24 bp DNA linear GSS 20-FEB-200 2M0070014R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0070014 R, genomic survey sequence.
 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
 Gaps
 .
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 Query Match
2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 31;
Matches 22; Conservative 0; Mismatches 1; Indels
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seg primer: CACACAGGAAACAGCTAATGACC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers

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/strain="C57BL/6J"

 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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 1793 TGTGTGTGTGTGTGTGTAT 1815
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 Mus musculus (house mouse)
 AZ807762.1 GI:12972432
GSS.
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indeportation of Maria Continual Liberatory Mouse DNA Resources documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.065 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF12972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coll Xi10-Gold (Stratagene) cells and selected for ampicillin resistance."
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (baess 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von plasmid inserts
plasmid inserts
 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 ö
 AZ813106
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/lab_host="B. Coli strain XL10-Gold, Tl-resistant, F-"
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Best Local Similarity 95.7%; Pred. No. 31;
Matches 22; Conservative 0; Mismatches 1; Indels
 Tel: 801 585 5606
Fax: 801 585 7177
Email: dduun@genetics.utah.edu
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Plate: 0880 row: A column: 16
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 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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 High quality sequence stop: 24. Location/Qualifiers
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 Unpublished (2000)
 USA
 Rm. 308,
84112, U
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AZ813106/c
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AUTHORS
 JOURNAL
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musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources (Jocuments/Anares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with 74 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarces gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD4 (1732114) gpl AR129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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 ö
 24 bp DNA linear GSS 20-FEB-200 MONGAGIAF Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCZM0146F14 F, genomic survey sequence.
 Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,M., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
plasmid inserts
plasmid inserts
Compublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC,
 /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
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 Fmail: ddunnagenetics.utah.edu
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 AZ846178.1 GI:13016086
 Tel: 801 585 5606
Fax: 801 585 7177
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 LOCUS
DEFINITION
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VERSION
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SOURCE
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 RESULT 43
AZ846178
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 TITLE
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Gaps

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Indels

..

0; Mismatches

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Matches 22; Conservative
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84112, US
 Query Match
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KEYWORDS
SOURCE
ORGANISM
 DEFINITION
 REFERENCE
AUTHORS
 JOURNAL
 RESULT 45
 FEATURES
 AZ345553
 TITLE
 COMMENT
 à
 musucula c.) who was the borathed the backson importatory Mouse DNR Resource (http://www.jax.org/resources/documents/dhares/). The DNR was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNR was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonacleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 k range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|RF129702.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 1 (Sabes 1.0.24).

Edilingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project; Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 isA, B-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREUS27/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing Projects. In Genome Sequencing Projects. In Barrell, Oxford University Press, 1999).
 TA163H11P 24 bp DNA linear GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 163h11, forward sequence,
 ö
 Email: nelsayed@tigr.org
Details of T. bruce; sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
 /clone_lib="Mouse 10kb plasmid UUGCIM library"
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musculus C57BL/6J (male) was obtained from the Jackson
 Gaps
 Trypanosoma brucei
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
 ö
 2.0%; Score 21.4; DB 1; Length 24; 95.7%; Pred. No. 31;
 2.0%; Score 21.4; DB 1; Length 24; 95.7%; Pred. No. 31; tive 0; Mismatches 1; Indels
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/clone="163h11"
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 Trypanosoma brucei
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Best Local Similarity 95.7
Matches 22; Conservative
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 Query Match
Best Local Similarity
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TA163H11P/c
 VERSION
KEYWORDS
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/elone="unclimousbate"
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// pape="male" | Jab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
// clone lb="whouse lokb plasmid UUGCIM library"
// note="Vector: PWDAIN: Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
imboratory Mouse DNA Resource
// hotp://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWNAT2 (gil H732114[gb|AR129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
 ö
 A2345553 29-SEP-2000 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M08016 F, genomic survey sequence.
 Б
 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
 Gaps
 ö
 DB 1; Length 25;
 Indels
 Hall, USB 5606
Fax: 801 585 5006
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: E column: 16
Seg primer: CGTTGTAAAACGACGCCAGT
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 Mus musculus (house mouse)
Mus musculus
 AZ345553.1 GI:10424790
 Similarity
 Best Local
Matches 2
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g

1793 TGTGTGTGTGTGTGTGTAT 1815

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g
 (thtp://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymcleotide kinase. Adaptor oligomocleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi/4732114) pb lAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptores complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XL10.601d (Stratagene) cells and selected for ampicillin resistance."
 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 GSS 03-OCT-2000
 Mus musculus Butazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Maukaryote, Metazoa, Chordata, Craniata, Vertebrata, Eutleria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 25)
1 (bases 1 to 25)
2 (bann, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longaore, S., Mahmoud, M., Menen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Miderhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 A2404057

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 /lab_host="B. Coli strain XL10-Gold, T1-resistant, F-" /clone_lib="Mouse lokb plaemid UVGCIM library" /note="Vector: PMP42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
 Tel: 801 585 5606
Fax: 801 585 7177
Fax: 801 585 7177
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Seg primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 25.
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 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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1793 TGTGTGTGTGTGTGTGTAT 1815
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 /sex="Male"
 USA
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 JOURNAL
 FEATURES
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TITLE

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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymicleotide kinase. Adaptor oligomicleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWAP2 (gil 47321141gb| BNE29072.1); a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed inco chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 ö
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Buthoria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. L. (basea, 1 to 23.)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Nese, M., Rose, M., Meright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 AZ467470 25 bp DNA linear GSS 04-OCT-200
IM0278E21R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
Clone UUGCIM0278E21 R, genomic survey sequence.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
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Laboratory Mouse DNA Resource
 Gaps
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 2.0%; Score 21.4; DB 1; Length 25; larity 95.7%; Pred. No. 32; Conservative 0; Mismatches 1; Indels
 Email: ddunn@genetics.utah.edu
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Fax: 801 585 7177
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SOURCE
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 JOURNAL
 FEATURES
 TITLE
 COMMENT
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1793 TGTGTGTGTGTGTGTGTAT 1815

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Gaps ö

Query Match 2.0%; Score 21.4; DB 1; Length 25; Best Local Similarity 95.7%; Pred. No. 32; Matches 22; Conservative 0; Mismatches 1; Indels

GSS.

ORGANISM

SOURCE

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ACCESSION VERSION KEYWORDS

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GSS 16-FEB-2001

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Laboratory Mouse DNA Resources Adocuments/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifica at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated mol area and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gfrom a derivative
of pwD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli X110-Gold (Stratagene) cells
and selected for ampicillin resistance."
 Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 23).

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Miderfausern,A. and Wright,D., Weiss,R.
 AZ771881
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 Score 21.4; DB 1; Length 25;
Pred. No. 32;
0; Mismatches 1; Indels
 Email: ddunn@genetics.utah.edu
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 Mus musculus (house mouse)
 AZ771881.1 GI:12894610
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 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
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VERSION
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ORGANISM
 DEFINITION
 RESULT 49
AZ771881
 JOURNAL
 REFERENCE
 AUTHORS
 FEATURES
 TITLE
 COMMENT
 ઠે
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/ note="Vector: FWD42nv; Purified genomic DNA from M.
musculus C57B1/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifica at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated by sheared DNA
was hydrodynamically sheared by repeated and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli Xi10-Gold (Stratagene) cells
and selected for ampicillin resistance."
 Mus musculus

Eukaryota, Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Butaryota; Matazoa; Chordata; Sciurognathi; Muridae; Musinae; Loss;

I (bases 1 to 25)

S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B.; Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.,

Muse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

AL Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah Genome Center
University of Utah
 AZ769673 16-FEB-2001 1MO570D12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0570D12 R, genomic survey sequence.
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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 0; Gaps
 Query Match 2.0%; Score 21.4; DB 1; Length 25; Best Local Similarity 95.7%; Pred. No. 32; Matches 22; Conservative 0; Mismatches 1; Indele
 Email: ddunn@genetics.utah.edu
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Plate: 0570 row: D column: 12
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 Mus musculus (house mouse)
AZ769673.1 GI:12890050
 Tel: 801 585 5606
Fax: 801 585 7177
 USA
 84112,
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source

FEATURES

Gaps ô

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AZ419877 GSS.

KEYWORDS SOURCE ORGANISM ACCESSION

/ERSION

AUTHORS REFERENCE

JOURNAL

TITLE COMMENT

RESULT 50 AZ419877/c LOCUS DEFINITION

GSS 04-OCT-2000

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.05 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.05 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 14 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarces get electrophoresis. Vector DNA was prepared from a derivative of pwHD42 (gi[4732114]gb[AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xi10-Gold (Stratagene) cells and selected for ampicillin resistance."
 Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
84112, USA
Fax: 801 585 506
Fax: 801 585 506
Fax: 801 587 177
Email: dumn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0278 row: 0 column: 07
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 26.
 Bukaryotai Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (Dases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenn, E., Pedersen, T., Niederhausern, A. and Wright, D., Weise, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
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1M0278007F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0278007 F, genomic survey sequence.
AZ467063
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/note="Yotcor: PWD42nv; Purified genomic DNA from M.
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Laboratory Mouse DNA Resource
 Query Match 2.0%; Score 21.4; DB 1; Length 26; Best Local Similarity 95.7%; Pred. No. 33; Matches 22; Conservative 0; Mismatches 1; Indels
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 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
 /db_xref="taxon:10090"
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 1793 TGTGTGTGTGTGTGTGTAT 1815
 4 rerererererererererer
 Mus musculus (house mouse)
Mus musculus
 AZ467063.1 GI:10625188
 /sex="Male"
 plasmid inserts
Unpublished (2000)
 source
 LOCUS
 ORGANISM
RESULT 51
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 AZ467063
 FEATURES
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 SOURCE
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(clone_lib="Wouse 10kb plasmid UUGCIM library"

/note="Vector: PWD4Znv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources (Accuments/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA

was hydrodynamically sheared by repeated by respected through a
0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from, a derivative
of pWD42 (gi|4732114|gb|AF129702.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 GSS 03-OCT-2000
 ö
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (2025) 1 to 26)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
 AZ419877 208 03-OCT-200 AM linear GSS 03-OCT-200 MO196N03R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0196N03 R, genomic survey sequence.
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Fax: 801 585 7177
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Location/Qualifiers
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Matches 22; Conservative
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 plasmid inserts
Unpublished (2000)
 Mus musculus
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source

FEATURES

USA

0; Gaps

26 TGTGTGTGTGTGTGTGTGTGT 4

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Query Match

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Bukaryota; Matazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musna.

1 (bases 1 to 26)

2 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Nouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
University of Utah
 AZB30551 200-FEB-2001
2M0109C19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0109C19 R, genomic survey sequence.
 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0109 row: C column: 19
Seq primer: CACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
 Mus musculus (house mouse)
 AZ830551.1 GI:13000459
 Tel: 801 585 5606
Fax: 801 585 7177
 Rm. 308, E
84112, USA
 source
 VERSION
KEYWORDS
SOURCE
ORGANISM
 JOURNAL
COMMENT
 DEFINITION
 REFERENCE
 AUTHORS
 ACCESSION
 FEATURES
AZ830551
 TITLE
 / General Control Structure of the property of the process of the
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Butaryota, Metazoa, Chordata, Sciurognathi, Muridae, Murinae, Mus. Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 26)

B. Junn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 AZ646850 26 bp DNA linear GSS 14-DEC-2000 1M0513L06F Mouse 10kb plasmid UUGclM library Mus musculus genomic clone UUGClM0513L06 F, genomic survey sequence.
AZ646850. GI:11777730
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Location/Qualifiers
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Mus musculus
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AUTHORS
 JOURNAL
 FEATURES
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/sex="Male"

Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

USA

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/clone="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gfrom a derivative
of pMD42 (gi|4732114|gb|AP129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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 DB 1; Length 26;
 1; Indels
 2.0%; Score 21.4; Dilarity 95.7%; Pred. No. 33; Conservative 0; Mismatches
 1793 TGTGTGTGTGTGTGTGTAT 1815
 rerererererererererer 25
 Similarity
 22;
 Query Match
Best Local S:
Matches 22;
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RESULT 54 AZ310642

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DB 1; Length 26; 1; Indels

2.0%; Score 21.4; DE 95.7%; Pred. No. 33; tive 0; Mismatches

Query Match
Best Local Similarity 95.77
Matches 22; Conservative

1793 TGTGTGTGTGTGTGTGTAT 1815 3 rererererererererereres

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23 RESULT

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL

TITLE

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pmap. [4] 4732114[9]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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1M0062213F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
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musculus C57BL/6J (male) was obtained from the Jackson
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Roses, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunogenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0062 row: P column: 13
Seq primer: CGTTGTAAAACGACGCCAGT
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 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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 /db_xref="taxon:10090"
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 Mus musculus (house mouse)
Mus musculus
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 Query Match
Best Local Similarity 100.*
Matches 21; Conservative
 plasmid inserts
 RESULT 56
AZ762904
LOCUS
DEFINITION
 DEFINITION
 ORGANISM
 ACCESSION
VERSION
KEYWORDS
SOURCE
 REFERENCE
AUTHORS
 JOURNAL
COMMENT
 FEATURES
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 / Jabones= Cooling Strain XIIO-Gold, Ti-resistant, F-"
/ Jab host="E. Coli strain XIIO-Gold, Ti-resistant, F-"
/ Jab host="E. Coli strain XIIO-Gold, Ti-resistant, F-"
/ Clone lib="wouse lobe plasmid UUGCIM library"
/ note="Vector: PWD42ny; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
/ (http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide Kinase. Adaptor oligonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb ange using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1) a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adappored vector DNA, and transformed into
chemically-competent B. coli XiiO-Gold (Stratagene) cells
and selected for ampicillin resistance."
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 GSS 29-SEP-2000
 GSS 29-SEP-2000
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. I (bases I to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Lorgacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niderhausern,A. and Wright,D.,Weiss,R., Tingey,A., von Mouse whole genome scaffolding with paired end reads from 10kb from hished force.
 AZ310642 10kb plasmid UUGCIM library Mus musculus genomic
 Gaps
 ó
 Query Match 2.0%; Score 21; DB 1; Length 21; Best Local Similarity 100.0%; Pred. No. 30; Matches 21; Conservative 0; Mismatches 0; Indels
 linear
 clone UUGC1M0025N09 R, genomic survey sequence.
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 Email: ddunn@genetics.utah.edu
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clone="UUGC1M0025N09"
 1793 TGTGTGTGTGTGTGTGTGT 1813
 21
 Mus musculus (house mouse)
Mus musculus
 rererererererererer
 AZ310642.1 GI:10352832
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
 AZ333309
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source

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AZ762904 11near GSS 16-FEB-2001 1M0558G12F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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2.0%; Score 21; DB 1; Length 21;
 Indels
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RESULT 55 AZ333309 LOCUS

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM JOURNAL

TITLE

AUTHORS REFERENCE

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muscular Crybly (Marle Margource Indocratic Louis Checker, Indocratory Mouse DNR Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymorlectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XII.0-Gold (Stratagene) cells and selected for ampicillin resistance."
 AZ484090 22 bp DNA linear GSS 05-OCT-200 1M0310115F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0310115 F, genomic survey sequence.
 Mus musculus Euklayota, Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Ciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)
1 (bases 1 to 21)
2 (bases 1 to 21)
1 (bases 1 to 21)
2 (bases 1 to 21)
3 (bases 1 to 21)
4 (bases 1 to 21)
5 (bases 1 to 21)
8 (bases 1 t
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 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
 2.0%; Score 21; DB 1; Length 21;
100.0%; Pred. No. 30;
ive 0; Mismatches 0; Indels
 Email: ddunnagenetics.utah.edu
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 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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 /db xref="taxon:10090"
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 Mus musculus (house mouse)
 AZ854856
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 Rm. 308, Biomedical
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
 Unpublished (2000)
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Best Local Si
Matches 21;
 RESULT 58
AZ484090
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VERSION
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SOURCE
ORGANISM
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 REFERENCE
AUTHORS
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 ठ
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (basea 1 to 21)
Bunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of pwMD42 (gilfyla) [4]plAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chamically-competent B. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
 AZB54856 2001 2005 21 bp DNA linear GSS 21-FEB-2001 2M0158109R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0158109 R, genomic survey sequence.
 ô
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 clone UUGC1M0558G12 F, genomic survey sequence.
 Email: ddunn@genetics.utah.edu
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 Mus musculus (house mouse)
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GSS.
 sex="Male"
 Query Match
Best Local Similarity 100.
Matches 21; Conservative
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
 . 21
 Mus musculus
 USA
 84112,
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source

FEATURES

GSS 05-OCT-2000

RESULT 57 AZ854856 LOCUS DEFINITION

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Gaps .; 0

KEYWORDS SOURCE ORGANISM

/ERSION

REFERENCE AUTHORS JOURNAL COMMENT

TITLE

FEATURES

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GSS.

Mus musculus (house mouse)

Mus musculus musculus (hordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

1 (bases 1 to 22)

1 (bases 1 to 22)

2 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

AL Ontact: Robert B. Weiss

University of Utah Genome Center

University of Utah Genome Center

University of Utah

Research Bldg., 20 S. 2030 E., SLC, UT
 muscular Cylebron terminals, was obtained from the box muscular dynamical by Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xiii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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/note="Vector: FWN42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
 2.0%; Score 21; DB 1; Length 22; 100.0%; Pred. No. 31; arive 0; Mismatches 0; Indels
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Insert Length: 10000 Std Error: 0.00
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 Rm. 308, Biomedical
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
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Best Local Similarity
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DEFINITION
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SOURCE
ORGANISM
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VERSION
KEYWORDS
 RESULT 60
AZ328763
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AUTHORS
 JOURNAL
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 TITLE
 COMMENT
 / Jean-Bornary Controller of the control of the control of the controller of the con
 Eukaryotta; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryotta; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1. (bases 1 to 22)
Bunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Waiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah
Res. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT
 AZ985497
2M0267D23F Mouse 10kb plasmid UUGC2M library Mus musculus genomic cone UUGC2M0267D23 F, genomic survey sequence.
 ö
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0
 Query Match 2.0%; Score 21; DB 1; Length 22; Best Local Similarity 100.0%; Pred. No. 31; Matches 21; Conservative 0; Mismatches 0; Indels
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Plate: 0310 row: I column: 15
Seq primer: CGTFGTAAAACGACGCCAGT
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/mol_type="genomic DNA"
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 /db_xref="taxon:10090"
/clone="UUGC1M0310115"
 High quality sequence stop: 22.
Location/Qualifiers
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 1 TGTGTGTGTGTGTGTGTGT 21
 Mus musculus (house mouse)
Mus musculus
 AZ484090.1 GI:10648679
 Rm. 308, B:
84112, USA
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Gaps

AZ985497.1 GI:13856724

ACCESSION VERSION

LOCUS

RESULT 59 AZ985497

SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL

TITLE

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1 (bases 1 to 23)

2 1 (bases 1 to 24)

1 Sand, H., Longacree, S., Mahmuud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Thngey, A., von Diamid inserts

1 Unpublished (2000)

2 Contact: Robert B. Weiss

3 University of Utah Genome Center

3 University of Utah

3 Contact: Robert B. Weiss

4 University of Utah

5 Contact: Robert B. Weiss

6 Contact: Robert B. Weiss

7 Contact: Robert B. Weiss

8 University of Utah

8 Contact: Robert B. Weiss
 Induction of Marse of
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/lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
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 Tail: 801 585 5606
Fax: 801 585 7177
Famil: ddunnagenetics.utah.edu
Email: ddunnagenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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/strain="C57BL/6J"
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/clone="UUGC1M0122K19"
 1793 IGIGIGIGIGIGIGIGIGI 1813
 3 rererererererererer 23
 Mus musculus (house mouse)
Mus musculus
 AZ824638.1 GI:12994546
 Rm. 308, Bj
84112, USA
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 DEFINITION
 ORGANISM
 ORGANISM
 ACCESSION
 REFERENCE
 AUTHORS
 JOURNAL
 RESULT 62
 KEYWORDS
SOURCE
 AZ824638
 FEATURES
 TITLE
 VERSION
 ઠ
 Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XII0-Gold (Stratagene) cells and selected for ampicillin resistance."
 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 AZ371475 22-OCT-2000 1MO122K19R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0122K19 R, genomic survey sequence.
 ö
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. I. (bases 1 to 2).

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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Laboratory Mouse DNA Resource
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 Email: ddunm@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0052 row: L column: 12
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
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Location/Qualifiers
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 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/clone="UUGC1M0052L12"
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Mus musculus (house mouse)
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Mus musculus
 /sex="Male"
 Tel: 801 585 5606
Fax: 801 585 7177
 USA
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 84112,
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source

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Query Match 2.0%; Score 21; DB 1; Length 23; Best Local Similarity 100.0%; Pred. No. 32; Matches 21; Conservative 0; Mismatches 0; Indels
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DEFINITION

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AZ371475

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 JOURNAL
 AZ647335
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/lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/clon= 11b="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/G1 (male) was obtained from the Jackson
Laboratory Mouse DNA Resources (documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gf con a derivative
of pwD42 (gi|4732114|gb|AR129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent B. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
 ö
 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 GSS 20-FEB-2001
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 23)

Bunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Ralam, H., Longacree, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Underwoole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
 AZ828969
2M0106013F Mouse 10kb plasmid UUGCIM library Mus musculus genomic Clone UUGC2M0106013 F, genomic survey sequence.
 Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 0; Gaps
 2.0%; Score 21; DB 1; Length 23;
 0; Indels
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0099 row: A column: 22
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 /db_xref="taxon:10090"
/clone="UUGC2M0099A22"
 High quality sequence stop: 23.
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AZ828969.1 GI:12998877
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 SOURCE
ORGANISM
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KEYWORDS
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/note="Westor: PWD42nv; Purified genomic DNA from M.
/note="Westor: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNR Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to.
10.5 kb range using preparative agarose get a copy-number
of pWD42 (gi|q732114) gb|AR129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli Xil0-Gold (stratagene) cells
and selected for ampicillin resistance."
 GSS 14-DEC-2000
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 ö
 24 bp DNA linear GSS 14-DEC-200
1MOS13J1SR Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1MO513J15 R, genomic survey sequence.
AZ647335
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 23)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Railly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Unnuse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
 0; Gaps
 Query Match 2.0%; Score 21; DB 1; Length 23; Best Local Similarity 100.0%; Pred. No. 32; Matches 21; Conservative 0; Mismatches 0; Indels
 Email: ddunn@genetics.utah.edu
Insert Length; 10000 Std Error: 0.00
Plate: 0106 row: 0 column: 13
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Class: plasmid ends
High quality sequence stop: 23.
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 /db_xref="taxon:10090"
/clone="UUGC2M0106013"
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 /sex="Male"
 Tel: 801 585 5606
Fax: 801 585 7177
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Best Local Similarity 100.04
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 REFERENCE
AUTHORS
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 RESULT 66
 ACCESSION
 VERSION
KEYWORDS
 FEATURES
 AZ506209
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 a
 Attribed Annual Control of the contr
1 (bases 1 to 24)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Lorgacces., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Dlasse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
Rm. 308, Elomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 AZ459694 100 25 bp DNA linear GSS 04-OCT-2000 1M0264PlOR Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0264PlO R, genomic survey sequence.
 ö
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
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 Query Match 2.0%; Score 21; DB 1; Length 24; Best Local Similarity 100.0%; Pred. No. 34; Matches 21; Conservative 0; Mismatches 0; Indels
 84112, USA
Tel: 801585 5606
FAX: 801 585 7177
Email: ddunn@genetics.utah.edu
 Laboratory Mouse DNA Resource
 Insert Length: 10000 Std Error: (Plate: 0513 row: J column: 15 Seq primer: CACACAGGAAACAGCTATGACC
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 /mol_type="genomic DNA"
/strain="CS7BL/6J"
 db_xref="taxon:10090"
/clone="UUGC1M0513J15"
 High quality sequence stop: 24. Location/Qualifiers
 1793 TGTGTGTGTGTGTGTGTGT 1813
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 Mus musculus (house mouse)
Mus musculus
 AZ459694.1 GI:10617819
 Class: plasmid ends
 USA
 source
 REFERENCE
AUTHORS
 DEFINITION
 SOURCE
ORGANISM
 JOURNAL
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 REFERENCE
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 AZ459694
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 COMMENT
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Abbratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymerase and T4 polymerase and T4 polymerase and T4 polymerase and T6 polymerase and T7 polymerase and T7 polymerase and T8 polymerase and T9 polymera
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 GSS 05-OCT-2000
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
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/note="Vector: PWD42nv; Purlited genomic DNA from M.
musculus C5/BL/6J (male) was obtained from the Jackson
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longarce, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Ungey, A., von Dussmid inserts
Unpublished (2000)
Unpublished (2000)
University of Utah Genome Center
University of Utah Genome Center
 0; Gaps
 2.0%; Score 21; DB 1; Length 25; 100.0%; Pred. No. 35; tive 0; Mismatches 0; Indels
 Tel: 801 585 5606
Fax: 801 585 7177
Email: dduun@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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 Mus musculus (house mouse)
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2.0%
Best Local Similarity 100.0
Matches 21; Conservative
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 DEFINITION
 ORGANISM
 REFERENCE
AUTHORS
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KEYWORDS
SOURCE
 RESULT 68
 JOURNAL
 AZ602037
 FEATURES
 TITLE
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 Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|q132114|gb|RR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. ooli XLLU-Gold (Stratagene) cells and selected for ampicillin resistance."
 AZ494629

1M0330F01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0330F01 F, genomic survey sequence.
 ö
 Б
 Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
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/note="Weetor: PWD42Lr; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
 plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Thogey, A., von Niederhausern, A. and Wright, D. Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb Mouse
 Gaps
 2.0%; Score 21; DB 1; Length 25; ilarity 100.0%; Pred. No. 35; Conservative 0; Mismatches 0; Indels
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Class: plasmid ends

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/strain="C57BL/6J"

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 24
 AZ494629.1 GI:10669392
GSS.
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 Query Match
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Matches 21; Conserv
 AZ494629
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KEYWORDS
SOURCE
ORGANISM
 LOCUS
 RESULT 67
AZ494629
 ACCESSION
 AUTHORS
 REFERENCE
 JOURNAL
 TITLE
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셤

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musuculas c.) tunies un Resource (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared bNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonacleotides were joilymucleotide kinase. Adaptor oligonacleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarese gel electrophoresis, vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF12972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
 GSS 13-DEC-2000
 Mus musculus (house mouse)
Mus musculus
Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Musmmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,B., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 AZ602037
1M0420A10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0420A10 R, genomic survey sequence.
 Unpublished (2000)
Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah
Am. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
 /sex="Male"
/lab host="B. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCLM library"
/note="Wetcr: PWD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
 Gaps
 ó
 2.0%; Score 21; DB 1; Length 26; 100.0%; Pred. No. 36; trive 0; Mismatches 0; Indels
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunnegenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends

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/db_xref="taxon:10090"
/clone="UUGC1M0330F01"
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JOURNAL COMMENT

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GSS.
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Best Local Similarity 88.0°
Matches 22; Conservative
 AZ368875
 AZ368875
LOCUS
DEFINITION
 ACCESSION
VERSION
KEYWORDS
SOURCE
 ORGANISM
 REFERENCE
AUTHORS
 JOURNAL
COMMENT
 RESULT 70
 FEATURES
 TITLE
 ઠે
 g
 Importance of Notice DNR Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|RR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XIIO-Gold (Stratagene) cells and selected for ampicillin resistance."
 ô
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Mus musculus (house mouse)
Mus musculus
Mus musculus
Mus musculus
Mus repease (hordata; Craniata; Vertebrata; Euteleostomi;
Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
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/note="Vector: PWD421v; Purified genomic DNA from M.
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Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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 Score 20.4; DB 1; Length 23; Pred. No. 37; 0; Mismatches 1; Indels
 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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High quality sequence stop: 23.
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AZ465273.1 GI:10623398
GSS.
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Best Local Similarity 95.5%;
Matches 21; Conservative
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@qenet
```

RESULT 69 AZ465273 LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

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Unpublished (2000)
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Ru. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
112, USA
113, USA
114: 801 585 7177
Email: ddunn@genetics.utah.edu
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// Calone lib= Mouse loke plasmid UnGCIM library"
// note="Weetor: PWD4DATM; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Labozatory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWDA2 (gel 4732114|gpl)AP129072.1), a copy number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
 AZ168875 10 bp DNA linear GSS 02-OCT-2000 1M0119112F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0119112 F, genomic survey sequence.
 ö
 Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
I (basea I to 20)
Eurn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Islam, H., Rose, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weise, R.
Mouse whole genome scaffolding with paired end reads from 10kb
 o
 1.9%; Score 20.2; DB 1; Length 25; 88.0%; Pred. No. 41; trive 0; Mismatches 3; Indels
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5

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gol electrophoresis. Vector DNA was prepared from a derivative of pMAP2 (gif 4722114[gb]AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent 2. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 Mus musculus (house mouse)
Mus musculus (house mouse)
Mus musculus
Mus musculus
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Eukaryota, Metazoa; Chordata, Sciurognathi, Muridae, Murinae, Mus.
1 (base 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
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MPQ2587809F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0285H09 F, genomic survey sequence.
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/clone lib="Mouse lokb plasmid UUGCIM library"
/note="Twetcr: PWD42nry Purified genomic DNA from Musculus C57BL/63 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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1.9%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 36; Matches 20; Conservative 0; Mismatches
 Tel: 801 585 5606
Fax: 801 585 7177
Eaal: ddundgenetics.utah.edu
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Plate: 0275 row: F column: 24
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 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Rese
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/sex="Male"
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 AZ470768.1 GI:10628893
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SOURCE
ORGANISM
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 RESULT 72
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/note="Weator: PWD42nv; Purifited genomic DNA from M.
macoulus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/Anares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated proceded to a
polynuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose get
adaptored DNA was purified and size-selected from a derivative
of pWD42 (gil #4732114|gpl AR129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouses DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
 ö
 AZ465453 1002 DNA linear GSS 04-OCT-2000 1M0275F24F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0275F24 F, genomic survey sequence.
 S. 2030 E., SLC, UT
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 20)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niderhausern,A. and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Gaps
 Query Match 1.9%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 36; Matches 20; Conservative 0; Mismatches 0; Indels
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
84112, USA
 Email: ddunn@genetics.utah.edu
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 Mus musculus (house mouse)
Mus musculus
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 sex="Male"
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
 VERSION
KEYWORDS
SOURCE
ORGANISM
 LOCUS
 JOURNAL
COMMENT
 RESULT 71
AZ465453
 ACCESSION
 REFERENCE
 AUTHORS
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TITLE

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AZ634201
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KEYWORDS
SOURCE
ORGANISM
 LOCUS
DEFINITION
 REFERENCE
AUTHORS
 JOURNAL
 ACCESSION
 AZ634201
 TITLE
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/ Jab host="B" Coli strain XL10-Gold, Tl-resistant, F-"
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/ note="Westor: PMD4Zav; Parified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end: repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gf rom a derivative
of pwD402 (gf 14732114 gb) [Ar29072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
 AZS80200
1M0368A20F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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 Bukaryocaria Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Musinae, Lusteria, Rodentia, Sciurognathi, Muridae, Murinae, Musina, Losae, 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Rallay, M., Rose, M., Rose, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Diasmid inserts

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 0; Indels
 Tel: 801 585 5606
Fax: 801 585 7177
Enail: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0:00
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 1793 TGTGTGTGTGTGTGTG 1812
 Mus musculus (house mouse)
 1 TGTGTGTGTGTGTGTGTG 20
 Contact: Robert B. Weiss
 AZ580200
AZ580200.1 GI:11694629
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DEFINITION
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AUTHORS
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KEYWORDS
SOURCE
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 COMMENT
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University of Utah Genome Center

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BELL 2019, Storedical Polymers Research Bidg., 20 S. 2010 E., SLC, UT

BELL 2019, Storedical Polymers Research Bidg., 20 S. 2010 E., SLC, UT

BEALL 2018, ST. 2018

Beall 501 Set Town A. Columnia C.

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Set Primer: CONTINUAL C.

Set District C.

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musculus G57BL/6" (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
/thtp://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWNA2 (gil 473214) glb AR129072.1); a copy-number inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed linc
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
 200226105R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0226105 k, genomic survey sequence.
 Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1. (bases 1 to 20)

Dun, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Island, H., Longarore, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.,

Mouse whole genome scaffolding with paired end reads from 10kb

Dhamid inserts

Unpublished (2000)
 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
 S. 2030 E., SLC,
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 Biomedical Polymers Research Bldg., 20
Rm. 308, Biomeaic...
84112, USA
121: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Location/Qualifiers
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 RESULT 76
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KEYWORDS
SOURCE
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AUTHORS
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Laboratory Mouse DNA Resources (documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated from state
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored bNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gfrom a derivative
of pWD42 (gi|4732114|gb|AF129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
 GSS 27-APR-2001
 S. 2030 E., SLC, UT
 Bukaryotts, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 AZ946508
2M0208P13F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0208P13 F, genomic survey sequence.
 Gaps
 ..
 1.9%; Score 20; DB 1; Length 20; ilarity 100.0%; Pred. No. 36; Conservative 0; Mismatches 0; Indels
 University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
84112, USA
 Email: ddurn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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clone="UUGC1M0489C19"
 1794 GIGIGIGIGIGIGIGIGI 1813
 Mus musculus (house mouse)
 1 GIGIGIGIGIGIGIGI 20
 AZ946508.1 GI:13815584
 sex="Male"
 Tel: 801 585 5606
Fax: 801 585 7177
 Query Match
Best Local Similarity
Matches 20; Conserv
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AUTHORS
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ACCESSION

TITLE

RESULT 75

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DEFINITION
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 RESULT 78
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 ò
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.05 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.05 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 14 DNA polymerase and 74 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarces gel electrophoresis. Vector DNA was prepared from a derivative of pwh92 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.
 AZ635627 21 bp DNA linear GSS 13-DEC-2000 LMO493DO6F Mouse 10kb plasmid UUGCIM library Mus musculus genomic UUGCIM0493D06 F, genomic survey sequence.
 Conteact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
 /sex="Female"
/lab host="B. coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC2M library"
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Laboratory Mouse DNA Resource
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. [Dases 1 to 21]

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Railam, H., Longacres, S., Mahmoud, M., Menen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Divouse whole genome scaffolding with paired end reads from 10kb plasmid innerts
 0; Gaps
 Query Match
1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 0; Indels
 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Class: plasmid ends
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/strain="C57BL/64"
 db xref="taxon:10090"
/clone="UUGC2M0226L05"
 1793 TGTGTGTGTGTGTGTGTGTG 1812
 Mus musculus (house mouse)
Mus musculus
 20 TGTGTGTGTGTGTGTGTG 1
 AZ635627.1 GI:11757817
Tel: 801 585 5606
Fax: 801 585 7177
 AZ635627
 AZ635627
 source
 AZ635627
LOCUS
DEFINITION
 ORGANISM
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KEYWORDS
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligomuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gi|4732114|gb|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 21)
Dun,D.; Aoyagi,A.; Barber,M.; Beacorn,T.; Duval,B.; Hamil,C.;
Islam,H.; Longadze,S.; Mahmoud,M.; Menen,E.; Pedersen,T.;
Reilly,M.; Rose,M.; Rose,R.; Stokes,R.; Tingey,A.; von
Niederhausern,A. and Wright,D.; Weiss,R.;
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
L Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
 AZ641805

21 bp DNA linear GSS 14-DEC-2000
1M0504J04R Mouse 10kb plasmid UJGCIM library Mus musculus genomic
clone UJGCIM0504J04 R, genomic survey sequence.
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
 ö
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 0; Gaps
 1.9%; Score 20; DB 1; Length 21;
100.0%; Pred. No. 37;
tive 0; Mismatches 0; Indels
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Email: 10000 Std Brror: 0.00
Plate: 0493 row: D column: 06

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 1 Gréferérérérérérérér
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Best Local Similarity 100.09
Matches 20; Conservative
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 AZ514387/c
 ORGANISM
 RESULT 80
 JOURNAL
 ACCESSION
 REFERENCE
 AUTHORS
 KEYWORDS
 FEATURES
 TITLE
 COMMENT
 SOURCE
 SM Mus musculus (note) musculus Eby Musculus E 1 (bases 1 to 21)

1 (bases 1 to 21)

1 (bases 1 to 21)

1 (bases 1 to 21)

1 (bases 1 to 21)

1 (bases 1 to 21)

1 (bases 1 to 21)

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1 (bases 1 to 21)

1 (bases 1 to 21)

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1 (bases 1 to 21)

1 (bases 1 to 21)

1 (bases 1 to 21)

2 (bases 1 to 21)

2 (bases 1 to 21)

2 (bases 1 to 21)

3 (bases 1 to 21)

4 (bases 1 to 21)

4 (bases 1 to 21)

5 (bases 1 to 21)

6 (bases 1 to 21)

7 (bases 1 to 21)

8 (bases 2 to
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end:repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agances gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Laboratory Mouse DNA Resource
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Insert Length: 10000 Std Error: 0.00
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/clone="UUGC1M0504J04"
 1794 GIGIGIGIGIGIGIGIGI 1813
 Mus musculus (house mouse)
 1 Grerererererererer 20
 AZ991225.1 GI:13862452
 sex="Male"
 Tel: 801 585 5606
Fax: 801 585 7177
Fax: 801 585 7177
 USA
 AZ991225
 AZ991225/c
LOCUS
 VERSION
KEYWORDS
SOURCE
ORGANISM
 DEFINITION
 ACCESSION
 REFERENCE
 AUTHORS
 JOURNAL
 RESULT 79
 FEATURES
 TITLE
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d

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/ note="WeatOr: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resources (documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch ond repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose get a 9.5 to
10.5 kb range using preparative agarose get of a 9.5 to
10.5 kb range using preparative agarose from a derivative
of pMD42 (gil 4732114 | gb | AR129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XiliO-Gold (Stratagene) cells
and selected for ampicillin resistance."
 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 AZ514387
22 bp DNA linear GSS 05-OCT-2000 1M0361H03F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0361H03 F, genomic survey sequence.
 Mus musculus (house mouse)

Mus musculus

Mus musculus

Mus musculus

Mus musculus

Muscarca, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

1 (bases 1 to 22)

10 (bases 1 to 22)

Muscarca, Muscarca, Muscarca, Muscarca, Muscarca, Mus.

11 (bases 1 to 22)

12 (bases 1 to 22)

Muscarca, Muridae, Murinae, Muscarca, Musc
 0; Gaps
 Query Match 1.9%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches 0; Indels
Email: ddunn@genetics.utah.edu
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Class: plasmid ends
High quality sequence stop: 21.
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 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/clone="UUGC2M0275K17"
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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 21 GTGTGTGTGTGTGTGT 2
 AZ514387.1 GI:10695703
GSS.
 /sex="Female"
 AZ514387
 84112,
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```
Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunngenetics.utah.edu

Insert Length: 10000 Std Error: 0.00

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 Mus musculus (house mouse)
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Best Local Simi
Matches 20;
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KEYWORDS
SOURCE
ORGANISM
 DEFINITION
 JOURNAL
COMMENT
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 RESULT 82
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 AUTHORS
 AZ780118
 FEATURES
 TITLE
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Weetor: PWD42nv; Purified genomic DNA from M.
musculus C578H/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/horter, Ackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gfrom a derivative
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AP129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adapprored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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 GSS 16-FEB-2001
 Mus musculus (house mouse)

Mus musculus

Mus musculus

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae, Murinae; Mus.

(bases 1 to 22)

Dunn,D., Aoyagi, B., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Menen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts
 AZ780002
2M0016J20R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0016J20 R, genomic survey sequence.
 Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC,
 Gaps
 ô
 Query Match 1.9%; Score 20; DB 1; Length 22; Best Local Similarity 100.0%; Pred. No. 38; Matches 20; Conservative 0; Mismatches 0; Indels
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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LOCUS
DEFINITION
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 JOURNAL
COMMENT
 ACCESSION
 REFERENCE
 AUTHORS
 FEATURES
 TITLE
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/note="Weetor: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
laboratory Mouse DNA Resources/Accuments/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically shaared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gfrom a derivative
of pwD42 (gil #732114 |gb|AF129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coll XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. Basaryota; Butheria; Rodentia; Sciurognathi; Muridae; Musnae; Mus. Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Railly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Dasmid inserts Muse scaffolding with paired end reads from 10kb plasmid inserts (2000) Contact: Robert B. Weiss University of Utah Genome Center University of Utah Genome Center Plda 20 R. 2013 P. SIC. ITT PR. 2018 P. Mondical Polymers Presearch Plda 20 R. 2013 P. SIC. ITT PR. 2018 P. Mondical Polymers Presearch Plda 20 R. 2013 P. SIC. ITT PR. 2018 P. Mondical Polymers Presearch Plda 20 R. 2013 P. SIC. ITT PR. 2018 P. Mondical Polymers Presearch Plda 20 R. 2013 P. SIC. ITT PR. 2018 P. Mondical P. 2018 P. SIC. ITT PR. 2018 P. Mondical P. 2018 P. SIC. ITT PR. 2018 P. 2018 P. 2018 P. SIC. ITT P. 2018 P. 2018 P. 2018 P. 2018 P. SIC. ITT P. 2018 P.
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 GSS 16-FEB-2001
 AZ780118
2M0017G07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0017G07 F, genomic survey sequence.
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
 ö
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High quality sequence stop: 2
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Best Local Similarity
Matches 20; Conserv
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KEYWORDS
SOURCE
ORGANISM
 LOCUS
 JOURNAL
COMMENT
 RESULT 84
AZ452951
 REFERENCE
AUTHORS
 ACCESSION
 FEATURES
 TITLE
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 d
 / Jab host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/ Jab host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/ Jab host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/ Jab host="Wouse loke plasmid UUGCIM library"
/ Jote="Wector: PWD42nv; Purified genomic DNA from M.
musculus C578lb/60 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gal
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1) a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XIIO-Gold (Stratagene) cells
and selected for ampicillin resistance."
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)

B Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Rally,M., Rose,M., Rose,R., Tingey,A., Von Niederhausern,A. and Wright,D.,Weiss,R. Tingey,A., von Dasmid inserts

L Unpublished (2000)

L Unpublished (2000)

L Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah Genome Center
 AZ309945

1M0017K22F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0017K22 F, genomic survey sequence.
 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 ö
 Gaps
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Insert Length: 10000 Std Error: 0.00
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Mus musculus (house mouse)
Mus musculus
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 AZ309945
AZ309945.1 GI:10351443
 Tel: 801 585 5606
Fax: 801 585 7177
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 Rm. 308,
84112, US
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musculus G57Bl/60 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomodleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil 473214 [gb]AP129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
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 ö
 chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 Mammalia; Butheria; Rodentia; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases I to 23).

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,M., St., Stokes,R., Tingey,A., von Niderhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid innerts
 AZ452951
1M0254M05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0254M05 F, genomic survey sequence.
 S. 2030 E., SLC,
 .
0
 ch 1.9%; Score 20; DB 1; Length 23; I Similarity 100.0%; Pred. No. 40; 20; Conservative 0; Mismatches 0; Indels
 Biomedical Polymers Research Bldg., 20
 Std Error: 0.00
 Rm. 308, Biomedical Polymers Researce 84112, USA For February 1885 506 February 1985 506 February 1985 506 February 1985 5177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0 Plate: 0254 row: M column: 05 Seg primer: CGTTGTAAAACGACGGCCAGT Class: plasmid ends
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 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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 Mus musculus (house mouse)
 drefererererererer
 AZ452951.1 GI:10610264
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunm@genetice.utah.edu
Email: ddunm@genetice.utah.edu
Ensert Length: 10000 5td Error: 0.00
Plate: 0251 row: I column: 05
Seq primer: CGTTGTAAAACGACGGCCAGT
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 AZ451588/c
LOCUS
DEFINITION
 VERSION
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ORGANISM
 JOURNAL
COMMENT
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 REFERENCE
AUTHORS
 ACCESSION
 RESULT 86
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/lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/lone lib="Mouse 10kb plasmid UUGCIM library"
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musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources /documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
clectrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gil #1912|14|19||AP129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
E. 1 (Dases I to 24)
E. 2 (Dases I to 25)
E. 2 (Dases I to 24)
E.
 AZ645446 140021 MOUSE 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0510H22 R, genomic survey sequence.
 E., SLC, UT
 ö
 ..
 1.9%; Score 20; DB 1; Length 23; 100.0%; Pred. No. 40;
 0; Indels
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0510 row: H column: 22
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/strain="C57BL/6J"
 'db_xref="taxon:10090"
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 Mus musculus (house mouse)
Mus musculus
 4 GTGTGTGTGTGTGTGTGT 23
 AZ64546.1 GI:11774942
 1794 GTGTGTGTGTGTGTGT
 Local Similarity
ses 20; Conserv
 Rm. 308, B:
84112, USA
 Query Match
Best Local Si
Matches 20;
 VERSION
KEYWORDS
SOURCE
ORGANISM
 LOCUS
DEFINITION
 JOURNAL
 REFERENCE
AUTHORS
 RESULT 85
AZ645446
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lone lib="Mouse 10kb plasmid UUGCIM library"
/notc="Twoctor: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from Hrom M.
imboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwy2 (qi|4732114|gb|AR129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
 Mus musculus (house mouse)

Mus musculus

Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;

Mummalia; Butheria; Rodendia; Sciurognathi; Muridae, Murinae; Mus.

1 (bases 1 to 25)

1 (bases 1 to 25)

1 (bases 1 to 25)

2 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

1 Islam, H., Longacze, S., Malmoud, M., Meenen, B., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von

Unjublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

RM. 201 Contact Robert B.
 5
 GSS 04-OCT-2000
 ô
 AZ451588
1M0251105F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 ..
 Score 20; DB 1; Length 24;
Pred. No. 41;
 0; Indels
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mcgarry191-19.rst

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muscular C7) Man Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared but one fine at constant velocity. The sheared but one inch orifica at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwM92 (gi|q132114|gb|Ar129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xiii0-Gold (stratagene) cells and selected for ampicillin resistance."
 Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Enkaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
E. 1 (Dases 1 to 21)
E. 1 (Dases 1 to 22)
E. 2 (Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacze,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von
Diasmid inserts
I. Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 ö
 AZ513902
1M0360A13F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
 /sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. Coli strain XL10-Gold, Iibrary"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
 Gaps
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Best Local Similarity 100.0%; Pred. No. 42;
Matches 20; Conservative 0; Mismatches 0; Indels
 Tel: 801 585 5606
Fax: 801 585 7177
Fax: 801 585 7177
Insert Length: 10000 Std Error: 0.00
Plate: 0360 row: A column: 13
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
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organism="Mus musculus"
mol_type="genomic DNA"
strain="C57BL/6J"
 High quality sequence stop: 21.
Location/Qualifiers
 db_xref="taxon:10090"
clone="UUGC1M0251105"
 25 GTGTGTGTGTGTGTGT 6 ·
 1794 GIGIGIGIGIGIGIGI 1813
 Mus musculus (house mouse)
 AZ513902.1 GI:10695218
 USA
 Rm. 308,
84112, U
 VERSION
KEYWORDS
SOURCE
ORGANISM
 LOCUS
DEFINITION
 source
 AZ513902/c
 REFERENCE
AUTHORS
 ACCESSION
 JOURNAL
 RESULT 87
 FEATURES
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/lab_host="E. Coli strain XLI0-Gold, T1-resistant, F-"
/lab_host="E. Coli strain XLI0-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/mote="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources
/chtp://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant velocity. The sheared DNA
was bunt end-repaired with T4 DNA polymerses and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwn22 (gil 4722114)gpl/AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XLI0-Gold (Stratagene) cells
and selected for ampicillin resistance."
 SM Muss musculus

Bukaryota, Metazoa; Chordata; Craniata, Vertebrata; Buteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus

mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

1 (Dases 1 to 22)

5 Dum, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Rella, L., Longacze, S., Mahmoud, M., Menen, E., Pedersen, T.,

Relly, M., Rose, M., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Duiversity of Utah

Duiversity of Utah
 5
 ö
 AZ784203
2M0026G16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0026G16 R, genomic survey sequence.
 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
 1.8%; Score 19.4; DB 1; Length 21; 95.2%; Pred. No. 42; ative 0; Mismatches 1; Indels
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0026 row: G column: 16
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 sex="Male"
 Conservative
 Query Match
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Matches 20; Conserv
 USA
 Rm. 308,
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 27
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DEFINITION
 ORGANISM
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/ clone lib="Wouse 10kb plasmid UUGCIM library"
/ note="Vector: PWD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources (documents/dnares). The Jackson (http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
10.005 inch orifice at constant velocity. The sheared DNA
was bunt end-repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gp|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli X110-Gold (Stratagene) cells
and selected for ampicillin resistance."
 Eukaryota; Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
E 1 (bases 1 to 22)
E 1 (bases 1 to 22)
S Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 AZ793094
2MC045H20R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
 Query Match 1.8%; Score 19.4; DB 1; Length 22; Best Local Similarity 95.2%; Pred. No. 43; Matches 20; Conservative 0; Mismatches 1; Indels
 Tel: 801 585 5606
Fax: 801 585 7177
Email: dduun@genetics.utah.edu
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 High quality sequence stop: 22.
Location/Qualifiers
db_xref="taxon:10090"
clone="UUGC2M0026G16"
 1793 IGTGTGTGTGTGTGTGTGT 1813
 1 reretrierererererer 21
 Mus musculus (house mouse)
Mus musculus
 AZ793094.1 GI:12937525
 USA
 Rm. 308, F
84112, US
 VERSION
KEYWORDS
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ORGANISM
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DEFINITION
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 AUTHORS
 RESULT 89
 AZ793094
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E., SLC, UT

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Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Bases 1 to 22)

1 (Bases 1 to 22)

2 Dunn,D., Aoyagai,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

1 Islam,H., Longacze,S., Mahmoud,M., Menen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid innearts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Duniversity of Utah

Duniversity of Utah
 AZ801266 10Kb plasmid UUGCIM library Mus musculus genomic clone UUGCZM0059107 R, genomic survey sequence.
AZ801266
 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 ö
 Gaps
 ö
 1.8%; Score 19.4; DB 1; Length 22; 95.2%; Pred. No. 43; tive 0; Mismatches 1; Indels
 Univer.

Rm. 308, Biomecarc.
84112, USA
Tel: 801 585 5606
Fax: 801 585 717
Email: ddunm@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0059 row: 1 column: 07
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High quality sequence stop: 22.
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Location/Qualifiers
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 1793 TGTGTGTGTGTGTGTGT 1813
 2 rérérérérésérérérérer 22
 AZ801266.1 GI:12953589
GSS.
 Query Match
Best Local Similarity 95.2
Matches 20; Conservative
 source
 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AZ801266
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AUTHORS
 JOURNAL
 FEATURES
 TITLE
 COMMENT
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(210me 11b="Wouse 10kb plasmid UUGCIM library"

/note="Wouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at conscant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polymucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptored mouse DNA was annealed to

adaptored vector DNA, and transformed into

chamically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."
 Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 AZ356191 23 bp DNA linear GSS 02-0CT-2000 1M0097L07F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0097L07 F, genomic survey sequence.
 ö
 Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
 1 (bases 1 to 2.3.)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 0; Gaps
 Query Match 1.8%; Score 19.4; DB 1; Length 22; Best Local Similarity 95.2%; Pred. No. 43; Matches 20; Conservative 0; Mismatches 1; Indels
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0097 row: L column: 07
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 Mus musculus (house mouse)
 AZ356191.1 GI:10469235
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 Unpublished (2000)
 USA
 AZ356191
 GSS.
 source
 LOCUS
 RESULT 91
AZ356191/c
 ORGANISM
 REFERENCE
AUTHORS
 ACCESSION
 VERSION
KEYWORDS
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 FEATURES
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/Bab.maie".
/Jab.mose 10kb plasmid UUGCIM library."
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/clone_lib="Wouse 10kb plasmid UUGCIM library."
/motes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
10.5 inch orifice at constant velocity. The sheared DNA
was hydrodynamically shaper oligomuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gil #432114[gp]AR129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli Xillo-Gold (Stratagene) cells
and selected for ampicillin resistance."
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 GSS 20-FEB-2001
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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2M0095D03F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
 Dunn,D., Acyaci,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacze,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
 Gapa
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1.8%; Score 19.4; DB 1; Length 23;
Best Local Similarity 95.2%; Pred. No. 45;
Matches 20; Conservative 0; Mismatches 1; Indels
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 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0095 row: D column: 03
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Class: plasmid ends

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 Mus musculus (house mouse)
Mus musculus
 22 TGGGTGTGTGTGTGTGT 2
 AZ822069.1 GI:12991977
GSS.
 Tel: 801 585 5606
Fax: 801 585 7177
 USA
 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 DEFINITION
 RESULT 92
AZB22069
 AUTHORS
 REFERENCE
 JOURNAL
 FEATURES
 TITLE
 COMMENT
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1 TATATATATATATATATACA 24
 Location/Qualifiers
 Mus musculus (house mouse)
Mus musculus
 AZ431700
AZ431700.1 GI:10555713
 rel: 801 585 5606
Fax: 801 585 7177
 DEFINITION
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 RESULT 94
AZ431700
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 AUTHORS
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musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by reseated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by reseased and T4
polynuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarcse gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil #4722114]gbl R7129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. ooli XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
 Unpublished (2000)
Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
 linear GSS 14-DEC-2000
 Mus musculus (Montana Montana Montana Musculus Euteleostomi), Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 28)
1 (bases 1 to 28)
1 (bases 1 to 28)
1 (bases 1 to 28)
1 (bases 1 to 28)
1 (bases 1 to 28)
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1 (bases 1 to 28)
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1 (bases 1 to 28)
1 (bases 1 to 28)
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1 (bases 1 to 2
 AZ648796 14-DEC-200 18 DNA linear GSS 14-DEC-200 1M0518A05F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0518A05 F, genomic survey sequence.
 0; Gaps
 Score 19.4; DB 1; Length 24; Pred. No. 46; 0; Mismatches 1; Indels
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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 4 TGTGTGTGTGTGTGTGTGT 24
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 AZ648796.1 GI:11781618
 Query Match 1.8%;
Best Local Similarity 95.2%;
Matches 20; Conservative
 /sex="Male"
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 ORGANISM
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KEYWORDS
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Laboratory Mouse DNA Resources/Accuments/Anares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerses and T4
polymucleotide kinase. Adaptor oliganucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose general from a derivative
of pMD42 (gil #4732114 gb] PR1297072.1), a copy-unuber
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli Xiil0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Insert Length: 10000 Std Error: 0.00
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à
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/note="Tweetor: PWD42nv, Purified genomic DNA from M.

musculus C573L/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AP129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 ö
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (2019)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Railam, H., Longacre, S., Mahmoud, M., Mener, E., Pedersen, T., Reily, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Unpublished (2000)

Unpublished (2000)

Ontact: Robert B. Weiss

University of Utah Genome Center
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 0; Indels
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Class: plasmid ends
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Mus musculus
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 USA
 AZ461642
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VERSION
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SOURCE
ORGANISM
 AZ461642/c
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AUTHORS
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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus G57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was bydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g41/472114)[g4][A1129][A1129][A112][A11
 ö
 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. 1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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1M0518B17R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0518B17 R, genomic survey sequence.
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100.0%; Pred. No. 42;
ive 0; Mismatches 0; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: OS18 row: B column: 17
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Class: plasmid ends
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 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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 1794 GIGIGIGIGIGIGIGIG 1812
 19 drererererererere
 AZ649147.1 GI:11782334
 sex="Male"
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
 Conservative
 Best Local Similarity
Matches 19; Conserv
 Rm. 308, Bi
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VERSION
KEYWORDS
SOURCE
ORGANISM
 REFERENCE
AUTHORS
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musculus C573L/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarese gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4712114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
 A2774954 10-FEB-2001 2M0004N15R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0004N15 R, genomic survey sequence.
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 ö
 chemically-competent B. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. L. (basea 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Nese, M., Rose, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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Plate: 0004 row: N column: 15
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/db_xref="taxon:10090"
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 Mus musculus (house mouse)
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AZ774954.1 GI:12900943
GSS.
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Unpublished (2000)
 19; Conservative
 Tel: 801 585 5606
Fax: 801 585 7177
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Best Local Similarity
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KEYWORDS
SOURCE
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwn92 (gil #742114|gb]AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptore complementary to the insert adaptors and adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT
 GSS 16-FEB-2001
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. I Chases I to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Roilly, M., Rose, M., Rose, M., Rose, M., Rose, M., Rose, M., Weise, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R., Tingey, A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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/note=""Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Class: plasmid ends
Laboratory Mouse DNA Resource
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 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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 Mus musculus (house mouse)
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was Dlunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the Dlunt ends in high modar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pWD42 (41772114) galphart20072.11, a copyrunuber inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored meuse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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 GSS 20-FEB-2001
 Mammalia, Butheria, Rodentia, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. I (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
(http://www.jax.org/resources/documents/dnares/). The DNA
 A2822936
2M0096E08R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0096E08 R, genomic survey sequence.
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University of Utah Genome Center
University of Utah
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 /db_xref="taxon:10090"
 clone="UUGC2M0096E08"
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 Conservative
 Unpublished (2000)
 Tel: 801 585 5606
Fax: 801 585 7177
 Mus musculus
 Query Match
Best Local Similarity
Matches 19; Conserv
 USA
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 SOURCE
ORGANISM
 DEFINITION
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RESULT 99 AZ822936

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ACCESSION

KEYWORDS

REFERENCE AUTHORS JOURNAL

TITLE

FEATURES

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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoreass. Vector DNA was prepared from a derivative of pWD42 (gi[4732114]gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 AZB27177
2M0103A05R Mouse 10kb plasmid UUGCIM library Mus musculus genomic close UUGC2M0103A05 R, genomic survey sequence.
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a
 Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Bukammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. I (bases 1 to 19)

Dunn, D., Aoyadi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Niegelly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weises, R., Mouse whole genome scaffolding with paired end reads from 10kb
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 Score 19; DB 1; Length 19;
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 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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 100.0%; Pred. No. 42;
tive 0; Mismatches
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/strain="C578L/63"
 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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 High quality sequence stop: 19.
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 Mus musculus (house mouse)
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 AZ827177.1 GI:12997085
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Matches 19; Conservative
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Unpublished (2000)
 Query Match
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 RESULT 100
 ORGANISM
 REFERENCE
AUTHORS
 ACCESSION
 JOURNAL
 VERSION
KEYWORDS
 AZ827177
 FEATURES
 TITLE
 SOURCE
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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gellectrophoresis. Vector DNA was prepared from a derivative of pWD42 (4)4732114|gb|RR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT ö GSS 16-FEB-2001 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi; Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von. Niederhausern, A. and Wright, D., Weise, R. AZ785549
2M0029F01R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0029F01 R, genomic survey sequence. 0; Gaps Score 19; DB 1; Length 19; 0; Indels Tel: 801 585 5606
Fax: 801 585 7177
Enail: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0029 row: F column: 01
Seq primer: CACACAGGAAACAGCTATGACC
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1.84; course, 10, 42;
Best Local Similarity 100.0%; Pred, No. 42;
Matches 19; Conservative 0; Mismatches 1793 TGTGTGTGTGTGTGT 1811 Mus musculus (house mouse) 1 TGTGTGTGTGTGTGT 19 AZ785549.1 GI:12922419 plasmid inserts Unpublished (2000) USA GSS RESULT 101 AZ785549 DEFINITION ORGANISM VERSION KEYWORDS SOURCE ACCESSION REFERENCE AUTHORS JOURNAL TITLE

ACCESSION VERSION KEYWORDS

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was blunt end-repaired with T4 DNA polymerase and T4 polymerase bolymerate the polymerate kinase. Adaptor oligomeclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance." ISM Mus musculus

Rukaryota, Metazoa, Chordata; Craniata, Vertebrata; Euteleostomi;

Rukaryota, Metazoa, Chordata; Craniata, Vertebrata; Euteleostomi;

Rumanla; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

(CE 1 (Dases 1 to 21)

Rohan, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weise, R.,

Nouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weise

University of Utah Genome Center

University of Utah

Parania inserts

University of Utah /sex="Male"
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muculus C57BL/60 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
/http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4 AZ818214
2M0088B08F Mouse 10kb plasmid UUGCIM library Mus musculus genomic Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 1.8%; Score 19; DB 1; Length 20; 100.0%; Pred. No. 44; 0; Indels Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0088 row: B column. na 100.0%; Pred. .... Plate: 0088 row: B column: 08 Seq primer: CGTTGTAAAACGACGGCCAGT 1. .21 /organism="Mus musculus" /mol\_type="genomic DNA" /strain="C57BL/6J" /db xref="taxon:10090" /clone="UUGC2M0088B08" High quality sequence stop: 21. Location/Qualifiers 1792 TTGTGTGTGTGTGTGTG 1810
2 TTGTGTGTGTGTGTGTG 20 Mus musculus (house mouse) AZ818214.1 GI:12988122 Class: plasmid ends Query Match Best Local Similarity 100.0 Matches 19; Conservative Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genet Rm. 308, Bi 84112, USA RESULT 102 AZ818214 DEFINITION ORGANISM REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

FEATURES

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA

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/sex="Male"

High quality sequence stop: 20. Location/Qualifiers

Bource

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Bukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 20)

1 (bases 1 to 20)

1 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Waiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Inpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah Genome Center

University of Utah Rose Research Bldg., 20 S. 2030 E., SLC, UT
polynuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWB42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XIL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 GSS 04-OCT-2000
 / Journal of the control of the cont
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 AZ482421
1M0307P01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0307P01 R, genomic survey sequence.
 Query Match 1.8%; Score 19; DB 1; Length 21; Best Local Similarity 100.0%; Pred. No. 45; Matches 19; Conservative 0; Mismatches 0; Indels
 Tel: 801 585 5606
Fax: 801 585 7177
Famil: ddunn@genetics.utah.edu
Email: ddunn@genetics.utah.edu
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Mus musculus
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 Rm. 308,
84112, US
 ACCESSION
VERSION
KEYWORDS
SOURCE
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 LOCUS
 RESULT 103
AZ482421
 AUTHORS
 JOURNAL
 REFERENCE
 FEATURES
 TITLE
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셤

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/ Jack-Male"
/ Jab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/ Jab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/ Jab host="E. Coli strain YL10-Gold, T1-resistant, F-"
/ Jab host="B. Coli strain yellow Jackson Libbrary"
musculus C57BL/6J (male) was obtained from the Jackson
Libbrardory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonicleotides were
ligated to the blunt ends in high molar excess. The
 Bukaryota; Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Bukaryota; Metazoa, Chordata; Craniata, Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
E. (bases 1 to 20)
E. John, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meener, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah Genome Center
University of Utah Genome Research Bldg., 20 S. 2030 E., SLC, UT
ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agardse gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129772.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector LNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
 AZ632650
1M0487H23F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0487H23 F, genomic survey sequence.
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 1.8%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 49; ative 0; Mismatches 1; Indels
 Std Error: 0.00
 Rm. 308, Biomedical Polymers Researc 84112, USA
Fal: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Mus musculus (house mouse)
Mus musculus
 1 TGTGTGTGTGTGTATGTG 20
 AZ632650
AZ632650.1 GI:11754840
 Query Match
Best Local Similarity 95.03
Matches 19; Conservative
 Bource
 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 DEFINITION
 RESULT 104
 JOURNAL
 REFERENCE
 AUTHORS
 AZ632650
 FEATURES
 TITLE
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Mus musculus (house mouse)

Mus musculus

Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 20)

2 Dunn, D., Aoyagi, A., Barber, M., Meacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von

Noderhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center
adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X1.0-Gold (Stratagene) cells and selected for ampicillin resistance."
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 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch ordice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuchectide kinase. Adaptor oligomocleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
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/note="Vector: PWD42nv; Purified genomic DNA from N.
musculus C57BL/6J (male) was obtained from the Jackson
 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
 Gaps
 .
0
 Query Match
1.8%; Score 18.4; DB 1; Length 20;
Best Local Similarity. 95.0%; Pred. No. 49;
Matches 19; Conservative 0; Mismatches 1; Indels
 Tel: 801 585 5606
Fax: 801 585 777
Fax: 801 585 777
Faxil: ddunn@genetics.utah.edu
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 1792 TTGTGTGTGTGTGTGT 1811
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 USA
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 84112,
 VERSION
KEYWORDS
SOURCE
ORGANISM
 RESULT 105
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 LOCUS
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AUTHORS
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 FEATURES
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TITLE

COMMENT

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musculus C5PBL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources (documents/dnares/). The DNA
/http://www.jax.org/resources/documents/dnares/). The DNA
/was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleoride kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
 Mus musculus (house mouse)

Mus musculus

Bukaryota; Marazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Mateazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 20)

1 (bases 1 to 20)

2 I (bases 1 to 20)

3 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

1 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm., 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AP129072.11), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
 AZ/93887
2M0047G21F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCZM0047G21 F, genomic survey sequence.
AZ793887
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 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror:
Plate: 0047 row: G column: 21
Seq primer: CGTTGTAAAACGACGGCCAGT
 High quality sequence stop: 20.
Location/Qualifiers
 1793 TGTGTGTGTGTGTGTGTG 1812
 1 rererererererrererere 20
 AZ793887.1 GI:12939296
 Class: plasmid ends
 Rm. 308, B:
84112, USA
 source
 LOCUS
 RESULT 106
AZ793887/c
 VERSION
KEYWORDS
SOURCE
ORGANISM
 JOURNAL
 REFERENCE
AUTHORS
 ACCESSION
 FEATURES
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AC415089 21 bp DNA linear GSS 03-OCT-2000 clone UUGCIMO189G17R Mouse 10kb plasmid UUGCIM library Mus musculus genomic AZ415089
 (http://www.jax.org/reaces/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.05 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative
electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|A7123072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 ö
 Mus musculus Subtracta; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)
Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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/clone lib="Mouse 10kb plasmid UNGCIM library"
/note="Vector: PWD42Iry; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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0
 DB 1; Length 20;
 1.8%; Score 18.4; DB 1; Length 2 ilarity 95.0%; Pred. No. 49; Conservative 0; Mismatches 1; Indels
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Ext Exror: 0.00
Plate: 0189 row: G column: 17
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 Laboratory Mouse DNA Resource
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 Mus musculus (house mouse)
 rrererererererererrr 1
 AZ415089.1 GI:10539102
 Query Match
Best Local Similarity
Matches 19; Conserv
 USA
 gss.
 source
 VERSION
KEYWORDS
SOURCE
ORGANISM
 RESULT 107
AZ415089
 DEFINITION
 ACCESSION
 AUTHORS
 JOURNAL
 REFERENCE
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TITLE

COMMENT

FEATURES

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuleotide Kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AP129072.1), a copy-number
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 AZ579599 11-DEC-2000 1MO367P06F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0367P06 F, genomic survey sequence.
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 ö
 Mus musculus (house mouse)
Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
L (bases 1 to 21)
Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Nouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
 /sex="male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
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/note="Vector: PWD42IIV; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
 ö
 DB 1; Length 21;
 1; Indels
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0367 row: P column: 06
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95.0%; Pred. No. 51;
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 Unpublished (2000)
Context: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Best Local Similarity
Matches 19; Conserv
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 Rm. 308, 1
84112, US
 RESULT 108
AZ579599
 LOCUS
DEFINITION
 ORGANISM
 ACCESSION
 JOURNAL
 VERSION
KEYWORDS
 REFERENCE
 AUTHORS
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.05 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel ectrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|472114|jab|AT129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli K110-Gold (Stratagene) cells and selected for ampicillin resistance."
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 GSS 13-DEC-2000
 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1. (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Nederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
 Gaps
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 DB 1; Length 21;
 1; Indels
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0454 row: M column: 05
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Class: plasmid ends
 Laboratory Mouse DNA Resource
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 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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 High quality sequence stop: 21.
Location/Qualifiers
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Best Local Similarity 95.0%;
Matches 19; Conservative (
 Unpublished (2000)
 Mus musculus
 USA
 GSS.
 AZ621072/c
LOCUS
DEFINITION
 VERSION
KEYWORDS
SOURCE
ORGANISM
 RESULT 109
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JOURNAL

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FEATURES

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blutt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blutt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and
with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
 AZ665302 14-DEC-2000 1M546J09R Mouse 10kb plasmid UUGCIM library Mus musculus genomic close UUGCIM0546J09 R, genomic survey sequence.
 5
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
 Dunn, D. Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Refally, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wirght, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb blasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
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 Gaps
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 Std Error: 0.00
 Tel: 801 585 5606

Pax: 801 585 7177

Bmal: ddunnagenetics.utah.edu
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 1796 GIGTGTGTGTGTGTAT 1815
 Mus musculus (house mouse)
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 AZ665302.1 GI:11802448
 'sex="Male"
 RESULT 110
 AZ665302/c
 DEFINITION
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Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA incedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA inceded
 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
 Homo sapiens
 RESULT 113
AA995094/c
LOCUS
 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 DEFINITION
 REFERENCE
AUTHORS
TITLE
 JOURNAL
COMMENT
JOURNAL
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 ò
 AZ464442 1002-2000 1M0273N14R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0273N14 R, genomic survey sequence.
 Plasmodium chabaudi genome survey sequence, clone PC4c11.plt,
purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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 Mus musculus (house mouse)
Mus musculus
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

[bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Miderinausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
 AJ303878.1 GI:11140385
GSS; genome survey sequence.
Plasmodium chabaudi
Plasmodium chabaudi
Plasmodium chabaudi
Plasmodium chabaudi
I (bases 1 to 21)
Janssen, C.S., Barratt, M.P., Lawson, D., Quail, M.A., Harris, D.,
Bowman, S., Phillips, R.S. and Turner, C.M.
Gene discovery in Plasmodium chabaudi by genome survey sequencing
MOL. Biochem. Parasitol. 113 (2), 251-260 (2001)
 봊
 Direct Submission
Submitted (06-NOV-2000) Division of Infection & Immunity,
University of Glasgow, Joseph Black Building, Glasgow G12 8QQ,
bases 40 to 60 (5L to QR).
Location/Qualifiers
 Gaps
 Gaps
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0
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 . Match
Local Similarity 90.5%; Pred. No. 58;
les 19; Conservative 0; Mismatches 2; Indels
 DB 1; Length 21;
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 chabaudi"
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 (bases 1 to 21)
 Janssen, C.S.
 AJ303878
 AZ464442
 11295179
 GSS.
 Query Match
Best Local S
Matches 19
 AZ464442
LOCUS
DEFINITION
 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 RESULT 111
PCH303878/c
 source
 VERSION
KEYWORDS
SOURCE
ORGANISM
 LOCUS
 RESULT 112
 TITLE
JOURNAL
MEDLINE
PUBMED
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AUTHORS
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 COMMENT
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/db xref="taxon:10090"

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/sex="Wale"

/lone="UUGCIM0273N14"

/sor musculus C57BL/6"

/muse lokb plasmid UUGCIM library"

/note="Vector: PWD42N1', Purified genomic DNA from M.

musculus C57BL/6" (male) was obtained from the Jackson
Laboratory Mouse DNA Resource (fattp://www.jax.org/resources/documents/dnares/). The DNA

was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA

was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA

was bydrodynamically sheared with T4 DNA polymerase and T4

polymuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil | 14732114 | 1981 | 1818 | 1810 | 2029 | 1910 |
uith adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli Xill0-Gold (Stratagene) cells
and selected for ampicillin resistance."
 19 bp mRNA linear EST 27-AUG-1998 ou89g09.s1 NCI CGAP Kid3 Homo sapiens cDNA clone IMAGE:1635040 3' similar to TR:Q69566 (069566 ; contains TAR1.t2 MER35 repetitive element ;, mRNA sequence.
 ö
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 Chase; Lo 19. NOT-CGAP http://www.nobi.nlm.nih.gov/ncicgap. Not-CGAP http://www.nobi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Gaps
 ö
 Query Match
1.7%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 60;
Matches 19; Conservative 0; Mismatches 2; Indels
 Tumor Gene Index
Inpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
High quality sequence stop: 22.
Location/Qualifiers
 1793 rerererererererer 1813
 1 rererererereacherater 21
 AA995094,1 GI:3181583
 Homo sapiens (human)
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mcgarry191-19.rst

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/clone lib="Mouse lOkb plasmid UGGCIM library"
/note="Wector: MPM2Inv; Purified genomic DNA from M.
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Laboratory Mouse DNA Resource
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strain="C57BL/6J"
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clone="UUGC2M0032C01"
 location/Qualifiers
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
 Rm. 308, Bi
84112, USA
 AZ597939
 source
 RESULT 115
AZ597939
 DEFINITION
 ORGANISM
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KEYWORDS
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//lab_host="DH10B"
//lab_host="NLI CGAP_Kid3"
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 Inpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
University of Utah
Weiss Beinmedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCT-GGAP clone distribution: NCT-GGAP clone distribution: NCT-GGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
 AZ786779 11 bp DNA linear GSS 16-FEB-2001 2M0032C01R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0032C01 R, genomic survey sequence.
 ö
 Mus musculus sukrayota; Chordata; Craniata; Vertebrata; Euteleostomi; Musiaya, Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
1 (bases 1 to 19)
2 (bases 1 to 19)
3 (bases 1 to 19)
4 (bases 1 to 19)
5 (bases 1 to 19)
8 (
 0; Gaps
 Query Match
1.7%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 1; Indels
 Trace considered overall poor quality Insert Length: 1087 Std Error: 0.00 Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 1.
 Email: ddunm@genetics.utah.edu
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Plate: 0032 row: C column: 01
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"mol_type="mRNA"
db_xref="taxon:9606"
 Class: plasmid ends
High quality sequence stop: 19.
 1794 GIGIGIGIGIGIGIGIG 1812
 Mus musculus (house mouse)
 19 GCGTGTGTGTGTGTGTG 1
 AZ786779
AZ786779.1 GI:12924882
 Tel: 801 585 5606
Fax: 801 585 7177
 VERSION
KEYWORDS
SOURCE
ORGANISM
 RESULT 114
AZ786779
 DEFINITION
 JOURNAL
COMMENT
 ACCESSION
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of phalot (gri 4712114/gpl AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XII0-Gold (Stratagene) cells and selected for ampicillin resistance."
 AZ597939
1M0412F22F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0412F22 F, genomic survey sequence.
 5
 Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
 Unpublished (2000)
Contact: Robert B. Weiss
Contract: Your delian Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Mouse whole ganome scaffolding with paired end reads from 10kb plasmid inserts
 Gaps
 ;
0
 Query Match 1.6%; Score 17; DB 1; Length 19; Best Local Similarity 100.0%; Pred. No. 63; Matches 17; Conservative 0; Mismatches 0; Indels
 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0412 row: F column: 22
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
 1798 GIGIGIGIGIGIGIA 1814
 AZ597939.1 GI:11720129
 3 GIGIGIGIGIGIGIA 19
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Importatory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.065 inch crifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AF12972.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli Xili0-Gold (Stratagene) cells
and selected for ampicillin resistance."
 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 GSS 13-DEC-2000
 ö
 Mus musculus

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

1 (bases 1 to 21)

2 (bases 1 to 21)
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clone UUGCIM0412F22 F, genomic survey sequence.
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/lab host="B. Coli strain XLIO-Gold, Tl-resistant, F."
/clone_lib="Mouse lokb plasmid UUGCIM library"
/note="Vector: PWD42nr; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0412 row: F column: 22
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
 db_xref="taxon:10090"
clone="UUGC1M0412F22"
 High quality sequence stop: 21.
Location/Qualifiers
mol_type="genomic DNA'
strain="C57BL/6J"
 1811 TGTATATATATATGTA 1830
 Mus musculus (house mouse)
 AZS97939.1 GI:11720129
GSS.
 Query Match
Best Local Similarity 90.0°
Matches 18; Conservative
 Tel: 801 585 5606
Fax: 801 585 7177
 USA
 Rm. 308,
84112, US
 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 source
 RESULT 116
AZ597939/c
LOCUS
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 AUTHORS
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Laboratory Mouse DNR Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA polymerase and T4 polymerase and polymerase complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coll XIIO-Gold (Stratagene) cells and selected for ampicillin resistance."
 AZ401252
19 bp DNA linear GSS 03-OCT-2000
1M0167E20R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0167E20 R, genomic survey sequence.
 B
 ö
 Mus musculus
Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
 /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone lib="Mouse 10%b plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
 inclinearies, courseles, coursele
 ö
 Query Match 1.6%; Score 16.8; DB 1; Length 21; Best Local Similarity 90.0%; Pred. No. 70; Matches 18; Conservative 0; Mismatches 2; Indels
 Tel: 601 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0167 row: E column: 20
Seq primer: CACAGGAAACAGCTATGACC
Class: plasmid ends
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 High quality sequence stop: 19.
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mol_type="genomic DNA"
strain="C57BL/6J"
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 1811 TGTATATATATATGTA 1830
 AZ401252.1 GI:10516326
 USA
 84112,
 20
 source
 LOCUS
 RESULT 117
AZ401252
 ORGANISM
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AUTHORS
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SOURCE
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ACCESSION
 REFERENCE
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 FEATURES
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 /Bab. Marle"
/ Jab. Moste "E. Coli strain XLIO-Gold, Tl-resistant, F-"
/ clone lib="Mouse 10kb plasmid UUGCIM library"
/ clone lib="Mouse 10kb plasmid UUGCIM library"
/ note="Weetor: PWD4Znv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources (documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XIIO-Gold (Stratagene) cells
and selected for ampicillin resistance."
 AZ401252
IMO167E20R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0167E20 R, genomic survey sequence.
 Rm. 308. Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
 ö
 Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
 0; Gaps
 1.6%; Score 16.4; DB 1; Length 19; 94.4%; Pred. No. 71; ive 0; Mismatches 1; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0167 row: B column: 20
Seq primer: CACACAGGAAACAGCTAATGACC
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/mol_type="genomic DNA"
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
 High quality sequence stop: 19.
Location/Qualifiers
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clone="UUGC1M0167E20"
 1813 TATATATATATATGTA 1830
 2 TATATATATATA 19
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 Class: plasmid ends
 Query Match
Best Local Similarity 94.41
Matches 17; Conservative
 Tel: 801 585 5606
Fax: 801 585 7177
 AZ401252
 source
 RESULT 118
AZ401252/c
LOCUS
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was bluctory interest constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose get of a 9.5 to
10.5 kb range using preparative agarose grow a derivative
of pWD42 (gil4732114 |gb|AF129072.1), a copy-number
inducible derivative of plasmid Al. The vector was ligated
with adaptors complamentary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coll Xil0-Gold (Stratagene) cells
and selected for ampicillin resistance."
 19 bp DNA linear GSS 13-DEC-2000 IMO484B03F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0484B03 F, genomic survey sequence.
 ô
 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 Mis musculus (house mouse)
Mis musculus
Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases I to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Mederhausern, A. and Wright, D., Meiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
 Gaps
 ô
 1.6%; Score 16.4; DB 1; Length 19; 94.4%; Pred. No. 71; ive 0; Mismatches 1; Indels
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0484 row: B column: 03
Seg primer: cGTTGTAAAACGACGCCAGT
Class: plasmid ends

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 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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 High quality sequence stop: 19.
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 AZ630416.1 GI:11752606
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 Query Match
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Matches 17; Conservative
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 USA
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LOCUS
 DEFINITION
 ORGANISM
 RESULT 121
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 hatbotacory youbse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwalet (gql 47321141gb] AF129772.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xilio-Gold (Stratagene) cells and selected for ampicillin resistance."
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)

1 (bases 1 to 19)

1 (bases 1 to 19)

2 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Mennen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University, of Utah
 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 GSS 13-DEC-2000
 ö
 AZ630416
1M0484B03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0484B03 F, genomic survey sequence.
 /clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
 lab_host="E. Coli strain XL10-Gold, T1-resistant, F~"
 0; Gaps
 1.6%; Score 16.4; DB 1; Length 19; 94.4%; Pred. No. 71; tive 0; Mismatches 1; Indels
 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0484 row: B column: 03
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High quality sequence stop: 19.
Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="taxon:10090"
 db_xref="taxon:10090'
 Mus musculus (house mouse)
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 AZ630416.1 GI:11752606
 Query Match
Best Local Similarity 94.4
Matches 17; Conservative
 Tel: 801 585 5606
Fax: 801 585 7177
 AZ630416
 308,
 source
 RESULT 120
AZ630416/c
LOCUS
 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 DEFINITION
 REFERENCE
AUTHORS
 FEATURES
 TITLE
 COMMENT
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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMAP2 (gqi 4732114[gb]AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10.0304 (Stratagene) cells and selected for ampicillin resistance."
 AZ789396 10- DNA linear GSS 16-FEB-2001 2M0056N18R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0056N18 R, genomic survey sequence.
 Ē
 ö
 Mus musculus (house mouse)
Mus musculus (house mouse)
Mus musculus
Muscaryota,
 Unpublished (2000)
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
/lab host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/clone_lib="Mouse_lokb plasmid_UUGCIM_library"
/note=""vector: PMP4Znv; Purified genomic_DNA from M.
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Laboratory Mouse_DNA Resource
 Gaps
 ;
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 Email: ddunn@genetics.utah.edu
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musculus C57BL/6J (male) was obtained from He Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated from series
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose get a 9.5 to
10.5 kb range using preparative agarose get of a 9.5 to
10.5 kb range using preparative agarose get of plasmid kl. The vector was ligated
inducible derivative of plasmid Rl. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coll Xil0-Gold (Stratagene) cells
and selected for ampicillin resistance."
 AZ772074

1M0574M10R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0574M10 R, genomic survey sequence.
 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 ö
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longarer, S., Mahmoud, M., Menen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Plasmid inserts
 Gaps
 ;
0
 Query Match
1.6%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 1; Indels
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0574 row: M column: 10
Seq primer: CAQCAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
 organism="Mus musculus"
 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
 /mol_type="genomic DNA"
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clone="UUGC1M0574M10"
 Mus musculus (house mouse)
 1808 GIGIGIATATATATAT 1825
 AZ772074.1 GI:12895006
 19 Grandiarararar 2
 /sex="Male
 84112, USA
 RESULT 122
AZ772074
 LOCUS
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VERSION
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SOURCE
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 REFERENCE
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Wostcr: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from Hre Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwp. (prified. The sheared, adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XLI0-Gold (Stratagene) cells
and selected for ampicillin resistance."
 AZ345795 1000 DNA linear GSS 29-SEP-2000 1M0080H09R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0080H09 R, genomic survey sequence.
 É
 ö
 Mus musculus (house mouse)

Mus musculus

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,

Bukaryota, Metazoa, Chordata, Sciurognathi, Muridae, Murinae, Mus.

I (Dases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/strain="C57BL/6J"
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 1.5%; Score 16; DB 1; Length 20; 00.0%; Pred. No. 79;
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0860 row: H column: 09
Seg primer: CACACAGGAAACAGCTATGACC
Class: plesmid ends
 100.0%; Pred. No. 79; rative 0; Mismatches
 organism="Mus musculus"
 plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
 High quality sequence stop: 19.
Location/Qualifiers
 AZ345795.1 GI:10425032
 1794 GIGIGIGIGIGIGI 1809
 s didididididididi 20
 Query Match
Best Local Similarity 100.
Matches 16; Conservative
 Rm. 308, Bi
84112, USA
 AZ345795
 source
 LOCUS
 VERSION
KEYWORDS
SOURCE
ORGANISM
 RESULT 123
AZ345795/c
 REFERENCE
AUTHORS
 JOURNAL
COMMENT
 ACCESSION
 FEATURES
 TITLE
 c
C
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RESULT 125
AZ650575/c
 LOCUS
 ORGANISM
 JOURNAL
 VERSION
KEYWORDS
SOURCE
 ACCESSION
 REFERENCE
 AUTHORS
 FEATURES
 TITLE
 COMMENT
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 g
 Laboraty Mouse DNA Resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides ware ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
B. (Dases 1 to 19)
S. Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacze,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
 AZ491644 10022-2000 19 bp DNA linear GSS 05-0CT-2000 1M0325AZ0F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0325AZ0 F, genomic survey sequence.
 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 ö
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42rv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone_lib="Mouse 10kb plasmid UUGC1M library"
 Gaps
 ô
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 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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/strain="C57BL/6J"
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/clone="UUGC1M0325A20"
 High quality sequence stop: 19.
Location/Qualifiers
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 Mus musculus (house mouse)
Mus musculus
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 AZ491644
AZ491644.1 GI:10663543
 'sex="Male"
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
 Query Match
Best Local Similarity 89.5
Matches 17; Conservative
 USA
 GSS.
 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 DEFINITION
 RESULT 124
 JOURNAL
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 AUTHORS
 AZ491644
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 TITLE
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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a plut end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel. lo.5 kb range using preparative agarose gel. electrophoresis. Vector DNA was prepared from a derivative of pMNA2 (gil H732114|gbl=NR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 É
 AZESOS75

100520P13R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIMO520P13 R, genomic survey sequence.
 Mis musculus substances (Abordata; Craniata; Vertebrata; Buteleostomi; Butaryota; Metazoa; Chordata; Craniata; Vertebrata; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
1 (bases 1 to 19)
1 (bases 1, to 19)
1 (bas
 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
 Jab host="B. Coli strain XLIO-Gold, TI-resistant, F-"/lab host="B. Coli strain XLIO-Gold. library"/note="Vector: PWD42nv; Purified genomic DNA from M.
 Gaps
 ..
 Score 15.8; DB 1; Length 19;
Pred. No. 79;
 2; Indels
 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0520 row: P column: 13
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 0; Mismatches
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/clone="UUGC1M0520P13"
 High quality sequence stop: 19.
Location/Qualifiers
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 Mus musculus (house mouse)
 1 recentratererere 19
 AZ650575.1 GI:11785200
 Query Match 1.5%;
Best Local Similarity 89.5%;
Matches 17; Conservative
 sex="Male"
 Class: plasmid ends
 Tel: 801 585 5606
Fax: 801 585 7177
```

1865 TTTTTTTTTTTT 1881

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musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligomuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 (gql 47422114|gpl AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli Xiii0-Gold (Stratagene) cells and selected for ampicillin resistance."
 SM Oriza sativa

Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae, Oryzae, Oryzae.

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae, Oryza.

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.K., and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongli, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Fax: 82 31 321 6355
 CF276637 11 bp mRNA linear EST 14-AUG-2003 14ETL--01-N18.gl Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa cDNA clone 14ETL--01-N18, mRNA sequence.
 ö
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and Then used as templates for RT-PCR."
 /dev_stāge="14 days after germination"
/lab_host="B.coli DH108"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)
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 Query Match 1.5%; Score 15.8; DB 1; Length 19; Best Local Similarity 89.5%; Pred. No. 79; Matches 17; Conservative 0; Mismatches 2; Indels
 Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="148TL--01-NB"
/tissue_type="leaf"
 1865 TITTITITITITIAN 1883
 19 Tritritritritritritri
 CF276637.1 GI:33654023
 Oryza sativa
 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 RESULT 126
CF276637/c
LOCUS
DEFINITION
 TITLE
JOURNAL
COMMENT
 REFERENCE
AUTHORS
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Gaps

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Query Match 1.5%; Score 15.4; DB 1; Length 17; Best Local Similarity 94.1%; Pred. No. 79; Matches 16; Conservative 0; Mismatches 1; Indels

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/scione liberarious and state of the blank of the blank of state of strain XL10-Gold, T1-resistant, F-" /clone liberarious 10kb plasmid UUGCIM library /mouse IN was blank of securce (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a was blunt end-repaired with T4 DNA polymerase and T4 was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pMPAD (grid 14732114 [gp] AR129072.1); a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 AGDS4/47
1M0529F08F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0529F08 F, genomic survey sequence.
AZ654747
 premied and (2000)
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 ö
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I. (bases I to 19)
Dunn,D., Adyagi,A., Adyagi,A., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Nucderhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
 Gaps
 ö
 DB 1; Length 19;
 Indels
 rel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0529 row: F column: 08
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/mol type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGCIM0529F08"
 High quality sequence stop: 19.
Location/Qualifiers
 Mus musculus (house mouse)
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 Rm. 308, Bi
84112, USA
 DEFINITION
 ORGANISM
RESULT 127
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Location/Qualifiers
 Mus musculus (house mouse)
 1864 CITITIATITITITI 1881
 Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
 1 critiriritiritiriti
 AZ799396.1 GI:12950471
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 Query Match
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Matches 16; Conservative
 USA
 source
 source
 RESULT 130
AZ799396
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AUTHORS
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 COMMENT
 SOURCE
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 ઠે
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/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
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with oligoribonucleotides and Then used as templates for
RI-PCR."
 CF320418

HD--11-E22.gl OsHDAC1-overexpressing transgenic rice plasmid cDNA
Library (HD) Oryza sativa cDNA clone HD--11-E22, mRNA sequence.
 CF301151 18-AUG-2003 17-AUG-2003 15-AUG-2003 7LEAF--05-005.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--05-005, MRNA sequence.
 ö
 Oryza sativa
bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae; Oryzeae; Oryza,
I (bases I to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
 Bukaryotta, Wiridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryotta; Wiridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eppermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Enthartoideae; Oryzae; Oryzae; Oryzae; Lo. 18)

(bases 1 to 18)

Kan, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.X., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 Contact: Nam. B.H.

Contact: Nam. B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongin, KyeongGi, Korea
Tel: 82 31 330 6193

Fax: 82 31 321 6355
 0; Gaps
 DB 1; Length 18;
 2; Indels
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
 Score 14.8; D
Pred. No. 93;
0; Mismatches
 1865 TITITATITITA 1882
 1 ritiriritiriti
 CF301151
CF301151.1 GI:33672912
 CF320418.1 GI:33692179
Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
 Oryza sativa
Oryza sativa
 Oryza sativa
 CF320418
 EST
 EST
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 LOCUS
 DEFINITION
 ORGANISM
 RESULT 128
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 RESULT 129
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VERSION
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 CF301151
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 CF320418
 FEATURES
 COMMENT
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/mol type="mRNA"
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/dev stage="proliferated callus on 2N6 media for 2 weeks"
/dev stage="recoli bH108"
/clone lib="OshIAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
 Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 108, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 GSS 16-FEB-2001
 Mus musculus

Bukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metacoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

2 (bases 1 to 19)

3 (bases 1 to 19)

3 (bases 1 to 19)

4 (bases 1 to 19)

4 (bases 1 to 19)

5 (bases 1 to 19)

5 (bases 1 to 19)

6 (bases 1 to 19)

7 (bases 1 to 19)

7 (bases 1 to 19)

8 (bases 1 to 19)

9 (bases 1 to 19)

9 (bases 1 to 19)

9 (bases 1 to 19)

10 (bases 1 to 19)

11 (bases 1 to 19)

12 (bases 1 to 19)

13 (bases 1 to 19)

14 (bases 1 to 19)

15 (bases 1 to 19)

16 (bases 1 to 19)

16 (bases 1 to 19)

17 (bases 1 to 19)

18 (bases 1 to 1
 AZ799396
2M0056N18R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0056N18 R, genomic survey sequence.
 /note="Vector: pCR4-TOPO; Site_1: BcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR: mRNA was derived from tice Histone Deacetylase overexpression
 Gaps
 ö
 1.4%; Score 14.8; DB 1; Length 18; 88.9%; Pred. No. 93; 2; Indels tive 0; Mismatches 2; Indels
of Bioscience and Bioinformatics, MyongJi University
 Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr
Location/Qualifiers
 rel: 601 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0056 row: N column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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ö

```
/lab host="E. Coli strain XLI0-Gold, T1-resistant, F-"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note=="Weetor: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch norifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated by espeated
purcleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gil #732114|gp|AR129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli Kili0-Gold (Stratagene) cells
and selected for ampicillin resistance."
 Wilson, R.
The WashU-Marck EST Project
Unpublished (1995)
Contact: Wilson RK
Mashington University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax:
 N41929 15 Dp mRNA linear EST 24-JAN-1996 1970'D02.r1 Soares melanocyte 2NDH Homo sapiens cDNA clone IMAGE:270507 5' similar to gb:M92934 CONNECTIVE TISSUE GROWTH PACTOR PRECURSOR (HUMAN);, mRNA sequence.
 ô
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(bases 1 to 35)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lenno,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
 Gapa
 ..
0
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Pred. No. 96;
0; Mismatches 2; Indels
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 Homo sapiens (human)
 Query Match 1.4
Best Local Similarity 88.9
Matches 16; Conservative
 Homo sapiens
 EST.
 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 RESULT 131
N41929/c
 LOCUS
DEFINITION
 REFERENCE
AUTHORS
 FEATURES
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Eukaryotta, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Rukaryotta; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Eukaryotta; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 17)

RS NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

AL Unpublished (1999)

Other_ESTS: 2819575. Sprime

Contact: Robert Straubberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling

Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing

project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:

www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality

scorse: PRED From University of Washingtion Genome Center: PHRAP suite. PoTy-T Identification: patMatch.pl from Berkeley

Trimming: cross match from University of Washingtion Genome Center: PHRAP suite. PoTy-T Identification: edu Low Quality Sequence: 17

contiguous PHRED high quality bases following vector sequence: 17

contiguous PHRED high quality bases following vector sequence: Plate: LLCM2 row: D column: 12

High quality Sequence: Plate: Trace file contained 17 contiguous distinct peaks following vector sequence.

Plate: LLCM2 row: D column: 12

High quality Sequence: Property Roop 17.

Lond that LLCM2 row: D column: 12

High quality sequence Sequence.
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/dlone lib="NH10B (phage-resist
 AW247165
2819675.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819675.3',
 ö
 Gaps
 ö
 1.4%; Score 14.8; DB 1; Length 35; 80.0%; Pred. No. 1.2e+02; tive 0; Mismatches 4; Indels
 Location/Qualifiers
 1813 TATATATATATATGTACA 1832
 35 TATATATATANNTATACACA 16
 mRNA sequence.
AW247165
AW247165.1 GI:6590158
 Homo sapiens (human)
Homo sapiens
 Conservative
 Query Match
Best Local Similarity
 RESULT 132
AW247165
 VERSION
KEYWORDS
SOURCE
ORGANISM
 LOCUS
DEFINITION
 REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
 ACCESSION
 FEATURES
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1866 TITITITITITI 1881

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 17)

RS NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

AL Unpublished (1999)

Other_ESTS: 2821096.5prime;

Conteact: Robert Strausberg, Ph.D.

Email: Gapba-r@mail.nih.gov

Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling

Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.

Conscrtium (LIML) DNA sequencing by: Berkeley MGC sequencing

From Conteact: Robert Strausberg, Ph.D.

Consortium (LIML) DNA sequencing by: Berkeley MGC sequencing

project Clone distribution: WGC clone distribution information can be found through the I.M.A.G.E. Consortium/Libra at the consortium (LIML) DNA sequencing by: Gones: PHRED from University of Washingtion Genome Center: PHRAP sulte. Poly-T Identification: patMatch.pl from Berkeley

Drosophila Genome Project. University of Washingtion Genome Center: http://www.genome.washington.edu Low Quality Sequence: B contiguous fullowing vector sequence: Toolyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

PHRE LiCMS row: O column: 17

High quality sequence stop: 8

Location/Quality sequence stop: 8

Location/Quality sequence stop: 8

Location/Qualifiers

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//mol_type="maxNa"
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CoCRI, cDNA made by oliqo-dT priming. Directionally
cloned into EccRI/Xho1 sites using the following 5;
adaptor: GGCACGGG(G). Size-selected >SOODp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CNNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
 AW248574 1inear EST 07-JAN-2000 2821096.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821095 3',
 ö
insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
 Gaps
 ö
 1.4%; Score 14.4; DB 1; Length 17; 93.8%; Pred. No. 96; Live 0; Mismatches 1; Indels
 organism="Homo sapiens"
 1866 TITITITITITI 1881
 AW248574
AW248574.1 GI:6591567
 2 TITITITITITI 17
 Homo sapiens (human)
Homo sapiens
 Query Match
Best Local Similarity 93.8
Matches 15, Conservative
 mRNA sequence.
 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 RESULT 133
AW248574
 DEFINITION
 REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
 FEATURES
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Gaps

ö

1.4%; Score 14.4; DB 1; Length 17; larity 93.8%; Pred. No. 96; Conservative 0; Mismatches 1; Indels

Query Match Best Local Similarity Matches 15; Conserv

```
/lab host="E" Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/noce="Weetor: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/Accuments/Anares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifica at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose general from a derivative
of pWD42 (gi|q732114 |gb|AF12972.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
 ö
 Б
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. L. (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 AZ579599 13-DEC-200 NA linear GSS 13-DEC-200 NMO367P06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
 .
0
 1.4%; Score 14.2; DB 1; Length 21;
14.2%; Pred. No. 1.1e+02;
ve 0; Mismatches 3; Indels
 Email: ddunm@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0367 row: P column: 06
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
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 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
 /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0367P06"
 Mus musculus (house mouse)
Mus musculus
 ilarity 84.2%; Pre
Conservative 0;
 AZ579599
AZ579599.1 GI:11694028
 'sex="Male"
 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet:
 Unpublished (2000)
 Best Local Similarity
Matchès 16; Conserv
 Rm. 308,
 GSS.
 Query Match
 source
 RESULT 134
AZ579599/c
LOCUS
DEFINITION
 ACCESSION
VERSION
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ORGANISM
 REFERENCE
 AUTHORS
 JOURNAL
 FEATURES
 TITLE
 COMMENT
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

LOCUS

RESULT 135 BQ590128

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/clone_rib="weather root"

/clone="vector: property roots
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Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 17)
 Sp6-Sall-CCACGCCTCCG-Sprime-cDNA-polyA-CC-Not1-T7; Note: Sequencing granted in the context of the GABI-Beet project, local Pr: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
 Eukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

1 (Dases 1 to 17)
Hervig.R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes plant J. 32 (5), 845-857 (2002)
 BO12715-024-017-B22-T7 MPIZ-ADIS-024-storage root Beta Vulgaris E0591177
 1. .17
/organism="Beta vulgaris"
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line)"
 Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.
 1.3%; Score 13.8; DB 1; Length 17;
88.2%; Pred. No. 1.1e+02;
tive 0; Mismatches 2; Indels
 Contact: Weisshaar B
ADIS DNA core facility at MPIZ
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 0049221506288
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 17 Std Brror: 0.00
Plate: 18 row: B column: 24
Seg primer: 77; GTAATAGGACTCACTATAGGGC.
 1865 TTTTTTTTTTTT 1881
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BQ590687
BQ590687.1 GI:26120270
 17 TTTTTTTTTTTTTTTT 1
 orientation:
 Conservative
 Beta vulgaris
 Beta vulgaris
 Beta vulgaris
 Best Local Similarity
Matches 15; Conserv
 12472698
 Query Match
 VERSION
KEYWORDS
SOURCE
ORGANISM
 DEFINITION
 RESULT 137
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 REFERENCE
AUTHORS
 JOURNAL
MEDLINE
PUBMED
 ACCESSION
 AUTHORS
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LOCUS
 REFERENCE
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/tish host="EMDH:10B"
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/note="Vector: pCMVSPORT6; Site_1: Sal1; Site_2: Not1;
/note="Textor from sugar beet, library provided by KMS
/cloim anzlebener Seateroth AG Einbeck, Germany, context:
/b.schulz@kws.de; cloning sites Sal1-Not1, primer sites and
 BQ590687 17-024-018-B24-T7 MPIZ-ADIS-024-storage root Beta vulgaris cDNA clone 024-018-B24 3-PRIME, mRNA sequence.
 ô
 BQ590128 17 bp mRNA linear EST 06-DEC-2002 E012843-024-019-E19-T7 MPIZ-ADIS-024-storage root Beta vulgaris cDNA clone 024-019-E19 3-PRIME, mRNA sequence.
 Beta vulgaris
Beta vulgaris
Beta vulgaris
Beta vulgaris
Butayota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Butaryota, Viridiplantae, Beta.
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 17)
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., and Radelof, U.
 SP6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-Not1-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
 /organism="Beta vulgaris"
/mol type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
 Gaps
 1.3%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 1.1e+02; tive 0; Mismatches 2; Indels
 Contact: Weisshaar B
ADIS DNA core facility at MPIZ
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062818
Email: weisshaadmpiz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 19 row: E column: 19
Seg primer: 77; GTAATAGGACTCACTATAGGGC.
Location/Qualifiers
 1814 ATATATATATATGTACA 1832
 1866 TITTATITITATIN 1882
 20 AGATATATATATACACA 2
 BQ590128
BQ590128.1 GI:26119711
 orientation:
 15; Conservative
 Query Match
Best Local Similarity
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source

FEATURES

JOURNAL MEDLINE PUBMED COMMENT

TITLE

EST 06-DEC-2002

RESULT 136 BQ590687/c LOCUS DEFINITION

Matches

g à

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Gaps

.. 0

ö

Gaps

ö

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/organism="Oryza sativa"
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/mol type="mRNA"
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 Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enhartoidees; Oryzeae; Oryza.

1. (bases 1 to 17)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Bong,S.I., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
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cultive="mcM" coff
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with oligoribonucleotides and then used as templates for
RT-PCR."
 Diputing (207)

Contact: Nahm B.H.

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc., Division

Genomics and Boinformatics, MyongJi University

Yorgin, KyeongGi, Korea

Tel: 82 31 330 6193

Fax: 82 31 312 655

Exx: 82 31 321 655

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
 1.3%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 1.1e+02; ive 0; Mismatches 2; Indels
 1.3%; Score 13.8; DB 1; Length 17;
llarity 88.2%; Pred. No. 1.1e+02;
Conservative 0; Mismatches 2; Indels
 l. .17
/organism="Oryza sativa"
Location/Qualifiers
 1866 TITITITITITITI 1882
 1881
 17
 CF294668.1 GI:33663701
 rititititititi
 1865 TTTTTATTTTGTTT
 Oryza sativa
Oryza sativa
 Best Local Similarity
Matches 15; Conserv
 Best Local Similarity Matches 15; Conserv
 Query Match
 Query Match
 VERSION
KEYWORDS
SOURCE
ORGANISM
 DEFINITION
 TITLE
JOURNAL
COMMENT
 RESULT 139
 REFERENCE
AUTHORS
 ACCESSION
 FEATURES
 CF294668
 FEATURES
 ò
 d
 ò
 엄
 CF290854 linear EST 14-AUG-2003 14ROOT--01-A21.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa cDNA clone 14ROOT--01-A21, mRNA sequence.
 db_xref="GABI:188948"

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 ö
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
 orientation:
SP6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local P1: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
 Oryza sativa

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Ehrhartoideae, Oryzeae, Oryza, Liliopsida, Poales, Poaceae, Kim,J.S., Jun,K.M., Cheong,P.J., Xim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Xim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University YongJi, Kveonggi, Korea Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
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 Contact: Weisshaar B
ADIS DNA core facility at MPIZ
ADIS DNA core facility at MPIZ
Max-Plandk-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 04942215.062818
Fmai: weisshaa@mpiz-koeln.mpg.de
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 Contact: Nahm B.H.
 Oryza sativa
 CF290854
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 EST.
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CF290854
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DEFINITION
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 TITLE
JOURNAL
COMMENT
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 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Enhartoidaes, Oryzae, Oryza.

1 (Dases 1 to 17)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bloinformatics, MyongJi University
YongJin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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88.2%; Pred. No. 1.1e+02;
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Oryza sativa
Oryza sativa
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

Stm. J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-ecale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 331 6355
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 CF295988 114-AUG-2003 30DGS--06-C17.bl Rice leaf plasmid cDNA library I (30DGS) Oryza sativa cDNA clone 30DGS--06-C17, mRNA sequence.
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Best Local Similarity 88.2%; Pred. No. 1.1e+02;
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 1866 TITIATITITITA 1882
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16 bp mRNA linear EST 09-MAR-1999 tf51h06.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2102843 3' almilar to TR:Q69566 Q69566 ;, mRNA sequence.
 CONA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. and Ph.D. CONA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Conter Clore distribution: NCI-CSAP clore distribution information can be found through the I.M.A.G.B. Consortium/LIML at:
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Homo sapiens

Homo sap
 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Genetics Institute, MyongJi University
Youghi, KyeongGi, Korea
Tel: 82 31 330 6193
Fax: 82 31 312 655
Email: bhnahm@gdpio.com, bhnahm@bio.myongji.ac.kr.
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 Conservative
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Best Local Similarity
Matches 15; Conserv
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 Lyzza sativa

Cryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Enhartoidaae; Oryzaa.

Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Enhartoidaae; Oryzaa.

I (bases 1 to 17)

RS Kim, Js. S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Vongin, Kyeonggi, Korea
Tel: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
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1 (bases 1 to 17)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Large-scale Sequencing Analysis of Rice ESTs
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reaction. The driver was PCR-amplified cDNAs from a pool
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985608-986759, 1101192-11011959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
A1685758 107 CGAP Pr28 Homo sapiens cDNA clone IMAGE:2253280 3, similar to TR:\(\overline{Q}\)02393 HUMAN PAPILLOMAVIRUS 18 E5 CENTRAL SEQUENCE MOTIF POTEIN 1, contains element LTR4 repetitive element in mRNA, sequence.
 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NIT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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 Tumor Gene Index
Unpublished (1997)
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project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
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BD12E4-024-024-019-K18-T7 MPIZ-ADIS-024-storage root Beta vulgaris
CDNA clone 024-019-K18 3-PRIME, mRNA sequence.
 Beta vulgaris
Beta vulgaris
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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1 (bases 1 to 16)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
 ö
 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes plant J. 32 (5), 845-857 (2002)

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 Contact: Weisshaar B
ADIS DNA core facility at MPIZ
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 049221506288 B
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DEFINITION

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Caryophyllales, Amaranthaceae, Beta.

L (bases 1 to 16)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
and Radelof,U., Lehrach,H., Menze,A., O'Brien,J., Lehrach,H.
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(bases 1 to 16)

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S.; Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
 SP6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-Not1-T7; Note: Sequencing granted in the context of the GAB1-Beet project, local Pr: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GAB1-Primary database: http://gabi.rzpd.de"
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 Contact: Weisshaar B
ADIS DNA core facility at MPIZ
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
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Butaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
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Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
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 ô
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SP6-SalI-CCACGCGTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Best
project, local Pi: Dr. Katharina Schmeider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
 Contect: Weisshaar B
ADIS DNA core facility at MPIZ
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062681
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 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
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 Query Match 1.2%; Score 12.8; DB 1; Length 16; Best Local Similarity 87.5%; Pred. No. 1.2e+02; Matches 14; Conservative 0; Mismatches 2; Indels
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 BQ592600.1 GI:26122183
 1 rrrrrrrrrrrrr 16
 line)
 Beta vulgaris
Beta vulgaris
 Beta vulgaris
 12472698
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RESULT 149 BQ592600/c LOCUS DEFINITION

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ACCESSION VERSION KEYWORDS SOURCE

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Gaps ô mcgarry191-19.rst

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/note="Vector: pCMVSPORT6; Site_1: Sal1; Site_2: Not1;
/contact: b.schulz@kws.de; cloning sites Sal1-Not1, primer sites and
 Beta vulgaris
Beta vulgaris
Beta vulgaris
Beta vulgaris
Beta vulgaris
Beta vulgaris
Beta vulgaris
Beta vulgaris
Spermatophyta; Viridiplantae; Streptophyta; Embryophylata;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

1 (baess 1 to 16)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Dungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Phant J. 32 (5), 845-857 (2002)
 SP6-Sall-CCACGCGTCCG-Sprime-cDNa-polya-CC-Not1-T7; Note: Sequencing granted in the context of the GAB1-Beet project, local Pr: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GAB1-Primary database: http://gabi.rzpd.de"
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 Contact: Weisshaar B
ADIS DNA core facility at MPIZ
MAX-PlandA-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 0049221506288;
Fmax: weisshaa@mpiz-koeln.mpg.de
Insert Length: 16 Std Brror: 0.00
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BQ595717/c
LOCUS
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PUBMED
COMMENT
 REFERENCE
AUTHORS
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 BEST.

Beta vulgaris

Est.

Est.

Beta vulgaris

Enkaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Enkaryota, Varidiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermacophyta; Amaranthaceae, Beta.

Caryophyllales, Amaranthaceae, Beta.

NCE 1 (bases 1 to 16)

IORS 1 to 16)

Drungowski,M., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,

Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.

and Radelof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes

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BQ595369
BQ595369.1 GI:26124952
EST.
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 Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-keeln.mpg.de
Insert Length: 16 Std Error: 0.00
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ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
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Seg primer: T7; GTAATACGACTCACTATAGGGC.
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 JOURNAL
MEDLINE
PUBMED
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 ACCESSION
 FEATURES
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Gaps ö

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Oryza sativa

Oryza sativa

Oryza sativa

Oryza sativa

Oryza sativa

Eukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,

Epkratotoldeae; Oryzae;

Enkratoideae; Oryzae;

Enkratoideae; Oryzae;

E (bases 1 to 16)

S Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTS

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, MyongJi University
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/lab host="E.coli DHIND"
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APF--06-C03.gl ABF3-overexpressing transgenic rice plasmid cDNA
Library (ABF) Oryza sativa cDNA clone ABF--06-C03, mRNA sequence.
CF311057.1 GI:33682818
EST.
 CF296130 10-2003 16 bp mRNA linear EST 14-AUG-2003 30DGS--06-F22.bl Rice leaf plasmid cDNA library I (30DGS) Oryza sativa cDNA clone 30DGS--06-F22, mRNA sequence.
 Oryza sativa

Oryza sativa

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Strantatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Enhartochodae, Oryzae, Oryza.

I (bases 1 to 16)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
 Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Genetics Institute, MyongJi University
Vongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggio.com, bhnahm@bio.myongji.ac.kr.
 Query Match
1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
 Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
 1867 TTTATTTTTTTA 1882
 CF296130
CF296130.1 GI:33665163
 1 rrrrrrrrrrrrrr 16
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 RESULT 155
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COMMENT
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CDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, context:
b.schulz@kws.de; cloning sites Sal1-Not1, primer sites and
orientation:
Sp6-Sal1-CCAGGGTCGG-Sprime-cDNA-polyA-CC-Not1-77; Note:
Sequencing granted in the context of the GABI-Beet
project, local Pi: Dr. Katharina Schneider, coordinator:
project, local Pi: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZDD/GABI-Primary database: http://gabi.rzpd.de"
 LEK/9325
J4ETL--05-J09.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--05-J09, mRNA sequence.
CF279325
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 Oryza sativa

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Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Intractolodaes; Oryzae

Oryzae; Oryzae

Nam,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Large-scale Sequencing Analysis of Rice ESTS

Unpublished (2002)
 Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 62 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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 CF279325.1 GI:33656711
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Matches 14; Conserv
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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RESULT 153 CF279325 LOCUS

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Surviva sativa

Oryza sativa

Dukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Shrhartoideae; Oryzeae; Oryzaa.

En (Dasses Ito 16)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongdi University
Yongin, Kyeonggi, Korea

Tel: 83 31 321 6355

Bmail: bhaahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
 16 bp mRNA linear EST 15-AUG-2003
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library (HD) Oryza sativa cDNA clone HD--04-NIO, mRNA sequence.
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..
Mismatches
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0
 1865 TTTTTTTTTTTT 1880
 1882
 .1 TTTTTTTTTTT 16
 16
 1 Trirriririririr
 1867 TITATITITITA
Matches 14; Conservative
 Oryza sativa
Oryza sativa
 Query Match
Best Local Similarity
Matches 14; Conserv
 RESULT 158
CF315789
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VERSION
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VERSION
KEYWORDS
SOURCE
ORGANISM
 RESULT 157
CF314377
LOCUS
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 REFERENCE
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AUTHORS
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JOURNAL
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Orytac; Magnollophyta; Liliopsida; Poales; Poaceae; Exhartoideae; Orytac; Stim, 7.8., Unn, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
 CF314013

16 bp mRNA linear EST 15-AUG-2003

HD--02-G01.gl OsHDAC1-overexpressing transgenic rice plasmid cDNA

library (HD) Oryza sativa cDNA clone HD--02-G01, mRNA sequence.

CF314013.1 GI:33685774
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then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
 /note="Vector: pCR4-TOPO; Site 1: ECORI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR: mRNA was derived from rice Histone Deacetylase overexpression line."
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 ö
 1.2%; Score 12.8; DB 1; Length 16;
87.5%; Pred. No. 1.2e+02;
 Query Match
1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
 Email: bhrahm@ggbio.com, bhrahm@bio.myongji.ac.kr.
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/cultivar="Nackdong"
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 1 Tritritititi 16
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Best Local Similarity
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TITLE JOURNAL COMMENT

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REFERENCE AUTHORS

RESULT 156 CF314013 LOCUS DEFINITION

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Enhartoideae; Oryzae; Oryza.

I (bases 1 to 16)

Song, S. I. (Kim, V. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C., Song, S. I., Kim, J. K., Kim, Y. -K. and Nahm, B. H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B. H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongIn, Kyeonggi, Korea
Tel: 82 31 321 6355

Email: bhnahm@ggdbio.com, bhnahm@bio.myongji.ac.kr.
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/clone lib="OsHDACI-cverexpressing transgenic rice plasmid cDNA library (HD)"

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 HD--07-105.g1 OBHDAC1-overexpressing transgenic rice plasmid cD
library (HD) Oryza sativa cDNA clone HD--07-105, mRNA sequence.
 /note="Weetor: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr Oligo-capped mRNA was reverse transcribed and then used for PCR: mRNA was derived from rice Histone Deacetylase overexpression line."
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 1.2%; Score 12.8; DB 1; Length 16; 87.5%; Pred. No. 1.2e+02; rative 0; Mismatches 2; Indels
 1.2%; Score 12.8; DB 1; Length 16; 87.5%; Pred. No. 1.2e+02; tive 0; Mismatches 2; Indels
 mRNA
 1865 TITITATITITI 1880
 CF317718
CF317718.1 GI:33689479
 1865 TITITATITIT 1880
 16
 1 riririririririi 16
 14; Conservative
 Best Local Similarity 87.5
Matches 14; Conservative
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Oryza sativa
 Similarity
 CF317718
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Best Local
 Query Match
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CF320356
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 CF317718
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 a
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatoideae; Oryzeae; Oryza.

E 1 (bases 1 to 16)
S Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongdi University
Yongin, Kyenonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 316 6355
 /dev_stage="proliferated callus on 2N6 media for 2 weeks" lab host="E.col! DH10B" /clone lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
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 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
Yorgin, Kyeonggi, Korea
Fax: 82 31 321 6155
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
 CDNA
 /notes="Vector: pCR4-TOPO, Site 1: EcoRI, Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."
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library (HD) Oryza sativa cDNA clone HD--05-D07, mRNA sequence.
CF316056
CF316056.1 GI:33687817
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 .
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 Length 16;
 2; Indels
 Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Oryza sativa
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CF316056
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DEFINITION
 ORGANISM
 TITLE
JOURNAL
COMMENT
 REFERENCE
AUTHORS
 TITLE
JOURNAL
 ACCESSION
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KEYWORDS
SOURCE
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Gaps

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Gaps

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

FEATURES

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Cuyza Bacina Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Poaceae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enrhartoideae, Oryzae; Oryza.

Enrhartoideae, Oryzae; Oryza.

1 (base; 1c 16)

S Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355

Email: bhnahm@ggblo.com, bhnahm@bio.myongji.ac.kr.
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/esue type="callus"

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/lab host="E.coli DH108"

/lab host="E.coli DH108"

/lone lib="Rice callus plasmid cDNA library (NACL)"

/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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 CF329320

NACL--04-J1.bl Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--04-J17, mRNA sequence.
CF329320
CF329320.1 GI:33806877
 Ö
 ö
 1.2%; Score 12.8; DB 1; Length 16; ilarity 87.5%; Pred. No. 1.2e+02; Conservative 0; Mismatches 2; Indels
 tch 1.2%; Score 12.8; DB 1; Length 16; al Similarity 87.5%; Pred. No. 1.2e+02; 14; Conservative 0; Mismatches 2; Indels
 Location/Qualifiers
 1867 TITATITITIA 1882
 1865 TITITATITITI 1880
 1 rrrrrrrrrrrrr 16
 Oryza sativa
Oryza sativa
 Query Match
Best Local Similarity
Matches 14; Conserv
 Query Match
Best Local Similarity
Matches 14; Conserv
 source
 CF329320
LOCUS
DEFINITION
 VERSION
KEYWORDS
SOURCE
ORGANISM
 source
 TITLE
JOURNAL
COMMENT
 RESULT 163
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AUTHORS
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 FEATURES
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 1. 16

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1 (bases 1 to 16)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
 Oryza sativa

Duyza sativa

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,

Spermatophyta, Magnoliophyta, Liliopsida, Poales, Foaceae;

Shrhatroidaes, Oryzae, Oryza.

(bases 1 to 16)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
 Contact: Nahm B.H.
Contact: Nahm B.H.
Contact: Nahm B.H.
Contact: And Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
YongIn, Kyeonggi, Korea
YongIn, Kyeonggi, Korea
Far: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
 Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
Yorgin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mENA was reverse transcribed and then used for PCR: mRNA was derived from rice Histone Deacetylase overexpression line."
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CF320356
CF320356.1 GI:33692117
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1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
 1865 TITITATITITIT 1880
 Oryza sativa
Oryza sativa
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

DEFINITION RESULT 162 CF327722

8

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Gaps

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 Wilson, R.
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VERSION
KEYWORDS
SOURCE
ORGANISM
 RESULT 166
R06912
 DEFINITION
 TITLE
JOURNAL
 REFERENCE
AUTHORS
 COMMENT
FEATURES
 FEATURES
 COMMENT
 d
 à
 Cryza sativa

Cryza sativa

Cryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Enthartoideae; Oryzae; Oryzae.

CE (Masses 1 to 16)

RS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

AL Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJin, KyeongJi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
 16 bp mRNA linear EST 18-AUG-2003
JMT--02-E05.gl AtJMT-overexpressing transgemic rice plasmid CDNA
library (JMT) Oryza sativa CDNA clone JMT--02-E05, mRNA sequence.
CF333386
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reversee transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
 ô
 GSS 03-APR-2001
 Janssen, C.S., Barrett, M.P., Lawson, D., Quail, M.A., Harris, D.,
Bowman, S., Phillips, R.S. and Turner, C.M.
Gene discovery in Plesmodium chabaudi by genome survey sequencing
Mol. Biochem. Parasitol. 113 (2), 251-260 (2001)
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 Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
1 (bases 1 to 21)
 2 (bases 1 to 21)
Janssen, C.S.
Direct Submission
Submitted (06-NOV-2000) Division of Infection & Immunity,
 ;
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Plasmodium chabaudi
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 genomic survey sequence.
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Best Local Similarity 87.5
Matches 14; Conservative
 Mol. Bioc
21192558
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KEYWORDS
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ORGANISM
 RESULT 165
PCH303878
LOCUS
 LOCUS
 DEFINITION
 ORGANISM
RESULT 164
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JOURNAL
MEDLINE
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TITLE
JOURNAL
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AUTHORS
 TITLE
JOURNAL
COMMENT
 ACCESSION
 VERSION
KEYWORDS
SOURCE
 REFERENCE
 AUTHORS
 PUBMED
 REFERENCE
 ACCESSION
 FEATURES
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Email: est@watson.wustl.edu

Insert Size: 1597
High qality sequence starts: 1 High qality sequence stops: 1
High qality sequence starts: 1 High qality sequence stops: 1
Source: IMGE Consortium, LINL This clone is available royalty-free through LINL, contact the IMAGE Consortium (info@image.llnl.gov)
for further information. Trace considered overall poor quality
Insert Length: 1597
Std Brror: 0.00
Seq primer: -2nml3
High quality sequence stop: 1.
 ö
 ROG912 18 CORREST 137 bp mRNA linear EST 05-APR-1999 1872gOS.81 SOBRET 11872 HOMO SADJENS CDNA CLONE IMAGE:115680 3' SIMILAR tO GD:M92934 CONNECTIVE TISSUE GROWTH PACTOR PRECURSOR (HUMAN); mRNA sequence.
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
I (bases 1 to 37)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Materston,R., Williamson,A., Wohldmann,P. and
University of Glasgow, Joseph Black Building, Glasgow G12 8QQ, bases 40 to 60 (SL to QR).

Location/Qualifiers
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 ;
0
 The Washu-Merck EST Project Unpublished (1995)
Unpublished (1995)
Contact: Wisson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
 Query Match 1.1%; Score 12; DB 1; Length 21; Best Local Similarity 75.0%; Pred. No. 1.6e+02; Matches 15; Conservative 0; Mismatches 5; Indels
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

RESULT 167 CF280421/c LOCUS DEFINITION

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Kim, J. S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongGi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidaes; Oryzeae; Oryza.

1 (bases 1 to 14)

Kim, J. S., Jun, K.M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C., Song, S. I., Kim, J. K., and Nahm, B. H.

Unpublished (2003)

Contact: Nahm B. H.
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 Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongJi, Korea
Pal: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
 /mol_type="mkNA" | Collibration | Co
 Query Match
Best Local Similarity 92.3%; Pred. No. 1.46+02;
Matches 12; Conservative 0; Mismatches 1; Indels
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 organism="Oryza sativa"
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Oryza sativa
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KEYWORDS
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 source
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 RESULT 169
 TITLE
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COMMENT
 TITLE
JOURNAL
COMMENT
 REFERENCE
AUTHORS
 REFERENCE
AUTHORS
 ACCESSION
 CF300543
LOCUS
 FEATURES
 FEATURES
 δ
 13 bp mRNA linear EST 15-AUG-2003 7LEAF--03-L04.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--03-L04, mRNA sequence.
 CF280421 18TL--07-B11.g1 Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa cDNA clone 14ETL--07-B11, mRNA sequence.
CF280421. GI:33657807
 ö
 ö
 Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enthartoideae; Oryzee; Oryze.

1 (bases 1 to 13)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, Y.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
 Contact: Nahm B.H.

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Boinformatics, MyongJi University
YongJin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@plio.myongJi.ac.kr.

Location/Qualifiers
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with eligoribonuclectides and then used as templates for RT-PCR."
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(14ETL)"
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 Length 37;
 Indels
 Query Match 1.1%; Score 11.8; DB 1; 1
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 1320 rcccacccaarrcaaacarrerccarerc 1350
 CF299609.1 GI:33671370
 1767 TITITAAAATTIT 1779
 13 rrrrrrradarrr 1
 Oryza sativa
 Oryza sativa
 Oryza sativa
 Query Match
Best Local Similarity
Matches 12; Conserv
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EST.

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

RESULT 168 CF299609/c LOCUS DEFINITION

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RESULT 170 CF328966/c LOCUS DEFINITION

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

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Oryza sativa
Oryza sativa
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Shrattoideae; Oryzeae; Oryza.
Enhartoideae; Oryzeae; Oryza.
Enhartoideae; Oryzeae; Oryza.

Enhartoideae; Oryzeae; Oryza.

Enhartoideae; Oryzeae; Oryza.

SKim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,X.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Large-scale Sequencing Analysis of Rice ESTs
Contact: Nahm B.H.
Gendet: Nahm B.H.
Gendet: Nahm B.H.
Gendet: Nahm B.H.
Vongin, Kyeonggi, Korea
Tel: 82 31 330 6133
Fax: 82 31 321 6555
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Ehrhartoideae; Oryzeae; Oryzaa.

Ehrhartoideae; Oryzeae; Oryzaa.

Kim, Usaes i to 11)

Kim, Us., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

L Unpublished (2013)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University YongJi, KyeongGi, KyeongGi, KyeongGi, KyeongGi, Sorea

Tel: 82 31 321 6355

Bmail: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
 / OLIGINATION SETTING
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 TITLE
JOURNAL
COMMENT
 REFERENCE
AUTHORS
 TITLE
JOURNAL
COMMENT
 ACCESSION
 REFERENCE
 AUTHORS
 FEATURES
 FEATURES
 ð
 SM Oryza sativa

Oryza sativa

Oryza sativa

Oryza sativa

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzae; Dryza.

Ehrhartoideae; Oryzae; Oryzae;

El (Asses Ito 14)

S Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
 | 1. 14 | Angalism=10.000 | Angalism=10.000 | Angalism=10.000 | Angalism=10.000 | Angalism=10.000 | Angalism=10.000 | A
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 Oryza sativa
vyza sativa
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
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DEFINITION

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 ISM Oryza sativa

Oryza sativa

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Liliopsida; Poales; Poaceae;

Ehrhartoidae; Oryza.

CE 1 (bases 1 to 12)

RS Kim, J.S., Jun, K.M., Y. Kim, Y. K., Kim, M.J., Lee, T. H., Shin, Y. C.,

Song, S. I., Kim, J. K., Kim, Y. K. and Nahm, B. H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B. H.

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Yongin, Kyeonggi, Korea

Tel: 82 31 320 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.myongji.ac.kr.

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VERSION
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 RESULT 173
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AUTHORS
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Contact: Nahm B.H. Genencing Analysis of Rice ESTS

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Fax: 82 31 321 6355

Bmail: bhnahm@ggbbio.com, bhnahm@bio.myongji.ac.kr.
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzea.

Ehrhartoideae; Oryzeae; Oryzea.

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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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Yonglin, Kyeonggi, Korea

Tel: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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CF329947

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Enthartoddeae; Orygae; Oryga.

I (bases 1 to 13)

SKim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTS

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

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 Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
 Email: bhuahm@ggbio.com, bhuahm@bio.myongji.ac.kr
Location/Qualifiers
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Email: Gapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-iberk, M.D., Ph.D.
EDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennor, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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 EST 15-AUG-2003
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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

REFERENCE AUTHORS TITLE

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| n Ltd.                                                                                                                                                                                                                           | me 2 Seconds<br>alignments)<br>lion cell updates/sec         | gtatattttttctataaa 1049                                  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |               | 464                  |                                                 |                                                     |                            | d by chance to have a<br>the result being printed,<br>re distribution. |             | Description                                      | Sequence    | Sequence 400, App<br>Sequence 400, App<br>Sequence 9, Appli      | Sequence<br>Sequence       | Sequence        | Sequence    | Sequence                     | Sednence      | Sequence      | Sequence      | Sequence         | Sequence                       | Sequence      | Sequence                                        | Sequence<br>Sequence | Sequence      | Sequence       | Sequence<br>Sequence                       |
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Sequence<br>.2 15 1 US-08-291-932A-194 Sequence       | .2 15 1 US-08-291-932A-310 Sequence<br>.2 15 1 US-08-812-951B-1 Sequence       | .2 15 ·1 US-08-812-951B-2 Sequence<br>.2 15 1 US-08-784-747-2 Sequence                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          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Ap. 198 12.4 1.2 15 1 US-08-314-847-335 Sequence 132, Appl 198. Ap. 198 198 198 198 198 198 198 198 198 198 | 1857, Ap 186 12.8 1.2 17 1 US-08-35-628-1058 Sequence 1651, Ap 186 12.8 1.2 17 1 US-08-35-628-1058 Sequence 1660, Ap 188 12.4 1.2 14 1 US-08-155-628-1058 Sequence 1855, Ap 189 12.4 1.2 14 1 US-08-156-55 Sequence 1857, Ap 190 12.4 1.2 14 1 US-08-919-867-78 Sequence 1857, Ap 192 12.4 1.2 14 1 US-08-919-867-78 Sequence 1861, Ap 193 12.4 1.2 14 1 US-08-919-867-78 Sequence 16, App 194 12.4 1.2 14 1 US-08-919-867-78 Sequence 176, App 195 12.4 1.2 14 1 US-08-319-428-474 Sequence 178, App 12.4 1.2 15 1 US-08-319-428-474 Sequence 1988, Ap 12.4 1.2 15 1 US-08-319-428-474 Sequence 1988, Ap 12.4 1.2 15 1 US-08-319-43-33-3 Sequence 1989, Ap 12.4 1.2 15 1 US-08-319-43-33-3 Sequence 1989, Ap 12.4 1.2 15 1 US-08-319-43-33-3 Sequence 1989, Ap 201 12.4 1.2 15 1 US-08-319-43-33-3 Sequence 1989, Ap 201 12.4 1.2 15 1 US-08-313-43-33-3 Sequence 1989, Ap 201 12.4 1.2 15 1 US-08-313-43-33-3 Sequence 1989, Ap 201 12.4 1.2 15 1 US-08-313-33-3 Sequence 1989, Ap 201 12.4 1.2 15 1 US-08-313-31 Sequence 1989, Ap 201 12.4 1.2 15 1 US-08-313-51-51 Sequence 1989, Ap 201 12.4 1.2 15 1 US-08-313-31 Sequence 1989, Ap 201 12.4 1.2 15 1 US-08-313-31 Sequence 1989, Ap 201 12.4 1.2 15 1 US-08-313-31 Sequence 1989, Ap 201 12.4 1.2 15 1 US-08-313-31 Sequence 1989, Ap 201 12.4 1.2 15 1 US-08-313-31 Sequence 1989, Ap 201 12.4 1.2 15 1 US-08-313-31 Sequence 1989, Ap 201 12.4 1.2 15 1 US-08-313-31 Sequence 1989, Ap 201 12.4 1.2 15 1 US-08-313-31 Sequence 1989, Ap 201 12.4 1.2 15 1 US-08-313-31 Sequence 1989, Ap 201 12.4 1.2 15 1 US-08-313-31 Sequence 1980, Ap 201 12.4 1.2 15 1 US-08-313-31 Sequence 1980, Ap 201 12.4 1.2 15 1 US-08-313-31 Sequence 1980, Ap 201 12.4 1.2 15 1 US-08-313-31 Sequence 1980, Ap 201 12.4 1.2 15 1 US-08-313-31 Sequence 1980, Ap 201 12.4 1.2 12 12 12 12 12 12 12 12 12 12 12 12 12 | 1857, Ap. 186 12.8 1.2 17 1 US-08-375-GZ8-1058 Sequence 1857, Ap. 186 12.8 1.2 17 1 US-08-375-GZ8-1058 Sequence 1855, Ap. 189 12.4 1.2 14 1 US-08-155-GZ8-1058 Sequence 1855, Ap. 190 12.4 1.2 14 1 US-08-155-GZ8-1058 Sequence 1855, Ap. 190 12.4 1.2 14 1 US-08-151-477A-57 Sequence 1857, Ap. 191 12.4 1.2 14 1 US-08-191-677-78 Sequence 16. App. 192 12.4 1.2 14 1 US-08-98-090-351 Sequence 16. App. 193 12.4 1.2 14 1 US-08-378-535-78 Sequence 16. App. 194 12.4 1.2 14 1 US-08-319-667-79 Sequence 1948, Ap. 195 12.4 1.2 15 1 US-08-319-487-4 Sequence 1988, Ap. 195 12.4 1.2 15 1 US-08-319-491 Sequence 1988, Ap. 197 12.4 1.2 15 1 US-08-33-03-03-03-03-03-03-03-03-03-03-03-03- | 1857, Ap. 186 12.8 1.2 17 1 US-08-375-G8-1058 Sequence 1861, Ap. 188 12.8 1.2 17 1 US-08-375-G8-1058 Sequence 1861, Ap. 188 12.4 1.2 14 1 US-08-155-G8-1058 Sequence 1857, Ap. 199 12.4 1.2 14 1 US-08-16-16-16-16-16-16-16-16-16-16-16-16-16- | 1857, Ap 186 12.8 1.2 17 1 US-08-35-678-1058 Sequence 1855, Ap 188 12.4 1.2 17 1 US-08-35-678-1058 Sequence 1855, Ap 189 12.4 1.2 14 1 US-08-155-658 Sequence 1855, Ap 190 12.4 1.2 14 1 US-08-15-655 Sequence 1855, Ap 190 12.4 1.2 14 1 US-08-19-867-78 Sequence 1857, Ap 191 12.4 1.2 14 1 US-08-19-867-78 Sequence 16. App 192 12.4 1.2 14 1 US-08-398-099-351 Sequence 16. App 193 12.4 1.2 14 1 US-08-398-099-351 Sequence 17. App 194 12.4 1.2 14 1 US-08-319-867-78 Sequence 132. App 195 12.4 1.2 15 1 US-08-319-42B-474 Sequence 132. App 196 12.4 1.2 15 1 US-08-319-491 Sequence 132. App 20 12.4 1.2 15 1 US-08-31-335 Sequence 132. App 20 12.4 1.2 15 1 US-08-31-31 Sequence 132. App 20 12.4 1.2 15 1 US-08-31-31 Sequence 132. App 20 200 12.4 1.2 15 1 US-08-071-845-331 Sequence 132. App 20 200 12.4 1.2 15 1 US-09-071-85-331 Sequence 2047, Ap 20 204 12.4 1.2 15 1 US-09-071-845-331 Sequence 2047, Ap 20 204 12.4 1.2 15 1 US-09-071-845-331 Sequence 5.4 App 10 204 12.4 1.2 15 1 US-08-44-133 Sequence 233. App 20 205 12.4 1.2 15 1 US-08-44-133 Sequence 5.4 App 10 206 12.4 1.2 15 1 US-08-44-133 Sequence 233. App 20 205 12.4 1.2 15 1 US-08-44-133 Sequence 234. App 10 206 12.4 1.2 15 1 US-08-44-133 Sequence 235. App 10 206 12.4 1.2 15 1 US-08-44-133 Sequence 235. App 10 206 12.4 1.2 15 1 US-08-44-133 Sequence 235. App 10 206 12.4 1.2 15 1 US-08-44-133 Sequence 245. App 10 206 12.4 1.2 15 1 US-08-44-133 Sequence 245. App 10 206 12.4 1.2 15 1 US-08-44-133 Sequence 245. App 10 206 12.4 1.2 15 1 US-08-44-133 Sequence 245. App 10 206 12.4 1.2 15 1 US-08-44-133 Sequence 245. App 10 206 12.4 1.2 15 1 US-08-44-133 Sequence 245. App 10 206 12.4 1.2 15 1 US-08-44-133 Sequence 245. App 10 206 12.4 1.2 15 1 US-08-44-133 Sequence 245. App 10 206 12.4 1.2 15 1 US-08-44-133 Sequence 245. App 10 206 12.4 1.2 12 1 US-08-44-133 Sequence 245. App 10 206 12.4 1.2 12 1 US-08-44-133 Sequence 245. App 10 206 12.4 1.2 12 1 US-08-44-133 Sequence 245. App 10 206 12.4 1.2 12 1 US-08-44-13 Sequence 245. App 10 206 12.4 1.2 12 1 US-08-44-13 Sequence 245. App 10 206 | 1857, Ap. 186 12.8 1.2 17 1 US-08-375-G8-1058 1869, Ap. 187 12.8 1.2 17 1 US-08-375-G8-1058 187 12.8 1.2 14 1 US-08-155-G8-1058 1857, Ap. 189 12.4 1.2 14 1 US-08-155-G8-1058 1859, Ap. 190 12.4 1.2 14 1 US-08-151-477A-57 187 12.4 1.2 14 1 US-08-151-477A-57 187 12.4 1.2 14 1 US-08-151-477A-57 187 12.4 1.2 14 1 US-08-198-67-78 1874, App. 193 12.4 1.2 14 1 US-08-398-099-351 1889, Ap. 194 12.4 1.2 14 1 US-08-398-68-98 1989, Ap. 199 12.4 1.2 15 1 US-08-398-491 1989, Ap. 199 12.4 1.2 15 1 US-08-398-491 1989, Ap. 199 12.4 1.2 15 1 US-08-398-491 1989, Ap. 199 12.4 1.2 15 1 US-08-398-898-998-998-998-998-998-998-998-99                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 1857, Ap. 186 12.8 1.2 17 1 US-08-375-G8-1058 Sequence 1861, Ap. 188 12.8 1.2 17 1 US-08-375-G8-1058 Sequence 1862, Ap. 188 12.4 1.2 14 1 US-08-155-G8-1058 Sequence 1855, Ap. 189 12.4 1.2 14 1 US-08-160-160-95-25-5 Sequence 1857, Ap. 199 12.4 1.2 14 1 US-08-161-477A-57 Sequence 1851, Ap. 199 12.4 1.2 14 1 US-08-191-67-78 Sequence 1851, Ap. 199 12.4 1.2 14 1 US-08-191-67-78 Sequence 1851, Ap. 199 12.4 1.2 14 1 US-08-191-67-78 Sequence 1854, Ap. 199 12.4 1.2 14 1 US-08-319-428-47 Sequence 1854, Ap. 199 12.4 1.2 15 1 US-08-319-428-47 Sequence 1858, Ap. 199 12.4 1.2 15 1 US-08-319-428-47 Sequence 1858, Ap. 199 12.4 1.2 15 1 US-08-319-428-49 Sequence 1858, Ap. 199 12.4 1.2 15 1 US-08-319-428-49 Sequence 132, Ap. 199 12.4 1.2 15 1 US-08-31-431 Sequence 132, Ap. 199 12.4 1.2 15 1 US-08-31-07-164 Sequence 132, Ap. 199 12.4 1.2 15 1 US-08-31-07-164 Sequence 132, Ap. 199 12.4 1.2 15 1 US-08-31-07-164 Sequence 132, Ap. 199 12.4 1.2 15 1 US-08-31-07-164 Sequence 132, Ap. 199 12.4 1.2 15 1 US-08-31-07-164 Sequence 132, Ap. 199 12.4 1.2 15 1 US-08-31-07-164 Sequence 12.4 1.2 15 1 US-08-31-07-164 Sequence 12.4 1.2 15 1 US-08-31-07-164 Sequence 12.4 1.2 15 1 US-08-31-31 Sequence 12.4 1.2 15 1 US-08-32-177-18 Sequence 12.4 1.2 15 1 US-08-32-177-18 Sequence 12.4 1.2 15 1 US-09-31-31-31 Sequence 12.4 1.2 15 1 US-09-31-31-31 Sequence 12.4 Ap. 199 12.4 1.2 1 US-09-31-31-31 Sequence 12.4 Ap. 199 12.4 1.2 1 US-09-31-31-31-31 Sequence 12.4 Ap. 199 12.4 1.2 1 US-09-31-31-31-31 Sequence 12.4 Ap. 199 12.4 1.2 1 US-09-31-31-31-31-31-31-31-31-31-31-31-31-31- | 1857, Ap. 186 12.8 1.2 17 1 US-08-373-678-1058 Sequence 1861, Ap. 187 12.8 1.2 17 1 US-08-373-678-1058 Sequence 1865, Ap. 188 12.4 1.2 14 1 US-08-155-678-1058 Sequence 1859, Ap. 199 12.4 1.2 14 1 US-08-151-477A-55 Sequence 1859, Ap. 199 12.4 1.2 14 1 US-08-161-477A-55 Sequence 1859, Ap. 199 12.4 1.2 14 1 US-08-398-099-351 Sequence 1854, Ap. 199 12.4 1.2 14 1 US-08-398-099-351 Sequence 1968, Ap. 199 12.4 1.2 15 1 US-08-319-4928-477 Sequence 1968, Ap. 199 12.4 1.2 15 1 US-08-319-4928-477 Sequence 1968, Ap. 199 12.4 1.2 15 1 US-08-319-4928-491 Sequence 1968, Ap. 199 12.4 1.2 15 1 US-08-319-4928-491 Sequence 132, Appli 201 201 12.4 1.2 15 1 US-08-319-4928-491 Sequence 132, Appli 201 201 12.4 1.2 15 1 US-08-319-4928-491 Sequence 132, Appli 201 12.4 1.2 15 1 US-08-31-31 Sequence 132, Appli 201 12.4 1.2 15 1 US-08-31-31 Sequence 132, Appli 201 12.4 1.2 15 1 US-08-31-31 Sequence 134, Appli 201 12.4 1.2 15 1 US-08-31-31 Sequence 134, Appli 201 12.4 1.2 15 1 US-08-31-31 Sequence 134, Appli 201 12.4 1.2 15 1 US-08-32-1-31 Sequence 134, Appli 201 12.4 1.2 15 1 US-08-32-1-31 Sequence 134, Appli 201 12.1 1.2 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 | App 186 12.8 1.2 17 1 US-08-375-0518-57 Sequence 1.2 17 1 US-08-153-0518-57 Sequence 1.2 18 12.4 12.2 17 1 US-08-153-0518-57 Sequence 1.2 18 12.4 12.2 14 1 US-08-153-0518-57 Sequence 1.2 12.4 12.2 14 1 US-08-169-051.5 Sequence 1.2 12.4 12.2 14 1 US-08-99-91-51 Sequence 1.2 12.4 12.2 14 1 US-08-98-91-91 Sequence 1.2 12.4 12.2 14 1 US-08-98-91-91 Sequence 1.2 12.4 12.2 15 1 US-08-91-91-91-91 Sequence 1.2 12.4 12.2 15 1 US-08-91-91-91 Sequence 1.2 12.4 12.2 15 1 US-08-91-91-91 Sequence 1.2 12.4 12.2 15 1 US-08-91-91-91 Sequence 1.2 12.4 12.2 15 1 US-08-91-91 Sequence 1.2 12.4 12.2 12 1 US-08-91-91 Sequence 1.2 12 12 12 1 US-08-91-91 Sequence 1.2 12 12 12 12 12 12 12 12 12 13 Sequence 1.2 12 12 12 12 12 12 13 Sequence 1.2 12 12 12 12 12 12 13 Sequence 1.2 Sequence 1.2 12 12 12 12 12 13 Sequence 1.2 Sequence 1.2 12 12 12 12 12 13 Sequence 1.2 Sequence 1.2 12 12 12 12 13 Sequence 1.2 Sequence 1.2 12 12 12 12 13 Sequence 1.2 Sequence 1.2 12 12 12 12 12 13 Sequence 1.2 Sequence 1.2 12 12 12 12 12 12 12 13 Sequence 1.2 Sequence 1.2 12 12 12 12 12 12 12 12 Sequence 1.2 Sequence 1.2 12 12 12 12 12 Sequence 1.2 Sequence 1.2 Sequence 1.2 12 12 12 12 Sequence 1.2 Sequence | Ap 186 12.8 1.2 17 1 05-08-35-528-1058 Sequence 188 12.4 1.2 17 1 05-08-35-528-1058 Sequence 188 12.4 1.2 17 1 05-08-35-528-558 Sequence 189 12.4 1.2 14 1 05-08-35-5518-57 Sequence 199 12.4 1.2 14 1 05-08-38-628-1058 Sequence 199 12.4 1.2 14 1 05-08-38-98-09-351 Sequence 193 12.4 1.2 14 1 05-08-38-09-351 Sequence 193 12.4 1.2 1.2 14 1 05-08-38-09-351 Sequence 194 12.4 1.2 1.2 14 1 05-08-38-09-351 Sequence 195 12.4 1.2 1.2 14 1 05-08-38-474 Sequence 196 12.4 1.2 1.2 15 1 05-08-34-4928-474 Sequence 197 12.4 1.2 1.2 15 1 05-08-34-4928-474 Sequence 198 12.4 1.2 1.2 15 1 05-08-34-4928-474 Sequence 198 12.4 1.2 1.2 15 1 05-08-34-31 Sequence 198 12.4 1.2 1.2 15 1 05-08-34-31 Sequence 198 12.4 1.2 1.2 1.2 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 | Ap 186 12.8 1.2 17 1 US-08-455-628-1058 Sequence 188 12.4 1.2 17 1 US-08-455-628-1058 Sequence 188 12.4 1.2 17 1 US-08-455-628-1058 Sequence 189 12.4 1.2 14 1 US-08-455-628-1058 Sequence 190 12.4 1.2 14 1 US-08-98-095-51 Sequence 191 12.4 1.2 14 1 US-08-98-095-51 Sequence 192 12.4 1.2 14 1 US-08-98-095-51 Sequence 193 12.4 1.2 14 1 US-08-98-095-51 Sequence 194 12.4 1.2 14 1 US-08-98-095-51 Sequence 195 12.4 1.2 14 1 US-08-444-4118-56 Sequence 196 12.4 1.2 15 1 US-08-344-447-335 Sequence 196 12.4 1.2 15 1 US-08-344-447-335 Sequence 196 12.4 1.2 15 1 US-08-344-447-335 Sequence 199 12.4 1.2 15 1 US-08-32-60A-331 Sequence 199 12.4 1.2 15 1 US-08-32-1.4 43.4 3.3 Sequence 199 12.4 1.2 1.2 1.3 US-08-21-4348-2.1 Sequence 199 12.4 1.2 1.3 US-08-21-332 Sequence 199 12.4 1.3 US-08-31-4 43.4 3.3 Sequence 199 12.4 1.3 US-08-31-32-33 Sequence 199 12.4 1.3 US-08-31-33-33 Sequence 199 12.4 1.3 US-08-31-33- | App 186 12.8 1.2 17 1 US-08-1515.0518-57 Sequence 189 12.4 1.2 17 1 US-08-1515.0518-57 Sequence 189 12.4 1.2 14 1 US-08-151-57 Sequence 199 12.4 1.2 14 1 US-08-151-57 Sequence 199 12.4 1.2 14 1 US-08-151-57 Sequence 192 12.4 1.2 14 1 US-08-151-55 Sequence 192 12.4 1.2 14 1 US-08-151-55 Sequence 193 12.4 1.2 1.2 14 1 US-08-151-55 Sequence 193 12.4 1.2 1.2 14 1 US-08-151-55 Sequence 193 12.4 1.2 1.2 14 1 US-08-151-78 Sequence 195 12.4 1.2 1.2 14 1 US-08-151-78 Sequence 195 12.4 1.2 1.2 14 1 US-08-151-78 Sequence 195 12.4 1.2 1.2 15 1 US-08-151-78 Sequence 195 12.4 1.2 1.2 15 1 US-08-151-73 Sequence 195 12.4 1.2 1.2 15 1 US-08-151-74 Sequence 195 12.4 1.2 1.2 1.2 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 | App 187 12.8 1.2 17 1 US-08-455-658-1058 Sequence 188 12.4 1.2 17 1 US-08-455-658-1058 Sequence 189 12.4 1.2 14 1 US-08-455-658-1058 Sequence 199 12.4 1.2 14 1 US-08-455-658-1058 Sequence 199 12.4 1.2 14 1 US-08-459-659-1059 Sequence 199 12.4 1.2 14 1 US-08-498-1059-155 Sequence 199 12.4 1.2 14 1 US-08-498-1059-155 Sequence 199 12.4 1.2 12 14 1 US-08-105-155-78 Sequence 199 12.4 1.2 12 14 1 US-08-105-458-78 Sequence 199 12.4 1.2 12 14 1 US-08-105-458-78 Sequence 199 12.4 1.2 15 1 US-08-105-458-79 Sequence 199 12.4 1.2 15 1 US-08-105-458-49 Sequence 199 12.4 1.2 15 1 US-08-105-44-11 Sequence 199 12.4 1.2 15 1 US-08-105-44-11 Sequence 199 12.4 1.2 15 1 US-08-105-105-105 Sequence 199 12.4 1.1 15 1 US-08-105-105-105 Sequence 199 12.4 1.1 15 1 US-08-105-105-105-105-105-105-105-105-105-105 | App 186 12.8 1.2 17 1 US-08-435-628-158 Sequence App 187 12.4 1.2 17 1 US-08-435-628-158 Sequence App 188 12.4 1.2 14 1 US-08-435-628-159 Sequence App 188 12.4 1.2 14 1 US-08-98-099-35 Sequence App 189 12.4 1.2 1.2 14 1 US-08-98-099-35 Sequence App 189 12.4 1.2 15 1 US-08-319-4228-49 Sequence App 189 12.4 1.2 15 1 US-08-319-4228-49 Sequence App 189 12.4 1.2 15 1 US-08-319-4228-49 Sequence App 189 12.4 1.2 15 1 US-08-226-620-33 Sequence App 189 12.4 1.2 15 1 US-08-226-620-33 Sequence App 189 12.4 1.2 1.2 1.3 1 US-08-226-620-33 Sequence App 189 12.4 1.2 1.2 1.3 1 US-08-226-433 Sequence App 189 12.4 1.2 1.2 1.3 1 US-08-226-433 Sequence App 189 12.4 1.2 1.2 1.3 1 US-08-226-433 Sequence App 189 12.4 1.3 1 US-08-34-34-34 Sequence App 189 12.4 1.3 1 US-08-34-34 Sequence App 189 12.4 1.3 1 US-08-34-34-34 Sequence App 189 12.4 1.3 1 US-08-34-34-34 Sequence App 189 12.4 1.3 1 US-08-34-34 Sequence App 189 12.4 1.3 1 US-08-34-34 Sequence App 189 189 189 189 189 189 189 189 189 189 | Ap   186   12.8   1.2   17   103-08-435-628-1039   99quence   74   103-08-436-103-35   99q | App 186 12.8 1.2 17 1 02-08-435-628-1058 Sequence App 186 12.4 1.2 17 1 02-08-435-628-1058 Sequence App 186 12.4 1.2 17 1 02-08-435-628-1058 Sequence App 189 12.4 1.2 14 1 05-08-98-095-952-55 Sequence App 193 12.4 1.2 14 1 05-08-98-095-952-56 Sequence App 193 12.4 1.2 14 1 05-08-98-096-952-56 Sequence App 195 12.4 1.2 14 1 05-08-316-4628-491 Sequence App 195 12.4 1.2 14 1 05-08-316-4628-491 Sequence App 195 12.4 1.2 14 1 05-08-316-4628-491 Sequence App 196 12.4 1.2 15 1 05-08-316-4628-491 Sequence App 196 12.4 1.2 15 1 05-08-316-4628-491 Sequence App 196 12.4 1.2 15 1 05-08-316-4628-491 Sequence App 197 12.4 1.2 15 1 05-08-316-463-491 Sequence App 197 12.4 1.2 15 1 05-08-316-463-193 Sequence App 197 12.4 1.2 15 1 05-08-316-463-13 Sequence App 197 12.4 1.2 15 1 05-08-316-313 Sequence App 197 12.4 1.2 15 1 05-08-316-313 Sequence App 197 12.4 1.2 15 1 05-08-316-313 Sequence App 197 12.4 1.2 15 1 05-08-313-13 Sequence App 197 12 1.1 12 1 05-08-313-13 Sequence App 197 12 12 1.1 12 1 05-08-31-31 Sequence App 197 12 12 1.1 12 1 05-08-31-31 Sequence App 197 12 1 05-08-31-31 Sequenc | Ap                                                                               | Ap                                                                             | Ap   186   12.8   1.2   17   105.00-173.247.109. Sequence   Ap   187   12.8   1.2   17   105.00-173.247.109. Sequence   Ap   188   12.4   1.2   14   105.00-173.247.87 Sequence   Ap   189   12.4   1.2   14   105.00-173.247.87 Sequence   Ap   189   12.4   1.2   14   105.00-173.247.87 Sequence   Ap   189   12.4   1.2   14   106.00-173.247.87 Sequence   Ap   189   12.4   1.2   14   106.00-173.247.87 Sequence   Ap   189   12.4   1.2   14   106.00-173.247.87 Sequence   Ap   189   12.4   1.2   1.2   14   106.00-173.247.87 Sequence   Ap   189   12.4   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1. | Ap 186 12.4 1.2 17 105.00-175.68-105 69-105 69-105 74 Ap 187 12.4 1.2 17 105.00-175.68-105 69-105 69-105 74 Ap 188 12.4 1.2 14 105.00-175.68-105 69-105 74 Ap 189 12.4 1.2 14 105.00-175.68-105 69-105 75 12.4 1.2 14 105.00-175.68-105 75 89-101 75 12.4 1.2 14 105.00-175.69-105 75 89-101 75 12.4 1.2 14 105.00-175.69-105 75 89-101 75 12.4 1.2 14 105.00-175.40 12.4 1.2 1.2 1.4 105.00-175.40 12.4 1.2 1.2 1.4 105.00-175.40 12.4 1.2 1.2 1.4 105.00-175.40 12.4 1.2 1.2 1.4 105.00-175.40 12.4 1.2 1.2 1.4 105.00-175.40 12.4 1.2 1.2 1.4 1.2 1.2 1.4 1.2 1.2 1.4 1.2 1.2 1.4 1.2 1.2 1.4 1.2 1.2 1.4 1.2 1.2 1.4 1.2 1.2 1.4 1.2 1.2 1.4 1.2 1.2 1.4 1.2 1.4 1.2 1.2 1.4 1.2 1.2 1.4 1.2 1.2 1.4 1.2 1.2 1.4 1.2 1.2 1.4 1.2 1.2 1.4 1.2 1.2 1.4 1.2 1.2 1.4 1.2 1.2 1.4 1.2 1.2 1.4 1.2 1.4 1.2 1.2 1.4 1.2 1.2 1.4 1.2 1.2 1.4 1.2 1.2 1.4 1.2 1.2 1.4 1.2 1.2 1.4 1.2 1.2 1.4 1.2 1.2 1.4 1.2 1.2 1.4 1.2 1.2 1.4 1.2 1.3 1.4 1.2 1.3 1.4 1.2 1.3 1.4 1.2 1.3 1.4 1.2 1.3 1.4 1.2 1.3 1.4 1.2 1.3 1.4 1.2 1.3 1.4 1.2 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1.4 1.3 1 | Ap         186         12.4         1.2         1.7         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0         1.0 <td>Ap         186         12.8         1.2         1.7         18.0         12.4         1.2         1.7         18.0         12.4         1.2         1.7         18.0         12.4         1.2         1.7         18.0         12.4         1.2         1.7         18.0         12.4         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2</td> <td>  App   186   12   17   18   18   18   18   18   18   18</td> <td>Ap   186   12.8   1.2   17   10   10   10   12.5   1.2   17   10   10   10   12.5   1.2   17   10   10   12.5   1.2   17   10   10   12.5   1.2   17   10   10   12.5   1.2   17   10   10   12.5   1.2   17   10   10   12.5   1.2   17   10   10   12.5   1.2   17   10   10   12.5   1.2   17   10   10   12.5   1.2   17   17   1.2   17   17   1.2   17   17   1.2   17   17   1.2   17   17   1.2   17   1.2   17   1.2   17   1.2   17   1.2   17   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1</td> <td>  156, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7,</td> <td>  1867, Ap   187, Ap   187</td> | Ap         186         12.8         1.2         1.7         18.0         12.4         1.2         1.7         18.0         12.4         1.2         1.7         18.0         12.4         1.2         1.7         18.0         12.4         1.2         1.7         18.0         12.4         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2         1.2 | App   186   12   17   18   18   18   18   18   18   18                           | Ap   186   12.8   1.2   17   10   10   10   12.5   1.2   17   10   10   10   12.5   1.2   17   10   10   12.5   1.2   17   10   10   12.5   1.2   17   10   10   12.5   1.2   17   10   10   12.5   1.2   17   10   10   12.5   1.2   17   10   10   12.5   1.2   17   10   10   12.5   1.2   17   10   10   12.5   1.2   17   17   1.2   17   17   1.2   17   17   1.2   17   17   1.2   17   17   1.2   17   1.2   17   1.2   17   1.2   17   1.2   17   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1 | 156, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7,                          | 1867, Ap   187, Ap   187 |

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RESULT 3
US-09-225-201B-400/c
; Sequence 400, Application US/09225201B
; Sequence 400, Application US/09225201B
; Patent No. 64884710N:
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Chenchik, Alex
; APPLICANT: Chenchik, Alex
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
EXPRESSION
 Query Match 3.1%; Score 32; DB 1; Length 32; Best Local Similarity 100.0%; Pred. No. 1.8; Matches 32; Conservative 0; Mismatches 0; Indels
) SEQUENCE DESCRIPTION: Oligonucleotide primer ; SEQUENCE DESCRIPTION: SEQ ID NO: 400: US-09-225-928-400
 ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYBE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows55
SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA.

APPLICATION NUMBER: US/09/225,928
FILING DATE: 05-Jan-1999
CLASSIFICATION: vUnknown.

PRIOR APPLICATION DATA.

APPLICATION NUMBER: 08/89,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:

NAMM: Field, Bret E.

REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 37,620
 NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson, P.C.
STRET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
 NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
CORRESPONDENCE FISH & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
 1732 CTTGTGGCAAGTGAATTTGCCTGTAACAAGCC 1763
 32 cricicecaagicaariricecicraacaagee
EXPRESSION
 TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
 TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 400:
SEQUENCE CHARACTERISTICS:
 TYPE: nucleic acid
STRANDEDNESS: single
 CITY: Menlo Park
STATE: CA
 MOLECULE TYPE: DNA
 COUNTRY: US
 COUNTRY:
 셤
 à
 ö
 Sequence 296, App
Sequence 13, Appl
 3.1%; Score 32; DB 1; Length 32;
100.0%; Pred. No. 1.8;
iive 0; Mismatches 0; Indels
 | Sequence 400, Application US/0885998
| Patent No. 5994076
| GENERAL INFORMATION:
| APPLICANT: Chenchik, Alex
| APPLICANT: Bibilashvilli, Robert
| TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
| TITLE OF INVENTION: EXPRESSION
| NUMBER OF SEQUENCES: 1375
| CORRESPONDENCE ADDRESS:
| ADDRESSE: Fish & Richardson, P.C.
| STREET: 2200 Sand Hill Road, Suite 100
| STATE: CANNERS | CONTRACT | CO
 APPLICANT: Chenchik, Alex
Jokhadze, George
Bibliashvilli, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
 COMPUTER: US
ZIP: 94025
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows55
SOFTWARE: FastGEG for Windows55
SOFTWARE: Papel.CATION DATA:
APPLICATION NUMBER: US/08/859,998
FLING DATE: 21-MAY-1997
CLASSITECATION: 435
FILING DATE: APPLICATION: A35
FILING DATE: APPLICATION: A37
FILING DATE: APPLICATION: A37
FILING DATE: APPLICATION: A37
FILING DATE: APPLICATION: NUMBER: Sield, Bret E.
NAME: Field, Bret E.
NAME: Field, Bret E.
NAME: Field, Bret E.
TELEROMUNICATION INFORMATION:
TELEPRAY: 415-322-5070
TELEPRAY: A15-322-5070
 1732 CITGIGGCAAGIGAATITGCCTGTAACAAGCC 1763
 US-09-475-947A-296
US-09-375-673B-13
) OTHER INFORMATION: oligonucleotide primer US-08-859-998-400
 US-09-225-928-400/c
; Sequence 400, Application US/09225928
Patent No. 6352829
; GENERAL INFORMATION:
 Best Local Similarity 100.
Matches 32; Conservative
 LENGTH: 32 base pairs
 TYPE: nucleic acid
STRANDEDNESS: single
 14
 linea
 MOLECULE TYPE:
PEATURE:
 -08-859-998-400/c
 11.4
 Query Match
 ò
 셤
```

Gaps

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APPLICANT: SIGNAL Brian
APPLICANT: ALLEN; Margaret
APPLICANT: ALLEN; Margaret
APPLICANT: ALLEN; Margaret
APPLICANT: SYRRDRUP, Fran
APPLICANT: CARMICHARL, David
APPLICANT: CARMICHARL, David
TITLE OF INVENTION: COMPACTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS OF USE
FILE REFERENCE: FIRMOLIO0-1
CURRENT FILING DATE: 1999-04-14
PRIOR FILING DATE: 1999-04-14
PRIOR FILING DATE: 1999-04-14
PRIOR FILING DATE: 1999-104-14
PRIOR FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Version 3.0
LENGTH: 25
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 DB 1; Length 25;
 Indels
 VERSION 1.25
 ; OTHER INFORMATION: Antisense CTGF oligonucleotide US-09-292-036-10
 APPLICANT: WORGANTE, MICHELE
APPLICANT: VOGEL, JULIE M.
TITLE OF INVENTION: COMPOUND MICROSATELLITE
TITLE OF INVENTION: PRIMERS FOR THE
TITLE OF INVENTION: DETECTION OF GENETIC
TITLE OF INVENTION: POLYMORFHISMS
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND
 Query Match 2.2%; Score 23.4; D
Best Local Similarity 96.0%; Pred. No. 14;
Matches 24; Conservative 0; Mismatches
 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION 0478.
APPLICATION NUMBER: 08/346,456
FILING DATE: 28 NOVEMBER 1994
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
 AUDKESSE:
COUTY: WILMINGTON
STATE: DELAWARE
COUTY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT IN RELEASE #1.0, VER
CURRENT APPLICATION NUMBER: US/08/849,021
 1742 GIGAATITGCCIGTAACAAGCCAGA 1766
 Sequence 87, Application US/08849021
Patent No. 5955276
GENERAL INFORMATION:
Application US/09292036
 TYPE: DNA ORGANISM: Artificial sequence
 08-849-021-87/c
 ADDRESSEE:
 δ
 g
 APPLICANT: SCENIA, MARGAREL
APPLICANT: SURBRUP, Fran
APPLICANT: SVERDRUP, Fran
APPLICANT: CARMICHAEL, David
TITLE ON TIVENTHON: CONNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS OF USE
FILE REFERENCE: FIBROLIOG-1
FURENT APPLICATION NUMBER: US 09/22,036
FRICR FILING DATE: 1999-04-14
PRIOR FILING DATE: 1999-04-14
PRIOR FILING DATE: 1999-04-14
PRIOR FILING DATE: 1999-04-14
PRIOR FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
SEQ ID NO 9
LENGTH: 25
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 Gaps
 Query Match 3.1%; Score 32; DB 1; Length 32; Best Local Similarity 100.0%; Pred. No. 1.8; Matches 32; Conservative 0; Mismatches 0; Indels
 Query Match
2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 25; Conservative 0; Mismatches 0; Indels
) SEQUENCE DESCRIPTION: Oligonucleotide primer ; SEQUENCE DESCRIPTION: SEQ ID NO: 400: US-09-225-201B-400
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:

NAME: Field, Bret E.

REGISTRATION NUMBER: 37,620
REPERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-32-5070
TELEPHONE: 415-34-0875
INFORMATION POR SEQ ID NO: 400:
SEQUENCE CHARACTERISTICS:
 ; OTHER INFORMATION: Antisense CTGF oligonucleotide
US-09-292-036-9
 1732 CTTGTGGCAAGTGAATTTGCCTGTAACAAGCC 1763
 APPLICATION NUMBER: US/09/225,201B
FILING DATE: 05-Jan-1999
CLASSIFICATION: <UNKNOWN>
 1718 ATTAGACTGGACAGCTTGTGGCAAG 1742
 Sequence 9, Application US/09292036 Patent No. 6358741 GENERAL INFORMATION:
APPLICANT: FIBROGEN, INC.
APPLICANT: SCHMIDT, Brian
 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
 TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
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US-09-292-036-9/c

RESULT 5 US-09-292-036-10/c

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 S-08-22-177A-143/c
S-08-22-177A-143/c
Sequence 143, Application US/08222177A
Sequence 143, Application US/08222177A
Sequence 143, Application US/08222177A
SENERAL INFORMATION:
APPLICANT: Weber, James L.
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: LCC-dA)n.(dd-dT)n SEQUENCES AND METHODS OF USING SAME NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
ADDRESSEE: DeWilt Rose & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
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 Query Match 2.1%; Score 22.2; DB 1; Length 27; Best Local Similarity 88.9%; Pred. No. 22; Matches 24; Conservative 0; Mismatches 3; Indels
 Query Match 2.2%; Score 23; DB 1; Length 24; Best Local Similarity 100.0%; Pred. No. 15; Matches 23; Conservative 0; Mismatches 0; Indels
 SIGNE: WISCOMENTE, WISCOMENTE, WISCOMENTE, WISCOMENTER, WISCOMENTER, READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN PATCHIN NOWBER: US/08/222,177A
FILING APPLICATION NUMBER: US/03/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: SITA CHARLES 30,492
REGISTRATION NUMBER: 30,492
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 30,492
TELECOMMUNICATION INFORMATION:
TELEFRAX: (608) 831-2106
 1805 TGTGTGTATATATATATAT 1827
 24 rerererarararararar 2
 INFORMATION FOR SEQ ID NO: 87: SEQUENCE CHARACTERISTICS: LENGTH: 24 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear NOLECULE TYPE: DNA (genomic) US-08-849-021-87
 DNA (genomic)
 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
302-992-7949
 TYPE: nucleic acid
STRANDEDNESS: double
 linear
 SIKELI.
CITY: Madison
STATE: Wisconsin
 IMMEDIATE SOURCE:
CLONE: mfd31rs
 US-08-222-177A-143
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105-01-454-021-86/C
PREMENT NO. 5952701
PREPARATOR
PREP
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Gaps
 Gaps
 Branched and Multiply
 ö
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 GENERAL INFORMATION:
APPLICANT: Sergei M. Gryaznov
APPLICANT: Sergei M. Gryaznov
TITLE OF INVENTION: Convergent Synthesis of Branched and Mu
TITLE OF INVENTION: Connected Macromolecular Structures
NUMBER OF SEQUENCES: 26
CORRESPONDENCES:
ADDRESSEE: Cooley Godward LLP
STREET: Five Palo Alto Square, 3000 El Camino Real
CITY: Palo Alto Alto Square, 3000 El Camino Real
STATE: California
CONTRY: DAS ALTOS ALTO
 Length 27;
 Indels
 Indels
 2.1%; Score 21.8; DB 1; 92.0%; Pred. No. 25;
 DB 1;
 APPLICATION:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/455,627
APPLICATION NUMBER: US/08/455,627
ATORNEY/AGENT INFORMATION:
NAME: NARAMUTA, Jackie
REFERENCE/DOCKET NUMBER: 15,966
REFERENCE/DOCKET NUMBER: LYNX-003/01 US
TELECOMMUNICATION INFORMATION:
TELEPANS: 415-43-5000
TELEPANS: 415-827-0663
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 nucleotides
TUMBER: Nucleotides
TELEPANS: ALT-857-0663
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 nucleotides
 Query Match 2.1%; Score 21.8; DB Best Local Similarity 92.0%; Pred. No. 25; Matches 23; Conservative , 0; Mismatches
 0; Mismatches
 1793 TGTGTGTGTGTGTGTGTATAT 1817
 1793 TGTGTGTGTGTGTGTGTATAT 1817
 rerererererererererererer 2
 26 rererererererererererer
 Sequence 23, Application US/08689856
Patent No. 5830658
TELEFAX: 415-857-0663
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 27 nuclectides
TYPE: nucleic acid
STRANDEDNESS: single
 Query Match
Best Local Similarity 92.0
Matches 23; Conservative
 TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-455-627-23
 TOPOLOGY: linear MOLECULE TYPE: DNA
 RESULT 11
US-08-689-856-23/c
 RESULT
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 Gaps
 Sequence 23, Application US/08455627

Sequence 23, Application US/08455627

Sequence 23, Application US/08455627

GENERAL INFORMATION:

TITLE OF INVENTION: Convergent Synthesis of Branched and Mul
TITLE OF INVENTION: Convergent Synthesis of Branched and Mul
TITLE OF INVENTION: Convergent Synthesis of Branched and Mul
TITLE OF INVENTION: Connected Macromolecular Structures
NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward LiP
STREET: Five Palo Alto Square, 3000 El Camino Real
CITY: Palo Alto
STREET: Callifornia
COUNTRY: USA
ZIP: 94306-2155
COMPUTER: LIM PC Compatible
COMPUTER: LIM PC COMPAT:
STILING DATE: 31-MAX-1995
CURRENT APPLICATION NUMBER: US/08/455,627
STILING DATE: 31-MAX-1995
CURASIENCEATION: 435
CURASIENCEATION: 435
 DB 1; Length 25;
 Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
 ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Jackie N.
REGISTRATION NUMBER: 35,966
REFERENCE/DOCKET NUMBER: LYNX-003/01 US
TELECOMATUNICATION INFORMATION:
 Pred. No. 22;
0; Mismatches
 Query Match 2.1%; Score 21.8;
Best Local Similarity 92.0%; Pred. No. 25
Matches 23; Conservative 0; Mismatche
 CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 007/341,562
FILING DATE: 21-APR-1989
ATORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECHONE: (608) 831-2100
TELECHONE: (608) 831-2100
 1793 TGTGTGTGTGTGTGTGTGTATAT 1817
 25 rererererererererererer
 146:
 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
INMEDIATE SOURCE:
CLONE: mfd32rs
US-08-222-177A-146
 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
 .08-455-627-23/c
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DNA (genomic)
 Query Match 2.0%;
Best Local Similarity 95.7%;
Matches 22; Conservative
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
 24 base pairs
 LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
; MOLECULE TYPE:
US-08-222-177A-454
 RESULT 14
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 d
 Sequence 454, Application US/08222177A

Patent No. 5582979

GENERAL INFORMATION:
APPLICANT: Weber:, James L.
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460

CORRESPONDENCE ADDRESS: Aboresses: Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401

CITY: Madison
STATE: Wisconsin
COUNTRY: USA
 ö
 Gaps
 Length 27;
 2; Indels
 TYPE: DNA
CRGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Description of Artificial Sequence:
COTHER INFORMATION: oligonucleotide
US-08-787-321-23
 CORFUGATE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/22,177A
FILING DATE:
CLASSIPICATION: A35.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21.APR.1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles 5.
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
 Query Match
2.1%; Score 21.8; DB 1;
Best Local Similarity 92.0%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 2;
 1793 TGTGTGTGTGTGTGTGTATAT 1817
 26 rererererererererererer 2
 COUNTRIT USA

ZIP: 53717-1914

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 (608) 831-2100
 SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDENNES: double
TOPOLOGY: linear
 (608) 831-2106
 INFORMATION FOR SEQ ID NO:
 RESULT 13
JS-08-222-177A-454/c
 셤
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US-011-177A-445/c

Sequence 445, Application US/08222177A

Sequence 445, Application US/08222177A

Patent No. 5582979

JENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION:

TITLE OF INVENTION:

CORRESPONDENCE ADD

CORRESPONDENCE ADD

CORRESPONDENCE ADD

CORRESPONDENCE ADD

STREET: 8000 Excelsior Drive, Suite 401
 ö
 Gaps
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 DB 1; Length 24;
DB 1, Length 23;
 Indels
 1; Indels
 COMPARESTONDENCE ADDRESSES:
CONTEXT: Maddison.
STREET: 8000 Excelsior Drive, Suite 401
CITY: Maddison.
STATE: Wisconsin
COUNTRY: USA
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDLIUM TYPES: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PREFIT PC-DOS/MS-DOS
SOFTWARE: PREFIT PC-DOS/MS-DOS
SOFTWARE: PREFIT NG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PSETING SYSTEM: US/08/222,177A
PPLICATION NUMBER: US/08/222,177A
FLING DATE:
FLING DATE: 1-APR-1989
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 07/341,562
ATTORNEY/AGENT INFORMATION:
NAME: SATE. CHALLES S.
TELESPAXTION NUMBER: 30,492
REFERENCE/OPOCKET NUMBER: 09865.601
TELESPAXTING NUMBER: 1000
TELESPAXTING NUMBER: 1000
TELESPAXTING NUMBER: 1000
 RESULT 15

727-0892-10792-44

9 Sequence 44, Application PC/TUS9210792

1 GENERAL INFORMATION:
1 APPLICANT: Jayasena, Sumedha D.
2 APPLICANT: Johnston, Brian H.
3 PAPLICANT: Johnston, Brian H.
3 TITLE OF INVENTION: Triple Helix Formation at
 Query Match 2.0%; Score 21.4; Dest Local Similarity 95.7%; Pred. No. 23; Matches 22; Conservative 0; Mismatches
 Score 21.4; D
Pred. No. 22;
0; Mismatches
 1793 TGTGTGTGTGTGTGTGTAT 1815
 1793 TGTGTGTGTGTGTGTGTGTAT 1815
 24 refererererererererer
 ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-222-177A-445
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Sequence 125, Application US/08222177A
Sequence 125, Application US/08222177A
Batent No. 5582979
GENERAL INFORMATION:
APPLICANT: Weber:, James L.
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
ADDRESSEE: DeWitt Ross & Stevens, S.C.
STREET: 8000 Excelsion Drive, Suite 401
CITY: Madison
STREET: ANGEORGIA
 ö
 Length 21;
 0; Indels
 CURRENTING SISTEM: FC-LUCY, WG-EDON #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/22,177A
FILING DATE:
CLASSIFICATION 435
FILOR APPLICATION DATE:
APPLICATION NUMBER: US 07/341,562
FILOR APPLICATION DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REGISTRATION NUMBER: 30,492
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFERX: (608) 831-2106
 DB 1;
 Query Match 2.0%; Score 21; DB Best Local Similarity 100.0%; Pred. No. 21; Matches 21; Conservative 0; Mismatches
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles 30,492
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECHONE: (608) 831-2100
TELECHONE: (608) 831-2100
 US/08/222,177A
 COUNTRY: USA
ZIP: 53717-1914
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PR PC COMPATIBLE
COMPUTER: PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
 1793 TGTGTGTGTGTGTGTGT 1813
 INFORMATION FOR SEQ ID NO: 160:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: mucleic acid
STRANDEDNESS: double
TOPOLOCY: linear
NOLECULE TYPE: DNA (genomic)
INMEDIATE SOURCE:
CLONE: mfd37rs
 TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION DATA:
 APPLICATION NUMBER: FILING DATE:
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 Sequence 160, Application US/08222177A

Sequence 160, Application US/08222177A

Patent No. 5582979

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Weber, James L.

TITLE OF INVENTION: LENGTH POLYMORPHISMS IN

TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 46C

CORRESPONDENCE ADDRESS:

ADDRESSEE: DeMitt Ross & Stevens, S.C.

STREET: 8000 Excelsion Drive, Suite 401

CITY: Madison

STATE: Misconsin
 Score 21.2; DB 1; Length 26;
Pred. No. 27;
0; Mismatches 3; Indels
 COUNTRY: USAGE

ZIP: 94025

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IN PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10792
FILING DATE: 1921211
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 07/826,934
FILING DATE: 21-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/808,452
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fablan, GATY R.
RESISTANTON NUMBER: 33,875
REPERENCE/DOCKET NUMBER: 33,875
REPERENCE/DOCKET NUMBER: 93,816
RESISTANDONE: (415) 859-4550
ITELEPAX: (415) 859-4550
ITELEPAX: (415) 859-4550
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 Dase pairs
ITPE: NUCLEIC ACID
STRANDENESS: single
 INDIVIDUAL ISOLATE: FIGURE 14A, TARGET SEQUENCE #8 PCT-US92-10792-44
 (PuNPyN) - (PuNPyN) Tracts
 1787 AAATATTGTGTGTGTGTGTGTGTG 1812
 AArrcgrerererererererere 26
 STATE: Wisconsin
COUNTRY: USA
ZIP: 5317-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Painner.
 NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: SRI International
STREET: 333 Ravenswood Avenue
CITY: Menlo Park
 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
 Query Match
Best Local Similarity 88.5%;
Matches 23; Conservative
 FITLE OF INVENTION:
 US-08-222-177A-160/c
 USA
 STREET:
CITY: Me
STATE: C
 COUNTRY:
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PatentIn Release #1.0, Version #1.25

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Gaps

Page

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SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/840 ^^^
 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/346,456
FILING DATE: 28 NOVEMBER 1994
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFRENCE/DOCKET NUMBER: BB-1064-A
TELECOMMUNICATION:
TELECOMMUNICATION:
 1799 TGTGTGTGTGTGTATATA 1818
 ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) US-08-849-021-89
 TELEPHONE: (626) 796-4000
TELEFAX: (626) 795-6321
INFORMATION FOR SEQ ID NO: 32
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 TELEFAX: 302-992-7949
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
 TYPE: nucleic acid
STRANDEDNESS: sing
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 Query Match
2.0%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels
 RESULT 18
US-08-787-321-22/c
195-92-22 Application US/08787321A
196-92 Application US/08787321A
196-92 Application US/08787321A
196-92 Application US/08787321A
196-92 APPLICANT: Hornas
197-92 APPLICANT: Hornas
197-92 APPLICANT: Hornas
197-92 APPLICANTON NUMBER: US/08/767,321A
197-92 APPLICANTON NUMBER: US PROV 60/009,918
 Length 23;
 Indels
 CTHER INFORMATION: Description of Artificial Sequence:
COTHER INFORMATION: oligonuclectide
US-08-787-321-22
 GENERAL INFORMATION:
APPLICANT: MOGGANTE, MICHELE
APPLICANT: WOGGANTE, JULIE M.
TITLE OF INVENTION: COMPOUND MICROSATELLITE
TITLE OF INVENTION: PRIMERS FOR THE
TITLE OF INVENTION: PRIMERS FOR THE
TITLE OF INVENTION: POLYMORPHISMS
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: COMPANY
STREET: 1007 MARKET STREET
 Query Match
2.0%; Score 21; DB 1;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 21; Conservative 0; Mismatches
 1793 TGTGTGTGTGTGTGTGT 1813
 1793 TGTGTGTGTGTGTGTGTGT 1813
 Sequence 89, Application US/08849021
Patent No. 5955276
 22 rererererererererer 2
 21 rererererererererer
... 22 base pairs
.rPE. nucleic acid
STRANDEDNESS; double
TOPOLOCY: linear
MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: mfd2rs
US-08-222-177A-125
Bar
 ZIP: 19898
COMPUTER READABLE FORM:
COMPUTER: IBM PC COMPATIBLE
 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
 STREET: 1007 MARKE
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
 JS-08-849-021-89/c
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Query Match
1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels
```

```
Fisher, Robert
Fivesh, Matthew
Henderson, Louis E.
TITLE OF INVENTION: Oligonucleotides Which Specifically Bind
Retroviral Nucleocapsid Proteins
 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION NUMBER: US/09/180,903
FILING DATE: 12-Jul-1999
FILING DATE: 20-MAY-1966
APPLICATION NUMBER: W0 PCT/US97/08936
FILING DATE: 19-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Kachleen L.
REGISTRATION NUMBER: 43,433
REFRENCE/DOCKET NUMBER: 43,433
TELECOMUNICATION NUMBER: 43,433
TELECOMUNICATION NUMBER: 015280-279100US
 NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LL
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
 Query Match
1.9%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches
 TOPOLOGY: innar MOLECULE TYPE: DNA SEQUENCE DESCRIPTION: SEQ ID NO: 8: US-09-180-903-8
 TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
 Sequence 9, Application US/08529878B Patent No. 932556 GENERAL INFORMATION:
APPLICANT: Tam, Robert C.
 1794 GIGIGIGIGIGIGIGI 1813
 Sequence 8, Application US/09180903
Patent No. 6316190
GENERAL INFORMATION:
 RESULT 24
US-08-529-878B-9
 JS-09-180-903-8
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 | FERLIL AND SHARTION:
| FARELICANT: BATHER, Thomas C. | APPLICANT: BATHER, Dev P. |
| APPLICANT: BATHER, Dev P. |
| APPLICANT: ATTENDENT: APPLICANTION NUMBER: US/09/407,675 |
| CURRENT FILING DATE: 1999-09-28 |
| PRIOR APPLICATION NUMBER: 09/347,443 |
| PRIOR APPLICATION NUMBER: 09/347,443 |
| PRIOR APPLICATION NUMBER: 09/091,481 |
| PRIOR PRILING DATE: 1998-07-02 |
| PRIOR PRILING DATE: 1998-12-11 |
| NUMBER OF SEQ ID NOS: 5 |
| SEQ ID NO S |
| LENGTH: 20 |
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 Sequence 89, Application US/09488671A
| Sequence 88, Application US/09488671A
| Patent No. 6187545 |
| GENERAL INFORMATION |
| APPLICANT: Robert McKay |
| APPLICANT: Acqueline W. Butler |
| APPLICANT: Lex M. Cowsert |
| APPLICANT: Lex M. Cowsert |
| TITLE OF INVENTION: ANTISENSE MODULATION OF PEPCK-CYTOSOLIC EXPRESSION |
| FILE REPRENCE: RFS-0123 |
| CURRENT APPLICATION NUMBER: US/09/488,671A |
| CURRENT PILING DATE: 2000-01-21 |
| NUMBER OF SEQ ID NOS: 177 |
| LENGTH: 20 |
| LENGTH: 20 |
 Gaps
 Gaps
 TYPE: DNA
CRGANISM: Artificial Sequence
FEATUREN: PEATURENCE
COTHER INFORMATION: Description of Artificial Sequence: Oligo 5
US-09-407-675-5
 Length 20;
 Query Match
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels
 Query Match
1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels
 Query Match 1.9%; Score 20; DB 1;
Best Local Similarity 100.0%; Pred. No. 26;
 TYPE: DNA

GRGANISM: Artificial Sequence

FRATURE:

FORTHER INFORMATION: Antisense Oligonucleotide

US-09-488-671-88
 , MOLECULE TYPE: Other nucleic acid
US-08-863-639A-32
 1794 GIGIGIGIGIGIGIGI 1813
 Sequence 5, Application US/09407675 Patent No. 6169176
TOPOLOGY: linear
 US-09-488-671-88/c
```

Indels

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0; Mismatches

Conservative

20;

Matches

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Length 20, Indels

```
Sequence 442.7 Application US/08222177A

Sequence 442.7 Application US/08222177A

Patent No. 558299

GENERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: (dC-dA)n. (dG-dT)n SEQUENCES AND METHODS OF USING SAME
TITLE OF INVENTION: (dC-dA)n. (dG-dT)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460

CORRESPONDENCE ADDRESS:
ADDRESSEE: DeMitt Rose & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
CITY: Madison
STREET: MASCONSIN
COUNTRY: USA
ZIP: 53717-1914
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: DetentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILTMA PAPLICATION NUMBER: US/08/222,177A
FILTMA PAPEL
 DB 1; Length 21;
 Indels
 Query Match
1.8%; Score 19.4; E
Best Local Similarity 95.2%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches
 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION 10 DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: SATA, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELEPHONE: (608) 831-2100
 US 07/918,259
 1793 TGTGTGTGTGTGTGTGTGT 1813
 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 24-UUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Spewack, A. David
REGISTRATION NUMBER: 24,743
REFERENCE/DOCKET NUMBER: N.C.
TELECHOWNICATION INFORMATION:
TELECHONE: (202) 295-6759
TELEFAX: (202) 295-6759
 DNA (genomic)
 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
 TELEFAX: (608) 831-2106
 linear
 HYPOTHETICAL: NO ANTI-SENSE: YES
 ; TOPOLOGY: lir
; MOLECULE TYPE:
US-08-222-177A-442
 US-08-136-118-10
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 Gaps
 Jesus 10, Application US/08136118

| Patent No. 5580969 |
| GENERAL INFORMATION |
| GENERAL INFORMATION |
| APPLICANT HOKE, Glenn D |
| APPLICANT HILLAMS, Taffy J |
| APPLICANT WILLIAMS, Taffy J |
| TITLE OF INVENTION ANTISENSE OLIGONUCLEOTIDES DIRECTED |
| TITLE OF INVENTION AGAINST HUMAN ICAM-1 |
| NUMBER OF SEQUENCES: 15 |
| CORRESPONDENCE ADDRESS: 15 |
| CORRESPONDENCE ADDRESS: 15 |
| ADDRESSEE: Naval Medical Res. & Dev. Cmd.
 Length 21;
 0; Indels
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION NUMBER OF SEQUENCES: 48
CORRESPONDENCES: 48
CORRESPONDENCES: 48
CORRESPONDENCES: 48
CORRESPONDENCES: 48
CITY: La Habra
STREET: 3000 S. Augusta Court
CITY: La Habra
STREET: 4000 S. Augusta Court
CITY: La Habra
STREET: 4000 S. Augusta Court
CITY: La Habra
STREET: 4000 S. Augusta Court
CITY: La Habra
COUNTRY: California
COUNTRY: United States of America
ZIP: 90631
CANDUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,878B
PILING DATE: 13-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGBNT INFORMATION:
NAME: Fish, Robert D.
REGISTRATION NUMBER: 33,880
REBERRICE/OMMUTCATION INFORMATION:
TELEPRAM: 714-525-3303
TELEFRAM: 714-525-3303
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/136,118
FILING DATE:
CLASSIPICATION: 514
 Query Match
1.9%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 28;
Matches 20; Conservative 0; Mismatches
 STREE: 8901 Wisconsin Ave.
CITY: Bethesda
STATE: Maryland
COUNTRY: USA
ZIP: 20889-5606
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTE
 1794 GTGTGTGTGTGTGTGT 1813
 TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
 INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: 1.ENGTH: 21 base pairs TYPE: nucleic acid
 US-08-136-118-10/c
 US-08-529-878B-9
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Sequence 4, Application US/08915609;
Sequence 4, Application US/08915609;
Patent No. 6054300
GENERAL INFORMATION:
APPLICANT: MCKendree Jr., William L.,
ITILE OF INVENTION: Bingle-Site Amplification (SSA) Method for Accelerated
ITILE OF INVENTION: Development of Nucleic Acid Marker,
FILE REFERENCE: 0115.97
CURRENT APPLICATION WUMBER: US/08/915,609
CURRENT APPLICATION WUMBER: 60/028,775
EARLIER FILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0 - beta
SEQ ID NO 4
LENGTH: 19
 ö
TITLE OF INVENTION: Single-Site Amplification (SSA) Method for Accelerated TITLE OF INVENTION: Development of Nucleic Acid Marker FILE REFERENCE: 0115.97
CURRENT APPLICATION NUMBER: US/08/915,609
CURRENT FILING DATE: 1997-08-21
EARLIER FILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PALENT VET. OF DETA
SOFTWARE: PALENT VET. OF DETA
SOFTWARE: PALENT VET. OF DETA
 Gaps
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 OTHER INFORMATION: Description of Artificial Sequence: primer FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: primer
 Length 19;
 DB 1; Length 19; 32;
 Indels
 0; Indels
 DB 1;
32;
 Query Match
1.8%; Score 19; DB
Best Local Similarity 100.0%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches
 Query Match 1.8%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 32; Matches 19; Conservative 0; Mismatches
 1794 GIGIGIGIGIGIGIGIG 1812
 1794 GIGIGIGIGIGIGIGIG 1812
 RESULT 30
US-09-314-246-1
; Sequence 1, Application US/09314246
 1 drefererererererere 19
 19 drererererererere
 TYPE: DNA ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
 , NAME/KEY: primer bind
, LOCATION: (1)..(19)
US-08-915-609-4
 NAME/KEY: primer bind LOCATION: (1)..(19)
 NAME/KEY: primer bind LOCATION: (1)..(19)
 FEATURE:
NAME/KEY: primer bind
LOCATION: (1)..(19)
US-08-915-609-3
 US-08-915-609-4
 TYPE: DNA
 FEATURE:
 FEATURE:
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0
 1.8%; Score 19; DB 1; Length 19; 100.0%; Pred. No. 32;
 Indels
 DB 1; Length 19; 32;
 0; Indels
 MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,021
FILING DATE:
 APPLICATION SOURCES OF PACE OF A PAPILCATION OF PACENT. NO. 2955276

PRECENT. NO. 2955276

APPLICANT: WORGANTE, MICHELE APPLICANT: WORGANTE, WICHELE M. TITLE OF INVENTION: COMPOUND MICROSATELLITE TITLE OF INVENTION: PRIMERS FOR THE TITLE OF INVENTION: POLYMORPHISMS NUMBER OF SEQUENCES: 89

CORRESPONDENCE ADDRESS:
ADDRESSER: COMPANY
STREET: 1007 MARKET STREET
 Query Match
1.8%; Score 19; DB
Best Local Similarity 100.0%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches
 0; Mismatches
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,456
FILING DATE: 28 NOVEMBER 1994
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA ACAMETHY
REGISTRATION NUMBER: 33.692
REFERENCE/DOCKET NUMBER: BB-1064-A
TELECHONE: 302-892-8112
TELEPHONE: 302-992-7949
 ; APPLICANT: McKendree Jr., William L.
 1799 TGTGTGTGTGTGTATAT 1817
 1793 TGTGTGTGTGTGTGT 1811
 US-08-915-609-3/c
; Sequence 3. Application US/08915609
; Patent No. 6054300
; GENERAL INFORMATION:
 1 TGTGTGTGTGTGTATAT 19
 19 rerererererererer
 INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
 i MOLECULE TYPE: DNA (genomic)
US-08-849-021-74
 Best Local Similarity 100.
Matches 19; Conservative
 CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DI
 TYPE: nucleic acid
STRANDEDNESS: single
 Query Match
 RESULT 28
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Length 21;

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Query Match 1.8%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 37; Matches 19; Conservative 0; Mismatches
 rGTG 1812
 SEQUENCE CHARACTERISTICS:
LENGTH: 18 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single-stranded
 RESULT 33
US-08-734-973-5/c
| Sequence 5. Application US/08734973
| Patent No. 5912147
| GENERAL INFORMATION:
| STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY | STORY
 1791 ATTGTGTGTGTGTGTG 1808
 Sequence 4, Application US/08734973
Patent No. 5912147
 2 crerererererererere
 18 Arrererererererere 1
 1794 GTGTGTGTGTGT
 linear
 MOLECULE TYPE: DI
 US-08-734-973-4/C
 US-08-734-973-4
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 US-10Y-144-246-2
Sequence 2, Application US/09314246
Patent No. 6180349
Patent No. 6180349
GENERAL INFORMATION:
APPLICANT: Godfrey, Tony E.
APPLICANT: Godfrey, Tony E.
APPLICANT: Godfrey, Tony E.
APPLICANT: Godfrey, Ton W.
APPLICANT: Jone W.
APPLICANT: The Regents of the University of California
APPLICANT: The Regents OF W.
APPLICANT: The Regents of the University of California
APPLICANT: The Regents OF W.
APPLICANT: The Regents OF W.
APPLICANT: APPLICATION NUMBER: US/09/314,246
APPLICANT: APPLICATION NUMBER: US/09/314,246
APPLICANT: APPLICATION NUMBER: US/09/314,246
APPLICANT: APPLICATION NUMBER: US/09/314,246
APPLICANT: APPLICATION OF S. 2
APPLICANT: APPLICATION OF S. 2
APPLICANT: APPLICATION: Complementary to amplification products of OTHER INFORMATION: Camplementary to amplification products of OTHER INFORMATION: Camplementary to amplification products of OTHER INFORMATION: Camplementary to amplification products of CATER INFORMATION: CATEBER OF CAMPER INFORMATION: CATEBER OF C
 GENERAL INFORMATION:
APPLICANT: Glairinger, David G.
APPLICANT: Godfrey, Tony E.
APPLICANT: Godfrey, Romald H.
APPLICANT: Gray, Jobe W.
TITLE OF INVENTION: A Quantitative PCR Method to Enumerate DNA Copy Number: 2107AA-0962000US US/09/314,246
TILLE REFRENCE: 2307AA-096200US US/09/314,246
CURRENT APPLICATION NUMBER: US/09/314,246
CURRENT APPLICATION NUMBER: 1999-05-18
NUMBER OF SEQ ID NOS: 2.0
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: NOO!
I. LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: complementary to amplification products of OTHER INFORMATION: Camplementary to amplification products of OTHER INFORMATION: Camplementary to amplification products of OTHER INFORMATION: 3-t attached to 6-carboxy fluorescein (FAM)
NAME/KEY: moddified base
LOCATION: (1)
OTHER INFORMATION: 3'-t attached to 6-carboxy tetramethyl rhodamine OTHER INFORMATION: (TAMEA)
NAME/KEY: moddified base
LOCATION: (2)
OTHER INFORMATION: (TAMEA)
US-09-314-246-1
 ö
 Gaps
 Query Match
1.8%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 19; Conservative 0; Mismatches 0; Indels
 OTHER INFORMATION: 3'-t attached to quenching dye-09-314-246-2
 1794 GIGIGIGIGIGIGIGI 1812
 US-09-314-246-2
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 Gaps
 Gapa
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 GENERAL INFORMATION:
APPLICANT: SOLET, Daniel L.
APPLICANT: Basik, Mark
APPLICANT: Anderson, Garth R.
TITLE OF INVENTION: Genomic Instability
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One W&T Plaza
CITY: Buffalo
STREET: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER: Diskette, 3.5 inch
COMPUTER: Ompatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows
SOFTWARE: October 1996
ATTORNEY AGENT INFORMATION:
FILEPHONE: (716) 849-0349
INFORMATION FOR SEQ ID NO: 4:
INFORMATION FOR SEQ ID NO: 4:
INFORMATION FOR SEQ ID NO: 4:
 DB 1; Length 18; 39;
 Indels
 0; Indels
 APPLICANT: Stoler, Daniel L.
APPLICANT: Basik, Mark
APPLICANT: Basik, Mark
TITLE OF INVENTION: A Rapid Means For Quantitating
TITLE OF INVENTION: Genomic Instability
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
DB 1;
37;
 Query Match
1.7%; Score 18; DB
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches
```

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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: EXIDS, Roger P
APPLICANT: EXIDS, Roger P
TITLE OP INVENTION: Binding assay using binding agents with tail groups FILE REFERENCE: 0380-P01180US0
CURRENT APPLICATION NUMBER: US/08/700,530
CURRENT FILING DATE: 1995-03-10
PRIOR APPLICATION NUMBER: PCT/GB95/00521
PRIOR APPLICATION NUMBER: GB 9404709.9
PRIOR APPLICATION NUMBER: GB 9404709.9
PRIOR FILING DATE: 1994-03-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 18
 Gaps
 Gaps
 APPLICANT: Head, Steven R. APPLICANT: Head, Steven R. APPLICANT: Geolet, Philip APPLICANT: Boolet, Philip APPLICANT: Boolet, Jonathan APPLICANT: Boyce-Jacino, Michael APPLICANT: Boyce-Jacino, 6.5229680 or "Universal" Sequencing Array FILE REFERENCE: 04990.0049 CURRENT APPLICATION NUMBER: US/08/976,427A CURRENT FILING DATE: 1997-11-21 NUMBER OF SEQ ID NOS: 31
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 0; Indels '
 Length 18;
 DB 1; Length 18; 39;
 Indels
 FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
CTHER INFORMATION: Oligonucleotide
US-08-700-530-2
 DB 1;
39;
 Query Match 1.7%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 39; Matches 18; Conservative 0; Mismatches
 1.7%; Score 18;
100.0%; Pred. No.
 Jequence 28, Application US/08976427A
Patent No. 6322968
 , OTHER INFORMATION: Synthetic primer US-08-976-427-28
 Sequence 28, Application US/09648312
Patent No. 6337188
 1793 TGTGTGTGTGTGTGTG 1810
 1794 GTGTGTGTGTGTGT 1811
 Sequence 2, Application US/08700530 Patent No. 6316186
 100.08;
 TYPE: DNA
ORGANISM: Artificial Sequence
 TYPE: DNA
ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 100.
Matches 18; Conservative
 INFORMATION
 RESULT 37
US-09-648-312-28
 SEQ ID NO 28
LENGTH: 18
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 WESOUR 1943
US-08-700-30-1/C

Sequence 1, Application US/08700530

Sequence 1, Application US/08700530

Patent No. 6316186

GENERAL INFORMATION:

APPLICANT: EKINS, Roger P

TITLE OF INVENTION: Binding assay using binding agents with tail groups;
FILE REPERENCE: 0380-P01180US0

CURRENT PELICATION NUMBER: US/08/700,530

CURRENT PILING DATE: 1995-03-10

PRIOR FILING DATE: 1995-03-10

PRIOR PPLICATION NUMBER: PCT/GB95/00521

PRIOR PPLICATION NUMBER: GB 9404709.9

PRIOR APPLICATION UNDER: 1994-03-11

NUMBER OF SEQ ID NOS: 4

SOFUTON 18

ILENGTH: 18

ILENGTH: 18
 Gaps
 Score 18; DB 1; Length 18; Pred: No. 39; 0; Indels 0; Indels
 Length 18;
 Indels
: Hodgson, Russ, Andrews, Woods & Goodyear
1800 One M&T Plaza
 ; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide
US-08-700-530-1
 MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows
OPTWARE: Wordperfect for Windows
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/08/734,973
ATLING DATE: October 1996
ATTORNEY/AGENT INFORMATION:
 1.7%; Scotton 100.0%; Pred. No. ...
 NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 03551.0021
TELECONMINICATION INFORMATION:
TELEPHONE: (716) 856-4000
TELEFAX: (716) 896-4000
TELEFAX: (716) 896-4000
TELEFAX: (716) 896-4000
SEQUENCE CHARACTERISTICS:
LENGTH: 18 nucleocides
 Query Match
1.7%; Score 18;
Best Local Similarity 100.0%; Pred; No.
Matches 18; Conservative 0; Mismatcl
 1793 TGTGTGTGTGTGTGTG 1810
 nucleic acid
EDNESS: single-stranded
 GTG 1808
 18 Arrerererererere
 ORGANISM: Artificial Sequence FEATURE:
 New York
: United States
 Local Similarity 100.
nes 18; Conservative
 COMPUTER READABLE FORM MEDIUM TYPE: Diskett
 MOLECULE TYPE: DNA HYPOTHETICAL: No
 1791 ATTGTGTGTG
 linear
 14203-2391
 STRANDEDNESS:
TOPOLOGY: lin
 ADDRESSEE:
 COUNTRY:
 US-08-734-973-5
 TYPE: DNA
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Query Match

Best Loca Matches

APPLICANT: Head, Steven R

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Query Match
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 RESULT 38
US-09-488-671-120
Sequence 120, Application US/09488671A
Factor No. 6187545
GENERAL INFORMATION
APPLICANT: Robert McKay
APPLICANT: Madeline M. Butler
APPLICANT: Madeline M. Butler
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF PEPCK-CYTOSOLIC EXPRESSION
FILE REFRENCE: RTS-0123
CURRENT APPLICANTION NUMBER: US/09/488,671A
CURRENT APPLICANTON NUMBER: US/09/488,671A
CURRENT FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 177
LENGTH: 20
APPLICANT: Goelet, Philip
APPLICANT: Karn, Jonathan
APPLICANT: Rarn, Jonathan
APPLICANT: Boyce-Jacino, Michael
APPLICANT: BOyce-Jacino, Michael
TITLE REFERENCE: 04990.0049
CURRENT PLING DATE: 2000-08-25
CURRENT PLING DATE: 2000-08-25
CURRENT PLING DATE: 2000-08-25
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: AsstSEQ for Mindows Version 3.0
SOFTWARE: SPECIAL 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE: CTHER INFORMATION: Synthetic primer
US-09-648-312-28
 Gaps
 Gaps
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 GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: C. Frank Bennett
APPLICANT: C. Frank Bennett
APPLICANT: Eric B. Swayze
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
FILE REPERENCE: ISP-0439
CURRENT APPLICATION NUMBER: US/09/496,694B
PRIOR APPLICATION NUMBER: 09/266,407
PRIOR APPLICATION NUMBER: 09/266,407
PRIOR PILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 09/163,162
 Length 20;
 1.7%; Score 18; DB 1; Length 18;
100.0%; Pred. No. 39;
tive 0; Mismatches 0; Indels
 Indels
 1.7%; Score 17.4; DB 1; ilarity 94.7%; Pred. No. 53; Conservative 0; Mismatches 1;
 TYPE: DNA
ORGANISM: Artificial Sequence
ORTURE:
OTHER INFORMATION: Antisense Oligonucleotide
 US-09-496-694B-235/c
; Sequence 235, Application US/09496694B
; Patent No. 6335194
 1794 GTGTGTGTGTGTGTG 1812
 1793 TGTGTGTGTGTGTGTG 1810
 1 Grerereagrererere
 1 rerererererererere
 Query Match
Best Local Similarity
Matches 18; Conserv;
 Best Local Similarity
Matches 18; Conserv
 US-09-488-671-120
 Query Match
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RESULT 40
US-08-222-177A-448/C
US-08-222-177A-448/C
Sequence 448, Application US/08222177A
Fatent No. 5582379
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: (dc-da)n.(dd-dT)n SEQUENCES AND METHODS OF USING SAME
NUMBER OP SEQUENCES:
NUMBER OP SEQUENCES:
ADDRESSEE: DeWitt Ross & Stevens, S.C.
ADDRESSEE: DeWitt Ross & Stevens, S.C.
TREET: 8000 Excelsior Drive, Suite 401
 ö
 ö
 Gaps
 Gaps
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 ö
 Length 20;
 1.6%; Score 17; DB 1; Length 17; larity 100.0%; Pred. No. 47; Conservative 0; Mismatches 0; Indels
 Indels
 SUFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
FILING DATE:
 DB 1;
 ; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-496-694B-235
 Query Match
1.7%; Score 17.4; D
Best Local Similarity 94.7%; Pred. No. 53;
Matches 18; Conservative 0; Mismatches
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 007/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REFERENCE/DOCKET NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
 CITY: Madison
STATE: Watsonsin
COUNTRY: USA
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OFFINARE: PATENTING SYSTEM:
PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V
 1811 TGTATATATATATGT 1829
 1793 TGTGTGTGTGTGTGT 1809
 MOLECULE TYPE: DNA (genomic) US-08-222-177A-448
 608) 831-2100
 TYPE: DNA
ORGANISM: Artificial Sequence
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 249
SEQ ID NO 235
LENGTH: 20
 17 rerererererererer
 TELEFAX: (608) 831-2106
 NPORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 17 base pairs
 TYPE: nucleic acid
STRANDEDNESS: double
 linear
 Best Local Similarity
Matches 17; Conserv
```

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;
 PATENTAL INFORMATION:
APPLICANT: Arnold Jr., Lyle J
APPLICANT: Reynolds, Mark
APPLICANT: Reynolds, Mark
APPLICANT: Reynolds, Mark
APPLICANT: Gadchett, Christina
TITLE OF INVENTION: Chimeric Oligonucleoside Compounds
NUMBER OF SEQUENCES:
CORRESPONDENCES:
ADDRESSE: Lyon & Lyon
STREET: 611 West Sixth St.
CITY: Los Angeles
STREET: 61 West Sixth St.
CITY: Los Angeles
STREET: 62
COUNTRY: U.S.A.
ZIP: BOONT
ZIP: POONT
ZIP: READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: BATE COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,774
FILING DATE:
CLASSIFICATION NUMBER: US/08/238,177
FILING DATE:
APPLICATION NUMBER: US/08/238,177
FILING DATE:
NAME: Melest, Paul H.
BEGISTRATION NUMBER: 207/174
BEGISTRATION NUMBER: 207/174
BEGISTRATION NUMBER: 207/174
BEGISTRATION NUMBER: 207/174
 Length 17;
 Indels
 MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: no
ANII-SENSE: yes
ANII-SENSE: yes
NAME/KEX: GT oligomers 2517-1, 2516-1
IDBNITE/CATION METHOD: synthesis experiments
OTHER INFORMATION: complementary to synthetic RNA
OTHER INFORMATION: target
 Ouery Match
1.6%; Score 17; DB 1;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 17; Conservative 0; Mismatches (
 207/174
 TOPOLOGY: linear MOLECULE TYPE: other nucleic acid HYPOTHETICAL: no
 US-09-490-774-11
; Sequence 11, Application US/09490774
; Patent No. 6262036
 1798 GIGIGIGIGIGIA 1814
 REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213/489-1600
TELEFAX: 213/955-0440
 1 drerererererera 17
 TELEX: 67-3510
INFORMATION FOR SEQ ID NO: SEQUENCE CHRACTERISTICS: LENGTH: 17 base pairs TYPE: nucleic acid STRANDEDNESS: single
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 17 base pairs
TYPE: nucleic acid
 single
 linear
 TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: li
 US-08-960-111-11
 δ
 ö
 Gaps
 ö
 Sequence ii, Application US/08960111

Patent No. 6060456

GENERAL INFORMATION:
APPLICANT: Arnold Jr., Lyle J
APPLICANT: Reynolds, Mark A
APPLICANT: Giachetti, Christina
TITLE OF INVENTION: Chimeric Oligonucleoside Compounds;
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Los Angeles
CITY: Los Angeles
SCHATE: CA
STATE: CA
 Length 17;
 0; Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,111
FILING DATE:
 TYPE: DNA CAGANISM: Artificial Sequence CAGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Chemically synthesized oligomer US-08-885-126-9
 Score 17; DB 1;
Pred. No. 47;
 1.6%; Scor.
100.0%; Pred. No. -...
'-- 0; Mismatches
 CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/238,177
FILING DATE: 04-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meier, Paul H.
REGISTRATION NUMBER: 32,274
REFERENCE/POCKET NUMBER: 207/174
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213/489-1600
 1798 GIGIGIGIGIGIGIA 1814
 Query Match
Best Local Similarity 100.
Matches 17; Conservative
 213/955-0440
 90017
8 7 7 7
 CITY: LOS
STATE: CA
COUNTRY:
 -08-960-111-11
 RESULT 42
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TYPE: nucleic aci
STRANDEDNESS: sir
 MOLECULE TYPE: DNA HYPOTHETICAL: No
 US-08-734-973-3/c
 US-08-734-973-1
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 Gaps
 Gaps
 ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-958-221A-16
 Sequence.1, Application US/08734973

Sequence.1, Application US/08734973

Sequence.1, Application US/08734973

SERRAL INFORMATION:
APPLICANT: Basik, Mark

APPLICANT: Basik, Mark

APPLICANT: Anderson, Garth R.

TITLE OF INVENTION: Genomic Instability

TITLE OF INVENTION: Genomic Instability

NUMBER OF SECURNCES: 38

CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE:
ADDRESSE: ADGRESS:
STREET: 1800 One M&T Plaza
 Query Match 1.6%; Score 17; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 47; Matches 17; Conservative 0; Mismatches 0; Indels
 Query Match
1.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 17; Conservative 0; Mismatches 0; Indels
 NAME/KEY: GT oligomers 2517-1, 2516-1
IDENTIFICATION METHOD: synthesis experiments
OTHER INFORMATION: complementary to synthetic RNA
OTHER INFORMATION: target
US-09-490-774-11
 RESULT 44
US-09-958-21A-16
Sequence 16, Application US/09958221A
Setent No. 6686160
GENERAL INFORMATION:
APPLICANT: Haeringen van, Willem A.
APPLICANT: Haeringen van, Hendrik
TITLE OF INVENTION: UNIVERSAL VARIABLE FRAGMENTS
FILE REPERENCE: 92750/64
CURRENT APPLICATION NUMBER: EP 00200757.3
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: EP COL-10-03
PRIOR PRILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 27
NUMBER OF SEQ ID NOS: 27
SEQ ID NO IN OF SEQ ID NOS: 27
SEQ ID NO IN OF SEQ ID NOS: 27
SEQ ID NO IN OF SEQ ID NOS: 27
SEQ ID NO IN OF SEQ ID NOS: 27
SEQ ID NO IN OF SEQ ID NOS: 27
SEQ ID NO IN OF SEQ ID NOS: 27
SEQ ID NO IN OF SEQ ID NOS: 27
SEQ ID NO IN OF SEQ ID NOS: 27
SEQ ID NO IN OF SEQ ID NOS: 27
SEQ ID NO IN OF SEQ ID NOS: 27
SEQ ID NO IN OF SEQ ID NOS: 27
SEQ ID NO IN OF SEQ ID NOS: 27
SEQ ID NO IN OF SEQ ID NOS: 27
SEQ ID NO IN OF SEQ ID NOS: 27
SEQ ID NOS: 27
 STREET: 1800 One Mer Plaza
CITY: Buffalo
SIME: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows
 1792 TIGIGIGIGIGIGIG 1808
 1798 GTGTGTGTGTGTGTA 1814
 1 rrerererererere 17
 1 dicicicicicidididid
 TYPE: DNA ORGANISM: Artificial Sequence
 RESULT 45
US-08-734-973-1/c
ANTI-SENSE:
FEATURE:
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

APPLICATION NUMBER:

APPLICATION NUMBER:

APPLICATION NUMBER:

ATCOMENY APPLICATION NUMBER:

ATTOMENY APPRICATION NUMBER:

ATTOMENY APPLICATION NUMBER:

ATTOMENY APPLIC
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NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFRENCE/DOCKET NUMBER: 03551.0021
TELECOMMUNICATION INFORMATION:
TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 18 nucleotides
TYPE: nucleic acid
STRANDENBES: single-gtranded
 REGISTRATION NUMBER: 35,300
REGISTRATION NUMBER: 35,300
REPERENCE!DOCKET NUMBER: 03551.0021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 856-4000
TELEFAX: (716) 849-0149
 1794 GIGIGIGIGIGIGIG 1810
 17 drérerererererere
 US-08-734-973-31/c
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 d
 ö
 Gaps
 Sequence 28, Application US/08734973

Patent No. 5912147

GENERAL INFORMATION:

APPLICANT: Stoler, Daniel L.

APPLICANT: Anderson, Garth R.

TITLE OF INVENTION: A Rabid Means For Quantitating
TITLE OF INVENTION: A Rabid Means For Quantitating
TITLE OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: Buffalo One M&T Plaza
 DB 1; Length 18;
51;
 0; Indels
 Sequence 30, Application US/08734973
Patent No. 5912147
GENERAL INFORMATION:
APPLICANT: Stoler, Daniel L.
APPLICANT: Basik, Mark
APPLICANT: Basik, Mark
APPLICANT: Anderson, Garth R.
TITLE OF INVENTION: A Rapid Means For Quantitating
TITLE OF INVENTION: Genomic Instability
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
 STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE PORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: BM COMPATIBLE
OPERATING SYSTEM: MS-DOS/ Microsoft Windows
SOFTWARE: Wordperfect for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/734,973
FILING DATE: OCCODER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 3351.0021
DB 1;
51;
 1.6%; Score 17; DB
100.0%; Pred. No. 51;
tive 0; Mismatches
Query Match 1.6%; Score 17; DB Best Local Similarity 100.0%; Pred. No. 51; Matches 17; Conservative 0; Mismatches
 single-stranded
 GTG 1808
 1792 TIGIGIGIGIGIGIG 1808
 TELEPAONE: (716) 856-4000
TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 28 :
SEQUENCE CHARACTERISTICS:
 1.67
Best Local Similarity 100.0
Matches 17; Conservative
 1792 TIGIGIGIGIGIG
 LENGTH: 18 nucleoti
TYPE: nucleic acid
STRANDEDNESS: singl
 linear
 RESULT 48
US-08-734-973-30/c
 US-08-734-973-28/c
```

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GENERAL INFORMATION:

Sequence 31. Application US/08734973

Patent No. 5912147

GENERAL INFORMATION:

APPLICANT: Stoler, Daniel L.

APPLICANT: Basik, Mark

APPLICANT: Anderson, Garth R.

ITLE OF INVENTION: A Rapid Means For Quantitating

ITLE OF INVENTION: A Rapid Means For Quantitating

ITLE OF INVENTION: Genomic Instability

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear

STREET: 1800 One M&T Plaza

CITY: Briffalo

STREET: New York

COUNTRY: United States

ZIP: 14203-229
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear STREET: 1800 One M&T Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS, Microsoft Windows
SOFTWARE: Wordperfect for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OS/734,973
FILING DATE: OCTOBE 1996
ATTORNEY/AGENT INFORMATION:
MANAY
 Query Match 1.6%; Score 17; DB 1; Length 18; Best Local Similarity 100.0%; Pred. No. 51; Matches 17; Conservative 0; Mismatches 0; Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IEM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows
SOFTWARE: Wordperfect for Windows
CURRET APPLICATION DATA:
APPLICATION NUMBER: US/08/734,973
FILING DATE: OCtOber 1996
ATTORNEY AGENT INFORMATION:
NAME: Nelson, WH. Bud
```

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DB 1; Length 20;
 2; Indels
 APPLICANT: Garner, Harold R.
APPLICANT: Wren, Jonathan D.
APPLICANT: Winna, John D.
APPLICANT: Minna, John D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes FILE REPERFOCE: UTSD0667
CURRENT APPLICATION NUMBER: US/09/475,947A
CURRENT FILING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 346
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 337
 VERSION 1.25
 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WORGANTE, MICHELE
APPLICANT: VOGEL, JULIE M.
TITLE OF INVENTION: COMPOUND MICROSATELLITE
TITLE OF INVENTION: PRIMERS FOR THE
TITLE OF INVENTION: DETECTION OF GENETIC
TITLE OF INVENTION: POLYMORPHISMS
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND
ADDRESSEE: COMPANY
 Query Match
1.6%; Score 16.8; D
Best Local Similarity 90.0%; Pred. No. 62;
Matches 18; Conservative 0; Mismatches
 ADDRESSE: COMPANY
STREET: 1007 WARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT IN RELEASE #1.0, VE
CURRENT APPLICATION NUMBER: US/08/849,021
PILING DATE:
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIORINEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION WIMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1064
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 302-992-8112
Sequence 337, Application US/09475947A Patent No. 6472154 GENERAL INFORMATION:
 Sequence 87, Application US/08849021
Patent No. 5955276
 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 1792 TIGIGIGIGIGIGI
 LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 TYPE: DNA
ORGANISM: human
 US-09-475-947A-337
 US-08-849-021-87
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 US-08-734-973-32/C
Sequence 3.2, Application US/08734973
Perent No. 5912H2.
GENERAL INFORMATION:
PAPPLICANT: Stoler, Daniel L.
APPLICANT: Anderson, Garth R.
TITLE OF INVENTION: A Rapid Means For Quantitating
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE:
ADDRESSE: ADDRESSE: ADDRESSE:
STREET: 1800 One W&T Plaza
 1.6%; Score 17; DB 1; Length 18; 100.0%; Pred. No. 51; tive 0; Mismatches 0; Indels
 Query Match
1.6%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 17; Conservative 0; Mismatches 0; Indels
 STREET: 1800 One M&T Plaza
CITY: Buffalo
STATE: 1800 One M&T Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
COMPUTER: READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IEM Compatible
COMPUTER: IEM Compatible
OPERATING SYSTEM:
MS-DOS/MICTOSOft Windows
SOFTWARE: MOORDETECT for Windows
SOFTWARE: MOORDETECT for Windows
SOFTWARE: OCCODER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REGISTRATION FOR SEQ 10 NO: 32
SEQUENCE CHARACTERISTICS:
LENGTH: 18 muclectides
TYPER: nuclectides
TYPER: NUCLECTION OF SEC 10 NO: 32
SEQUENCE CHARACTERISTICS:
LENGTH: 18 muclectides
TYPER: NUCLECTION OF SEC 10 NO: 32
SEQUENCE CHARACTERISTICS:
LENGTH: 18 muclectides
TYPER: nuclectides
TYPER: NUMBER: SEC 10 NO: 32
STREADBONESS: SINGle-Stranded
 TYPE: nucleic acid
STRANDEDNESS: single-stranded
POPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: No
US-08-734-973-31
 1794 GTGTGTGTGTGTGTG 1810
 GTG 1810
 17 Grerererererer 1
 SEQUENCE CHARACTERISTICS:
LENGTH: 18 nucleotides
 1.6
Best Local Similarity 100.
Matches 17; Conservative
 INFORMATION FOR SEQ ID NO:
 1794 GTGTGTGTGTGT
 TOPOLOGY: lines MOLECULE TYPE: DN HYPOTHETICAL: NO
 US-08-734-973-32
```

MOLECULE TYPE: DNA (genomic)

RESULT 51 US-09-475-947A-337/c

linear

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TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
 US-08-734-973-29/c
 US-08-734-973-8
 ö
 Gaps
 ö
 Sequence 7, Application US/08734973
| GENERAL INFORMATION:
| APPLICANT: Stoler, Daniel L. APPLICANT: Stoler, Mark
| APPLICANT: Anderson, Garth R. TILLE OF INVENTION: Genemic Instability
| TITLE OF INVENTION: Genemic Instability
| NUMBER OF SEQUENCES: 38
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: 1800 One MAT Plaza Andrews, Woods & Goodyear STREET: New York
| COUNTRY: United States | STREET: New YORK
| COUNTRY: United States | STREET: New YORK
| CONTRY: United States | STREET: New YORK
| CONTRY: United States | STREET: New YORK | TELEFAX: (716) 849-0349 | INFORMATION FOR SEQ ID NO: 7 | SEQUENCE CHARACTER: STREET: ST
 Ouery Match
Best Local Similarity 90.0%; Pred. No. 78;
Matches 18; Conservative 0; Mismatches 2; Indels
 Indels
 Sequence 8, Application US/08734973
Patent No. 5912147
GENERAL INFORMATION:
APPLICANT: Stoler, Daniel L.
APPLICANT: Basik, Mark
APPLICANT: Anderson, Garth R.
TITLE OF INVENTION: A Rapid Means For Quantitating
TITLE OF INVENTION: Genomic Instability
 Score 16.4; D
Pred. No. 60;
0; Mismatches
 1813 TATATATATATATGTACA 1832
 1 TATATATATATATACACA 20
 LENGTH: 18 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single-stranded
 1791 ATTGTGTGTGTGTGTG 1808
 Query Match 1.6%;
Best Local Similarity 94.4%;
Matches 17; Conservative (
 linea
 RESULT 54
US-08-734-973-8/c
 RESULT 53
US-08-734-973-7/C
US-08-849-021-87
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Sequence 35, Application US/08734973 Patent No. 5912147
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 DB 1; Length 18
 DB 1; Length 18;
 CONTRESPONDENCE ADDRESS:
ADDRESSEE:
ADDRESSEE:
BUffalo
CITY:
Buffalo
STATE:
New York
COUNTRY:
United States
COMPUTER:
LA103-231
COMPUTER:
BEBLIC TOMBOUSE:
COMPUTER:
MEDIUM TYPE:
DISKette, 3.5 inch
COMPUTER:
BEBLIC TOMBOUSE:
COMPUTER:
MEDIUM TYPE:
DISKette, 3.5 inch
COMPUTER:
MEDIUM TYPE:
DISKette, 3.5 inch
COMPUTER:
MEDIUM TYPE:
MEDIUM TYPE:
OFFERTION OFFERTION:
MEDIUM TYPE:
COMPUTER:
MEDICATION NUMBER:
US/08/734,973
FILING DATE:
OCTOBET 1996
ATTORNEY, AGENT INPORMATION:
NAME:
NAME
 1; Indels
 GENERAL INFORMATION:
APPLICANT: Stoler, Daniel L.
APPLICANT: Stoler, Mark
APPLICANT: Adderson, Garth R.
TITLE OF INVENTION: A Rapid Means For Quantitating
TITLE OF INVENTION: Genomic Instability
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodye
 Query Match 1.6%; Score 16.4; 1
Best Local Similarity 94.4%; Pred. No. 60;
Matches 17; Conservative 0; Mismatches
 Score 16.4; D
Pred. No. 60;
0; Mismatches
 Sequence 33, Application US/08734973
Patent No. 5912147
 single-stranded
 1793 TGTGTGTGTGTGTGTG 1810
 single-stranded
 18 rererererererere 1
TELEPHONE: (716) 856-4000
TELEFAX: (716) 849-0349
INPORMATION POR SEQ ID NO: 29
SEQUENCE CHARACTERISTIC:
LENGTH: 18 nucleotides
 Ouery Match
Best Local Similarity 94.4%;
Matches 17; Conservative
 TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

HYPOTHETICAL: NO

US-08-734-973-29
 TYPE: nucleic acid
STRANDEDNESS: sing
 TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
 RESULT 56
US-08-734-973-33/C
 US-08-734-973-33
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Gaps
 ö
 Score 16.4; DB 1; Length 18; Pred. No. 60;
 RESULT 58
US-08-734-973-37/c
; Sequence 37, Application US/08734973
; Patent No. 5912147
; GENERAL INFORMATION:
 APPLICANT: Stoler, Daniel L.
 APPLICANT: Anderson, Garth R.
 TITLE OF INVENTION: A Rapid Means For Quantitating
 TITLE New York
 COUNTRY: United States
 COUNTRY: United States
 COUNTRY: United States
 COUNTRY: United States
 CONFUTER: Is Diskette, 3.5 inch
 COMPUTER: ISM COMPATIBLE

GENERAL INCORMITION:
APPLICANT: Stoler, Mark
APPLICANT: Basik, Mark
APPLICANT: Basik, Mark
APPLICANT: Basik, Mark
APPLICANT: Basik, Mark
APPLICANT: Anderson, Garth R.
TITLE OF INVENTION: Genomic Instability
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREST: Buffalo
STATE: New York
CONFUTER: Diskette, 3.5 inch
COMPUTER: Diskette, 3.5 inch
COMPUTER
 Indels
 Query Match
1.6%; Score 16.4; E
Best Local Similarity 94.4%; Pred. No. 60;
Matches 17; Conservative 0; Mismatches
 TYPE: nucleic acid
STRANDEDNESS: single-stranded
 1791 ATTGTGTGTGTGTGTG 1808
 linear
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Indels

1791 ATTGTGTGTGTGTGTG 1808

Gabs

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 DB 1; Length 18;
 Query Match 1.6%; Score 16.4; DB 1; Length 18; Best Local Similarity 94.4%; Pred. No. 60; Matches 17; Conservative 0; Mismatches 1; Indels
 1; Indels
 US-09-475-947A-104
US-09-475-947A-104
| Sequence 104, Application US/09475947A
| Patent No. 647218.
| Patent No. 647218.
| APPLICANT: Minna, John D. | APPLICANT: Minna, John D. | TITLE OF INVERTION: POLYMOTPHIC Repeats in Human Genes FILE REPRENCY: US/09/475,947A
| CURRENT APPLICATION NUMBER: US/09/475,947A
| CURRENT PAPLICATION NUMBER: 1999-12-31
| NUMBER: OF SEQ ID NOS: 346
| SOFTWARE: PatentIn Ver. 2.1
| SER ID NO 104
 RESULT 61
US-09-475-947A-104/C
i Sequence 104, Application US/09475947A
j Patent No. 6472154
j GENERAL INFORMATION:
j APPLICANT: Garner, Harold R.
APPLICANT: Minna, John D.
TITLE OF INVENTION: Polymorphic Repeats.in Human Genes
FILE REFERENCE: UTSD0667
CURRENT PILING DATE: 1999-12-31
CURRENT FILING DATE: 1999-12-31
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 104
 1; Indels
 DB 1;
 1.6%; Score 16.4; Dl
94.4%; Pred. No. 60;
cive 0; Mismatches
 Query Match
1.6%; Score 16.4; D
Best Local Similarity 94.4%; Pred. No. 60;
Matches 17; Conservative 0; Mismatches
 RESULT 62
US-08-222-177A-439/c
; Sequence 439, Application US/08222177A
; Patent No. 5582879
; GENERAL INFORMATION:
 1814 ATATATATATATATGTAC 1831
 1810 GIGTATATATATATAT 1827
 1791 ATTGTGTGTGTGTGTG 1808
 1 Grafararararar 18
 18 AArdricididigidigid 1
 18 ATATATATATATATAC
 0.65
Best Local Similarity 94.43
Matches 17; Conservative
 TYPE: DNA
ORGANISM: human
 TYPE: DNA ORGANISM: human
 US-09-475-947A-104
 US-09-475-947A-104
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 Gaps
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 REBULT 59
US-08-734-973-38/C

j Sequence 38, Application US/08734973

j Patent No. 591247

GENERAL INFORMATION:
APPLICANT: Stoler, Daniel L.
APPLICANT: Stoler, Daniel L.
APPLICANT: Basik, Mark
APPLICANT: Anderson, Garth R.
TITLE OF INVENTION: A Rapid Means For Quantitating
TITLE OF INVENTION: A Rapid Means For Quantitating
TITLE OF INVENTION: Genomic Instability
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One M&T Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
STATE: New York
COUNTRY: United States
STATE: New York
COMPUTER: Diskette, 3.5 inch
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: SEADABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: ORGOBERIC FOR Windows
SOFTWARE: Wordperfect for Windows
SOFTWARE: Wordperfect for Windows
SOFTWARE: ORGOBER: 1996
FILING DATE: OCCODER: 1996
ATTORNEY APPLICATION NUMBER: UNINGOME
STATES OCCODER: 1996
ATTORNEY APPLICANTION
 Length 18;
 1; Indels
OPERATING SYSTEM: MS-DOS/ Microsoft Windows
SOFTWARE: Wordperfect for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/734,973
FILING DATE: October 1996
ATTORNEY/AGENT INFORMATION:
NAME: NABES: 03551.0021
REFERENCE/DOCKET NUMBER: 03551.0021
TELECOMUNICATION INPORMATION:
TELECOMUNICATION INPORMATION:
TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 nucleotides
 0; Mismatches
 Score 16.4;
Pred. No. 60
 03551.0021
 single-stranded
 TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
 1791 ATTGTGTGTGTGTGTG 1808
 NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REPERENCE/DOCKET NUMBER: 035
TELECOMMUNICATION: TELECOMMUNICATION:
 TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 38 :
SEQUENCE CHARACTERISTICS:
LENGTH: 18 nucleotides
 18 AATGIGIGIGIGIGIG 1
 Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative
 TYPE: nucleic acid
STRANDEDNESS: sing
 MOLECULE TYPE: DNA
HYPOTHETICAL: NO
US-08-734-973-37
 MOLECULE TYPE:
HYPOTHETICAL: N
 US-08-734-973-38
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0
 ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-958-221A-18
 FEATURE:
) OTHER INFORMATION: Description of Artificial Sequence: primer US-09-958-221A-17
 Length 17;
 DB 1; Length 17;
62;
 Query Match
Best Local Similarity 50.0%; Pred. No. 57;
Matches 8; Conservative 8; Mismatches 0; Indels
 WS-09-58-221A-18

WS-09-58-221A-18

WS-09-58-221A-18

Sequence 18, Application US/09958221A

Patent No. 668160

GENERAL INPORMATION:
APPLICANT: Haeringen van, Willem A.
APPLICANT: Haeringen van, Hendrik

TITE OF INVENTION: UNIVERSAL VARIABLE FRAGMENTS
FILE REFRENCE: 92756/64

CURRENT FILING DATE: 2001-10-03

PRIOR FILING DATE: 2000-13-03

PRIOR PILING DATE: 2000-03-03

PRIOR PILING DATE: 2000-03-03

PRIOR PILING DATE: 2001-05

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 18

LENGTH: 17
 GENERAL NO. 6200100);
GENERAL NO. 6200100);
GENERAL INFORMATION:
APPLICANT: Haeringen van, Willem A.
APPLICANT: Haeringen van, Hendrik
TITLE OF INVENTION: UNIVERSAL VARIABLE FRAGMENTS;
FILE REFERENCE: 92750/64
CURRENT APPLICATION NUMBER: US/09/958,221A
CURRENT APPLICATION NUMBER: BP 00200757.3
PRIOR APPLICATION NUMBER: PCT/NLO1/00177
PRIOR PILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 27
SEQ ID NOS: 27
SEQ ID NO 17
LENGTH: 17
 DB 1;
62;
 Query Match
1.5%; Score 16; DB
Best Local Similarity 100.0%; Pred. No. 62;
Matches 16; Conservative 0; Mismatches
 1.5%; Score 16;
100.0%; Pred. No.
 US-09-958-221A-17; Sequence 17, Application US/09958221A; Patent No. 6686160
 1793 TGTGTGTGTGTGTG 1808
 1794 GTGTGTGTGTGTGT 1809
 TYPE: DNA
ORGANISM: Artificial Sequence
 2 rererererererer 17
 1 GuguGuGuGuGuGuGu 16
 TYPE: DNA ORGANISM: Artificial Sequence
; ORGANISM: Homo sapiens
US-09-371-772B-6069
 Query Match
Best Local Similarity
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 Sequence 6069, Application US/09371772B

Sequence 6069, Application US/09371772B

Sequence 6069, Application US/09371772B

Sequence 6069, Application US/09371772B

Sequence 6069, Application US/09371772B

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Stinchcomb, Dan

APPLICANT: Scobedo, Jaime

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

FILE REFERENCE: MBH800,876-4 (237/198)

CURRENT FILING DATE: 1995-08-10

PRIOR FILING DATE: 1995-10-26

PRIOR FILING DATE: 1995-10-26

PRIOR PLING DATE: 1996-01-08

NUMBER OF SEQ ID NOS: 14225

SOFTWARE PATENTIN VETSION 3.0
 ö
 APPLICANT: Weber, James L.

TITLE OF INVENTION: LENGTH POLYMORPHISMS IN

TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME

NUMBER OF SEQUENCES: 460

NUMBER OF SEQUENCES: 460

CARRESPONDENCE ADDRESS:

ADDRESSEE: DeWitt Ross & Stevens, S.C.

STREET: 8000 Excelsior Drive, Suite 401
 Gaps
 Query Match
1.5%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 16; Conservative 0; Mismatches 0; Indels
 CITY: Madison
STATE: Wisconsin
COUNTRY: Misconsin
COUNTRY: 1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BATEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
 FILING DATE:
CLASCIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENI INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,4925
 30,492
ER: 09865.601
 1793 TGTGTGTGTGTGTG 1808
 REFERENCE DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-222-177A-439
 rerererererere
 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
 TYPE: nucleic acid
STRANDEDNESS: double
 -09-371-772B-6069
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nucleic ació
 US-08-734-973-2/c
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 Gaps
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 ; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-958-221A-20
 CTHER INFORMATION: Description of Artificial Sequence: primer US-09-958-221A-19
 1.5%; Score 16; DB 1; Length 17;
100.0%; Pred. No. 62;
tive 0; Mismatches 0; Indels
 1.5%; Score 16; DB 1; Length 17;
100.0%; Pred. No. 62;
tive 0; Mismatches 0; Indels
Indels
 APPLICANT: Haeringen van, Willem A.
APPLICANT: Haeringen van, Hendrik
TITLE OF INVENTION: UNIVERSAL VARIABLE FRAGMENTS
FILE REPERENCE: 92750/64
CURRENT APPLICATION NUMBER: US/09/958,221A
CURRENT FILING DATE: 2001-10-03
PRIOR PLILING DATE: 2000-03-03
PRIOR PLLING DATE: 2000-03-05
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO
 GENERAL INCRORATION:
APPLICANT: Haeringen van, Willem A.
APPLICANT: Haeringen van, Willem A.
APPLICANT: Haeringen van, Hendrik
ITILB OF INVENTION: UNIVERSAL VARIABLE FRAGMENTS
FILE REPERENCE: 92750/64
CURRENT APPLICATION NUMBER: US/09/958,221A
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: EP 00200757.3
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 27
SOFTWARR: Patentin Ver. 2.1
SEQ ID NO
ö
Mismatches
 US-09-958-221A-20/c
; Sequence 20, Application US/09958221A
; Patent No. 6686160
; GENERAL INFORMATION:
 Sequence 19, Application US/09958221A
Patent No. 6686160
;
0
 1793 TGTGTGTGTGTGTGTG 1808
 1793 TGTGTGTGTGTGTGT 1808
 1793 TGTGTGTGTGTGTG 1808
 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
 TYPE: DNA ORGANISM: Artificial Sequence
 2 refererererere 17
 Best Local Similarity 100.
Matches 16; Conservative
 16; Conservative
Matches 16; Conservative
 Best Local Similarity
Matches 16; Conserva
 -09-958-221A-19/c
 Query Match
 Query Match
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 Gaps
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 FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-958-221A-21
 Query Match 1.5%; Score 16; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 62; Matches 16; Conservative 0; Mismatches 0; Indels
 ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear STREET: 1800 One M&T Plaza CITY: Buffalo STATE: New York
 APPLICANT: Stoler, Daniel L.
APPLICANT: Basik, Mark
APPLICANT: Basik, Mark
APPLICANT: Anderson, Garth R.
AITLE OF INVENTION: A Sapid Means For Quantitating
TITLE OF INVENTION: Genomic Instability
 GENERAL INCORMATION:
APPLICANT: Haeringen van, Willem A.
APPLICANT: Haeringen van, Hendrik
APPLICANT: Haeringen van, Hendrik
FITLE OF INVENTION: UNIVERSAL VARIABLE FRAGWENTS
FILE REFERENCE: 92750/64
CURRENT APPLICATION NUMBER: US/09/958,221A
CURRENT PILING DATE: 2001-10-03
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-05
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver: 2.1
SEC ID NO 21
LENGTH: 17
 STATE: New York
COUNTRY: United States
ZIP: 14203-2391
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows
OSTWARE: WORDPETCE for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/734,973
ATTORNAY APPLICATION NUMBER: US/08/734,973
ATTORNAY AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: SA 300
REGISTRATION NUMBER: SA 300
REGISTRATION NUMBER: OBSION, M. Bud
 REFERENCE/DOCKET NUMBER: 03551.0021
Sequence 21, Application US/09958221A Patent No. 6686160
 Sequence 2, Application US/08734973
Patent No. 5912147
GENERAL INFORMATION:
 1793 TGTGTGTGTGTGTG 1808
 TELEPHONE: (716) 856-4000
TELEPAK: (716) 849-0349
INFORMATION FOR SEO ID NO: 2
SEQUENCE CHARACTERISTICS:
 TYPE: DNA
ORGANISM: Artificial Sequence
 NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
```

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Basik, Mark
 US-08-734-973-36/c
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 CONTRESPONDENCE ADDRESS:
STREET: 1800 One M&T Plaza
STREET: 1800 One M&T Plaza
CITY: Butfalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM COMPUTER: SANDER: Wordperfect for Windows
COMPUTER: IBM COMPUTER: US/OS/NICKOSOft Windows
SOFTWARE: Wordperfect for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OS/34,973
FILING DATE: October 1996
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAMICATION FOR SEQ ID No: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 18 nucleotides
TYPE: nucleo cid
 DB 1; Length 18; 67;
 1.5%; Score 16; DB 1; Length 18;
100.0%; Pred. No. 67;
tive 0; Mismatches 0; Indels
 0; Indels
 Sequence 6, Application US/08734973

Sequence No. 541247

Patent No. 541247

GENERAL INFORMATION:

APPLICANT: Stoler, Daniel L.

APPLICANT: Anderson, Garth R.

TITLE OF INVENTION: Genomic Instability

NUMBER OF SEQUENCE 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodvear
 Mismatches
 Sequence 34, Application US/08734973
Patent No. 5912147
 1.5%; Scc.
100.0%; Pre
0;
 STRANDEDNESS: single-stranded
 1793 TGTGTGTGTGTGTG 1808
 1793 TGTGTGTGTGTGTG 1808
 16 TGTGTGTGTGTGTG 1
 Query Match
Best Local Similarity 100.(
Matches 16; Conservative
 Query Match
Best Local Similarity 100.
Matches 16; Conservative
 TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
 MOLECULE TYPE: DNA HYPOTHETICAL: NO
 -08-734-973-34/c
 US-08-734-973-6
 US-08-734-973-2
```

GENERAL INFORMATION: APPLICANT: Stoler, Daniel L.

```
APPLICANT Adderson Garth X.

TITLE OF INVESTION: A Rapid Means For Quantitating TITLE OF INVESTION: A Rapid Means For Quantitating TITLE OF INVESTION: A Rapid Means For Quantitating MAREN OF SEQUENCE: June Address, Mode & Goodyear CITY. Black Display of Place and Compared to the Compar
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Length 15;
1.4%; Score 15; DB 1;
100.0%; Pred. No. 68;
tive 0; Mismatches C
 1.4%; Score 15; DB 100.0%; Pred. No. 68; tive 0; Mismatches
 NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFRENCE/DOCKET NUMBER: BB-1064-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
 FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/346,456
FILING DATE: 28 NOVEMBER 1994
ATTORNEY/AGENT INFORMATION:
 Sequence 9, Application US/08849021; Patent No. 5955276; GENERAL INFORMATION:
 US-08-849-021-8/c
; Sequence 8, Application US/08849021
; Patent No. 5955276
 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
 1794 GIGIGIGIGIGIG 1808
 1793 IGTGTGTGTGTGT 1807
 15 rerererererer
 Query Match
Best Local Similarity 100.0
Matches 15; Conservative
 TELEFAX: 302-992-7949
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
 Query Match
Best Local Similarity 100.
Matches 15; Conservative
 TYPE: nucleic acid
STRANDEDNESS: single
 US-08-849-021-8
 US-08-849-021-9
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0
 Gaps
 Score 16; DB 1; Length 18;
Pred, No. 67;
 0; Indels
 CITY: WILMINGTON STREET CITY: WILMINGTON STATE: DELAWARE COUNTRY: U.S.A.;
ZIP: 19898
COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY DISK COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25 CURRENT APPLICATION DATA: APPLICATION DATA:
 GENERAL INFORMATION:
APPLICANT: MORGANTE, MICHELE
APPLICANT: WORGANTE, JULIE M.
TITLE OF INVENTION: PRIMERS FOR THE
TITLE OF INVENTION: PRIMERS FOR THE
TITLE OF INVENTION: PETECTION OF GENETIC
TITLE OF INVENTION: POLYMORPHISMS
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESSE: E. I. DU PONT DE NEMOURS AND
ADDRESSEE: E. I. DU PONT DE NEMOURS AND
ADDRESSEE: COMPANY
SIRRET: 1007 MARKET STREET
 Mismatches
 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION 435
PRILAM DATE: 08/346,456
FILING DATE: 28 NOVEMBER 1994
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/POCKET NUMBER: BB-1064-A
TELEPHONE: 302-892-8112
 NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 03551.0
TELERATION INFORMATION:
TELEPAIN: (716) 849-0349
INFORMATION FOR SEQ ID NO: 36: SEQUENCE CHARACTERISTICS:
LENGTH: 18 mucleotides
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
 JS-08-849-021-7/c
; Sequence 7, Application US/08849021
; Patent No. 5955276
 Query Match
Best Local Similarity 100.0%; Pi
Matches 16; Conservative 0;
 1793 TGTGTGTGTGTGTGTG 1808
 MOLECULE TYPE: DNA (genomic)
 16 rererererererere
 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
 MOLECULE TYPE: DNA
HYPOTHETICAL: NO
US-08-734-973-36
 US-08-849-021-7
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 Gaps
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 DB 1; Length 15;
 Indels
 0; Indels
 GENERAL INCORNATION:
APPLICANT: MORGANTE,
APPLICANT: MORGANTE,
TITLE OF INVENTION: COMPOUND MICROSATELLITE
TITLE OF INVENTION: DETECTION OF GENETIC
TITLE OF INVENTION: DOLVMORPHISMS
NUMBER OF SEQUENCES: 89
CORRESPONDENCES: B. I. DU PONT DE NEMOURS AND
ADDRESSEE: COMPANY
STREET: 1007 MARKET STREET
CITY: WILMAINGTON
STREET: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPATIS PATIENT IN RELEASE #1.0, VERSION 1.25
SUCHREEN APPLICATION NUMBER: US/08/849,021
 APPLICANT:
```

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Gaps
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0
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 Sequence 24. Application US/08787321A

Patent No. 6180777

GENERAL INFORMATION:
TILLE OF INVENTION: SYNTHESIS OF BRANCHED NUCLEIC ACIDS
TILLE REFERENCE: (1300)-11999-002

CURRENT APPLICATION NUMBER: US/08/787,321A

CURRENT FILING DATE: 1997-01-03

EARLIER APPLICATION NUMBER: US PROV 60/009,918

EARLIER PEPLICATION NUMBER: US PROV 50/009,918

SAGINGER OF SEQ ID NOS: 27

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 24

LENGTH: 15

LENGTH: 15
 DB 1; Length 15; 68;
 Length 15;
 Indels
 Indels
 FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: oligonuclectide
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PATENT IN RELEASE #1.0, VERSION 1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,021
 1.4%; Score 15; DB 1;
100.0%; Pred. No. 68;
tive 0; Mismatches
 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,456
FILING DATE: 28 NOVEMBER 1994
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REPERRECE/DOCKET NUMBER: BB-1064-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-912
TELEFAX: 302-992-912
 1.4%; Score 15;
100.0%; Pred. No.
tive 0; Mismatc
 US-09-081-646-733
; Sequence 733, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 15 base pairs TYPE: mucleic acid STRANDEDNESS: single
 , MOLECULE TYPE: DNA (genomic)
US-08-849-021-10
 1794 GIGIGIGIGIGIG 1808
 CTGTG 1808
 TYPE: DNA ORGANISM: Artificial Sequence
 15 Gréréréréreren 1
 Kenneth
 Query Match
Best Local Similarity 100.0
Matches 15; Conservative
 Query Match
Best Local Similarity
Matches 15; Conserva
 1794 GTGTGTGTGT
 JS-08-787-321-24/c
 US-08-787-321-24
 ઠે
 ઠે
 유
 ö
 Gaps
 ..
0
 Length 15;
 Indels
 COUNTRY: WIGHLANDSON
STATE: DELAWARS
ZID: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,021
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/346,456
FILING DATE: 28 NOWENBER 1994
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AZAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/POCKET NUMBER: BB-1064-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
 Sequence 10, Application US/08849021
Sequence 10, Application US/08849021
Batent No. 5555276
GENERAL INFORMATION:
MORGANTE, MICHELE
APPLICANT: WOREL, JULIE M.
TITLE OF INVENTION: PRIMERS FOR THE
TITLE OF INVENTION: PRIMERS FOR THE
TITLE OF INVENTION: POLYMORPHISMS
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS: 80
CORRESPONDENCE ADDRESS: ADDRESSEE: COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAMBED
 TITLE OF INVENTION: COMPOUND MICROSATELLITE
TITLE OF INVENTION: PRIMERS FOR THE
TITLE OF INVENTION: DETECTION OF GENETIC
TITLE OF INVENTION: POLYMORPHISMS
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND
ADDRESSEE: COMPANY
STREET: 1007 WARKET STREET
CITY: MILMINGTON
 COMPOUND MICROSATELLITE PRIMERS FOR THE
 Mismatches
 Score 15;
Pred. No.
 Query Match

1.4%; Sc
Best Local Similarity 100.0%; P
Matches 15; Conservative 0;
 E: FLOPPY DISK
IBM PC COMPATIBLE
 / TOPOLOGY: linear
// MOLECULE TYPE: DNA (genomic)
US-08-849-021-9
 1793 TGTGTGTGTGTGT 1807
 TELEPHONE: 302-892-8112
TELEFAX: 302-92-7949
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
 rerererererer 15
 15 base pairs
 TYPE: nucleic acid
STRANDEDNESS: single
 COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
 COMPUTER:
```

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Sequence 2, Application US/07971978

Sequence 2, Application US/07971978

Patent No. 5614617

Patent No. 5614617

Patent No. 5614617

TITLE OF INVENTION: Modified Oligonaclectides that Detect and Modulate TITLE OF INVENTION: Modified Oligonaclectides that Detect and Modulate TITLE OF INVENTION: Gene Expression

TITLE OF INVENTION: Gene Expression

TITLE OF INVENTION: 65

CORRESPONDENCE ADDRESS: 65

CORRESPONDENCE ADDRESS: 65

CORRESPONDENCE ADDRESS: 65

CORRESPONDENCE ADDRESS: 65

COTT: Philadelphia Place - 46th Floor

CITY: Philadelphia Place - 46th Floor
 Query Match

1.4%; Score 15; DB
Best Local Similarity 100.0%; Pred. No. 74;
Matches 15; Conservative 0; Mismatches
 COMPUTER: 0.5.A.

ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/971,978
FILING DATE: February 18, 1993
CLASSIFICATION BATA:
APPLICATION NUMBER: 07/558,806
FILING DATE: JULY 27, 1990
ATTORNEY AGENT INFORMATION:
NAME: JOSEPH LUCCI.
RECISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: 15IS-0333
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 215-568-3100
 1813 TATATATATATAT 1827
 PEATURE:
NAME/KEY: Modified-site
 U.S.A.
 US-07-971-978-2/c
 COUNTRY:
 ò
 Sequence 2, Application US/07971978

Sequence 2, Application US/07971978

Patent No. 5614617

GENERAL INFORMATION:
APPLICANT: Cook and Sanghvi
TITLE OF INVENTION: Nuclease Resistant, Pyrimidine
TITLE OF INVENTION: Modified Oligonaleotides that Detect and Modulate
TITLE OF INVENTION: Gene Expression
TITLE OF INVENTION: Gene Expression
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
ADDRESSEE: No. 5614617xis
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
 ö
TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
TITLE OF INVENTION: Cancer Cells
FILE REPREMENCE: 01107.74664
CURRENT APPLICATION NUMBER: US/09/081,646
CURRENT PILING DATE: 1988-05-20
EARLIER APPLICATION NUMBER: 60/047,352
EARLIER PILING DATE: 1997-05-21
NUMBER OF SEQ ID NOS: 871
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 733
LENGTH: 15
TYPE: DNA
TYPE: DNA
CORGANISM: Homo sapiens
US-09-081-646-733
 Gaps
 ö
 Query Match 1.4%; Score 15; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 68; Matches 15; Conservative 0; Mismatches 0; Indels
 COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordberfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/971,978
FILING DATE: February 18, 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/558,806
FILING DATE: July 27, 1990
ATTORNEY AGENT INFORMATION:
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-0333
TELEPHONE: 215-568-3100
TELEPHONE: 215-568-349
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TVPF: nucleic acid
 2231 CATGITTGCACCITT 2245
 MOLECULE TYPE: DNA (genomic)
 NAME/KEY: Modified-site LOCATION: 2
 U.S.A.
 COUNTRY:
 US-07-971-978-2
 RESULT 79
 ò
```

```
ö
 DB 1; Length 16; 74;
 0; Indels
 NAME/KEY: Modified-site
| LOCATION: 12 | LOCATION: 14 |
| FEATURE: NAME/KEY: Modified-site |
| NAME/KEY: Modified-site |
| LOCATION: 14 |
| OTHER INFORMATION: 6-aza-thymidine substitution |
US-07-971-978-2
OTHER INFORMATION: 6-aza-thymidine substitution PEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: 6-aza-thymidine substitution
 LOCATION: 6-000 G-000 G-000 GOOSTITUTION FEATURE:
 NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: 6-aza-thymidine substitution
 FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
CTHEN: 10
CTHEN: NFORMATION: 6-aza-thymidine substitution
FEATURE:
```

```
RESULT 82
US-09-371-772B-6070

US-09-371-772B-6070

Sequence 6070, Application US/09371772B

Patent No. 6566127

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Rescoedy, Jaime

APPLICANT: Brinchcomb, Dan

APPLICANT: Brinch Dane: 1990-08-10

FILE REFERENCE: MBHB00, 876-J (237/198)

CURRENT APPLICATION NUMBER: US 60/005, 974

PRIOR FILING DATE: 1996-01-08

NUMBER OF SEQ ID NOS: 14225

SOFTWARE: Patentin version 3.0

SEQ ID NO 6070

LEARTH APPLICATION NUMBER: US 60/005, 974

PRIOR FILING DATE: 1996-01-08

NUMBER OF SEQ ID NOS: 14225

SOFTWARE: Patentin version 3.0

SEQ ID NO 6070
 Ouery Match
Best Local Similarity 53.3%; Pred. No. 74;
Matches 8; Conservative 7; Mismatches 0; Indels
Query Match
1.4%; Score 15; DB 1; Length 16;
Best Local Similarity 46.7%; Pred. No. 74;
Matches 7; Conservative 8; Mismatches 0; Indels
 COUNTRY:
21P: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: TESTER Windows Version 2.0
SOFTWARE: FastERQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,998
TI,ING DATE: 21-MAY-1997
 Sequence 400, Application US/08859998;
Sequence 400, Application US/08859998;
Patent No. 5994076;
APPLICANT: Chenchik, Alex
APPLICANT: Jokhadze, George
APPLICANT: Jokhadze, George
APPLICANT: Bibilashvilli, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIF
TITLE OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STREET: 220 Sand Hill Road, Suite 100
CITY: Menlo Park
STREET: CA
 1794 GIGIGIGIGIGIG 1808
 1793 TGTGTGTGTGTGT 1807
 2 ugugugugugugugu 16
 TYPE: RNA
CRGANISM: Homo sapiens
US-09-371-772B-6070
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 d
 RESULT 81
US-09-371-772B-6068

Sequence 6068, Application US/09371772B

Sequence 6068, Application US/09371772B

Sequence 6068, Application US/09371772B

Sequence 6068, Application

Resolution: Resolution: Pavco, Pam

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Revolution: Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Becobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases

CURRENT APPLICATION NUMBER: US 60/005,974

PRIOR APPLICATION NUMBER: US 60/005,974

PRIOR FILING DATE: 1996-01-08

NUMBER OF SEQ ID NOS: 14225

SEQ ID NO 6068

TANE: Battle APPLICATION NUMBER: US 60/005,974

SEQ ID NO 6068

TANE: Battle APPLICATION NUMBER: US 60/005,974

FILING DATE: 1996-01-08

SEQ ID NO 6068

TANE: Battle APPLICATION NUMBER: US 60/005,974

TANE: Battle APPLICATION NUMBER: US 60/005,974

PRIOR FILING DATE: 1996-01-08

SEQ ID NO 6068

TANE: Battle APPLICATION NUMBER: US 60/005,974

TANE: Battle APPLICATION NUMBER: US 60/005,974

SEQ ID NO 6068

TANE: Battle APPLICATION NUMBER: US 60/005,974

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 Gaps
 Query Match
1.4%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 15; Conservative 0; Mismatches 0; Indels
 FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: 6-aza-thymidine substitution
FRAURE:
 LOCATION: 12
OTHER INFORMATION: 6-aza-thymidine substitution
) LOCATION: 14
; OTHER INFORMATION: 6-aza-thymidine substitution
US-07-971-978-2
 LOCATION: 2
OTHER INFORMATION: 6-aza-thymidine substitution
 LOCATION: 4
OTHER INFORMATION: 6-aza-thymidine substitution FEATURE:
 LOCATION: 6
OTHER INFORMATION: 6-aza-thymidine substitution
 LOCATION: 8
OTHER INFORMATION: 6-aza-thymidine substitution
 1813 TATATATATATAT 1827
 MOLECULE TYPE: DNA (genomic)
FEATURE:
 NAME/KEY: Modified-site LOCATION: 12
 NAME/KEY: Modified-site LOCATION: 6
 FEATURE:
NAME/KEY: Modified-site
 NAME/KEY: Modified-site
 NAME/KEY: Modified-site
 NAME/KEY: Modified-site
 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 TYPE: RNA
CRGANISM: Homo sapiens
US-09-371-772B-6068
 linear
 LENGTH: 16 bas
TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: line
```

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FEATURE:
 Best Local
Matches
 RESULT 86
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 g
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 Gabs
 ò
 Length 32;
 1.4%; Score 15; DB 1; Length 32; 67.7%; Pred. No. 1.5e+02; tive 0; Mismatches 10; Indels
 APPLICANT: Chenchik, Alex
APPLICANT: Chenchik, Alex
Jokhadze, George
Bibilashvilli, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
EXPRESSION
 ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRING PAPLICATION DATA:
APPLICATION NUMBER: US/99/225,928
FILING DATE: 05-Jan-1999
CLASSIFICATION: «Unknown»
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:

NAME: Field, Bret E.

REGISSTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-322-5070
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
 1731 GCTTGTGGCAAGTGAATTTGCCTGTAACAAG 1761
) OTHER INFORMATION: oligonucleotide primer US-08-859-998-400
 2 GCTTGTTACAGGCAAATTCACTTGCCACAAG 32
 NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
INFORMATION FOR SEQ ID NO: 400:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
 US-09-225-928-400
; Sequence 400, Application US/09225928
; Patent No. 6352829
; GENERAL INFORMATION;
 TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 400:
 LENGIH: 32 base pairs
 TYPE: nucleic acid
STRANDEDNESS: single
 NUMBER OF SEQUENCES: 1375
 SEQUENCE CHARACTERISTICS
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
 LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
PEATURE:
 Query Match
Best Local Similarity 67.7%
Matches 21; Conservative
 COUNTRY: US
 RESULT 84
 8
```

```
ö
 / Match 1.4%; Score 15; DB 1; Length 32; Local Similarity 67.7%; Pred. No. 1.5e+02; No. 21; Conservative 0; Mismatches 10; Indels
 Length 32;
 10; Indels
 APPLICANT: Chenchik, Alex
APPLICANT: Chenchik, Alex
Jokhadze, George
Bibliashvilli, Robert
TITLE OF INVENTION: METHOD OF ASSAXING DIFFERENTIAL
EXPRESSION
 COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
CORPUTER: IBM Compatible
CORPUTER: IBM Compatible
SOFTWARE: FastSEQ for Windows Version 2.0
SOFTWARE: (100 NOTAE: (100 NOTAE
OTHER INFORMATION: oligonucleotide primer; SEQUENCE DESCRIPTION: SEQ ID NO: 400: US-09-225-928-400
) SEQUENCE DESCRIPTION: Oligonucleotide primer ; SEQUENCE DESCRIPTION: SEQ ID NO: 400: US-09-225-201B-400
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
 Query Match 1.4%; Score 15; DB 1; I
Best Local Similarity 67.7%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 10;
 1731 GCTTGTGGCAAGTGAATTTGCCTGTAACAAG 1761
 1731 GCTTGTGGCAAGTGAATTTGCCTGTAACAAG 1761
 2 derretracadecaaarreaerreceaeaa 32
 2 gcirigiracaggaaaaricacrigaaaaa 32
 Sequence 400, Application US/09225201B
Patent No. 6489455
GENERAL INFORMATION:
 LENGTH: 32 base pairs
 TYPE: nucleic acid
STRANDEDNESS: single
 NUMBER OF SEQUENCES: 1375
 TOPOLOGY: linear
MOLECULE TYPE: DNA
 COUNTRY: US
 RESULT 85
US-09-225-201B-400
 FEATURE:
 Query Match
```

Gaps

ö

1; Indels

```
GENERAL INCORMATION:
APPLICANT: Michael D. West
APPLICANT: Michael D. West
APPLICANT: Woodring E. Wright
APPLICANT: Woodring E. Wright
APPLICANT: Woodring E. Wright
APPLICANT: Blizabeth Blackburn
TITLE OF INVENTION: TELCMERASE ACTIVITY
TITLE OF INVENTION: TELCMERASE ACTIVITY
TITLE OF INVENTION: TELCMERASE ACTIVITY
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
CITY: Los Angeles
STRATE: California
COUNTRY: U.S.A.
ZIP: 90071-206
COMPUTER: READABLE FORM:
MEDIUM TYPE: Storest Since STRATE:
COUNTRY: U.S.A.
ZERATING SYSTEM: IBM P.C. DOS 5.0
COMPUTER: ROOMPERIECT S.I.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/060,952C
TILING DATE: May 13, 1993
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: 00/038,766
FILING DATE: May 13, 13, 293
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard U.
RECISTRATION NUMBER: 202/045
FELECOMMUNICATION NUMBER: 202/045
 DB 1; Length 16;
 DB 1;
 Query Match
1.4%; Score 14.4; D
Best Local Similarity 93.8%; Pred. No. 87;
Matches 15; Conservative 0; Mismatches
 1.4%; Score 14.4;
 Sequence 57, Application US/08060952C Patent No. 5695932
TELEPHONE: (213) 489-1600
TELEFAX: (713) 955-0440
TELEX: 67-3510
INPORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 1793 TGTGTGTGTGTGTG 1808
 : (213) 489-1600
(213) 955-0440
 TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
 TYPE: nucleic acid
 linear
 linear
 STRANDEDNESS
 TELEPHONE:
 ;
TOPOLOGY:
US-08-153-051B-58
 RESULT 88
US-08-060-952C-57
 Query Match
 ઠે
 g
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 Sequence 40, Application US/09344520

Patent No. 603176

GRNERAL INFORMATION:
APPLICANT: Fram Bennett
APPLICANT: Lex M. Cowsert
APPLICANT: Lex M. Cowsert
APPLICANTIN: ANTISENSE MODULATION OF integrin beta 3 EXPRESSION
FILE REFERENCE: RTS-0070
CURRENT APPLICATION NUMBER: US/09/344,520
CURRENT PILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 40
LENGTH: 18
FURNIT SECONDER COMMENT OF SEQ ID NOS: 47
SEQ ID NO 40
FILENGTH: 18
 Gaps
 ö
 DB 1; Length 18;
 2; Indels
 ; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-344-520-40
 Query Match
1.4%; Score 14.8; D
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches
 COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,051B
FILING DATE: No. 5645986ember 12, 1993
PRIOR APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: storage
 NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 204/195
TELECOMMUNICATION INFORMATION:
 APPLICATION NUMBER: 08/038,766
FILING DATE: March 24, 1993
TTORNEY/AGENT INFORMATION:
 E: Lyon & Lyon
633 West Fifth Street
Suite 4700
 1794 GIGIGIGIGIGIGI 1811
 18 Grererrrarerererer 1
 TYPE: DNA ORGANISM: Artificial Sequence
 NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Ly
 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
 90071
 -08-153-051B-58
 STREET:
STREET:
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```

Length 16;

```
APPLICANT: Michael J.
 Catherine M. Strahl
Michael J. Mceachern
Jerry Shay
Woodring E. Wright
Elizabeth H. Blackburn
 Sequence 80, Application US/08819867
Patent No. 6007989
 Michael D. West
Calvin B. Harley
Scott L. Weinrich
 TOPOLOGY:
US-08-819-867-80
 à
 ö
 Gaps
 ö
 1.4%; Score 14.4; DB 1; Length 16;
93.8%; Pred. No. 87;
 y cequence 58, Application US/08151477A

PRIERAL INFORMATION:
APPLICANT: Michael D. West
APPLICANT: Jerry W. Shay
APPLICANT: Blizabeth Blackburn
APPLICANT: Blizabeth Blackburn
APPLICANT: Blizabeth Blackburn
APPLICANT: Scott L. Weinrich
APPLICANT: Catharine Stranh
APPLICANT: Catharine Stranh
APPLICANT: Catharine Stranh
APPLICANT: Homayoun Vaziri
TITLE OF INVENTION: TERNAPY AND DIAGNOSIS OF
TITLE OF INVENTION: LENGTH AND/OR TELOMERAE
TITLE OF INVENTION: LENGTH AND/OR TELOMERASE
CORRESPONDENES: 58
CORRESPONDENES: 58
CORRESPONDENES: 1.vor. f. 1.
 Indels
 ;
 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 5.5" Diskette, 1.44 Mb
MEDIUM TYPE: 5.5" Diskette, 1.44 Mb
MEDIUM TYPE: 5.5" Diskette, 1.44 Mb
COMPUTER: 1BM COMPATION
COMPATION SYSTEM: 1BM P.C. DOS 5.0
SOFTWARE: Factory Oversion 1.5
CURRENT APPLICATION DATA: 78/08/151,477A
RILING DATE: No. 5830644ember 12, 1993
APPLICATION NUMBER: 08/038,766
FILING DATE: March 24, 1993
ATORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 202/189
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
TELERAX: (213) 955-0440
TELERAX: 67-3510
INFORMATION FOR SEQ ID NO: 58: SEDGUENCE CHARACTER/STICS: LENGTH: 16 base pairs
TYPE: nucled caid
STRANDEDNESS: single
93.8%; Pred. No. 87;
tive 0; Mismatches
 ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
 1793 TGTGTGTGTGTG 1808
 1 recerererererere
 Query Match
Best Local Similarity 93.8
Matches 15; Conservative
 Best Local Similarity 93.8
Matches 15; Conservative
 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
 US-08-151-477A-58
 ò
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0
 1.4%; Score 14.4; DB 1; Length 16; 93.8%; Pred. No. 87;
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage FORM:
COMPUTER: IBM COMPATIBLE FORM:
SOFTWARE: PRESENCE FORM:
APPLICATION NUMBER: US/08/819,867
FILING DATE: MARCH 14, 1997
CLASGIFICATION NUMBER: 08/153,051
FILING DATE: NO. 6007989ember 12, 1993
APPLICATION NUMBER: STORAGE FORM:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/232
TELECOMMUNICATION: INFORMATION:
TELESPHONE: (213) ASP.1600
 0; Mismatches
 Sequence 57, Application US/08464011B
Patent NO. 6368789
GENERAL INFORMATION:
APPLICANT: Michael D. West
 1793 TGTGTGTGTGTGTG 1808
 (213) 489-1600
(213) 955-0440
 TELEX: 67-3510
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 16 base pairs TYPE: nucleic acid STRANDEDNESS: single
 Query Match
Best Local Similarity 93.8
Matches 15; Conservative
 US-08-464-011B-57
 g
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Gaps

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Indels

0; Mismatches

1793 TGTGTGTGTGTGTGTG 1808

RESULT 90

```
APPLICANT: Ribozymenter Pharmaceuticals, Inc.
APPLICANT: Ribozymen
APPLICANT: Ribozymen
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
APPLICANT: Escobedo, Jaime
APPLICANT: Escobedo, Jaime
APPLICANT: Bacobedo, Jaime
TILLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TILLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
CURRENT APPLICATION NUMBER: US 60/005, 974
PRIOR FILING DATE: 1995-08-10
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
SEQ ID NO 6071
 Query Match
1.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 87;
Matches 15; Conservative 0; Mismatches 1; Indels
 TECLOMERE LENGTH AND/OR TELOMERASE ACTIVITY
 COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FESTESED for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/378,535
FILING DATE: 20-Aug-1999
CLASSIFICATION OF CHROOM->
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/819,867
FILING DATE: CURACOM->
ATTORNEY/AGENT INFORMATION:
NAME: CHAMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/232
TELEFRANCE/DOCKET NUMBER: 224/232
TELEFRAN: (213) 955-0440
CONDITIONS RELATED TO
 CITY: Los Angeles
STATE: California
COUNTX: U.S.A.
ZIP: 9071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 80:
 CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 Weet Fifth Street
Suite 4700
 RESULT 93
US-09-371-772B-6071
Sequence 6071, Application US/09371772B
; Patent No. 6566127
GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO: 80: SEQUENCE CHARACTERISTICS: LENGTH: 16 base pairs TYPE: nucleic acid STRANDEDNESS: single
 1793 TGTGTGTGTGTGTG 1808
 NUMBER OF SEQUENCES: 80
 US-09-378-535-80
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 Gaps
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 Jerry W. Shay
Woodring E. Wright
FITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
TELATED TO TELOMERE LENGTH AND/OR
TELOMERASE ACTIVITY
 Query Match 1.4%; Score 14.4; DB 1; Length 16; Best Local Similarity 93.8%; Pred. No. 87; Matches 15; Conservative 0; Mismatches 1; Indels
 Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
 COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PERFOCE 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,011B
FILING DATE: OS-Jun-1995
CLASSIFICATION OF-Jun-1995
CLASSIFICATION NUMBER: 07/882,438
FILING DATE: MAY 13, 1993
APPLICATION NUMBER: 08/038,766
FILING DATE: MAY 13, 1993
APPLICATION NUMBER: 08/060,952
FILING DATE: MAY 13, 1993
ATTORNEY/AGENT INFORMATION:
NAME: WARDLER: 31,337
REFERENCE/DOCKET NUMBER: 32,327
 COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
 TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 57: US-08-464-0118-57
 NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
 Sequence 80, Application US/09378535
Fatent No. 6551774
GENERAL INFORMATION:
Calvin B. Harley
Scott L. Weinrich
Catherine M. Strahl
Michael J. Meeachern
Jerry Shay
Woodring E. Wright
Blizabeth H. Blackburn
Nam Woo Kim
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
 1793 IGIGIGIGIGIGIG 1808
 TYPE: nucleic acid
STRANDEDNESS: single
 US-09-378-535-80
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 Query Match
1.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 50.0%; Pred. No. 87;
Matches 8; Conservative 7; Mismatches 1; Indels
 RESULT 94
US-08-105-483-235
is equence 215, Application US/08105483
j Patent No. 5494807
j Patent No. 5494807
j GENERAL INFORMATION:
j APPLICANT: Paoletti, Enzo
title OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
j NUMBER OF SEQUENCES: 462
correspondence Address: Addresses: Addresses: Curtis, Morris & Safford
hDRESSEE: Curtis, Morris & Safford
hDRESSEE: C/O William S. Frommer
city: New York
 COMPUTER LUGAA

ZIP: 1036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER PE FLOPPY DISK
FLOPPY APPLICATION DATA:
APPLICATION NUMBER: US 07/847,951
FLING DATE: US 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAMME: Frommer, William S.
REFERROCH/DOCKET NUMBER: 45.506
REFERROCH/DOCKET NUMBER: 45.506
REFERROCH/DOCKET NUMBER: 25.506
REFERROCH/DOCKET NUMBER: 25.506
REFERROCH/DOCKET NUMBER: 25.506
REFERROCH/DOCKET NUMBER: 25.506
TELEPAX: (212) 840-0313
INFORMATION FOR SEQ ID NO: 235:
LENGTH: 17 base pairs
LENGTH: 17 base pairs
LENGTH: 17 base pairs
LYPE: NUCLeic acid
STRANDENNESS: single
 1794 GIGIGIGIGIGIGI 1809
 LENGTH: 16
TYPE: RNA
CRGANISM: Homo sapiens
US-09-371-772B-6071
 USA
 COUNTRY:
```

ö DB 1; Length 17 1; Indels Query Match
1.4%; Score 14.4; Di
Best Local Similarity 93.8%; Pred. No. 94;
Matches 15; Conservative 0; Mismatches US-08-105-483-235

RESULT 95
US-08-373-124A-1058/c
; Sequence 1058, Application US/08373124A
; Patent No. 5546042
Patent No. 5546042
; PAPERRAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.

APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: TARGET USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 Weet Fifth Street
STREET: 633 Weet Fifth Street
STREET: 634 Weet Fifth Street
STREET: 634 Weet Fifth Street
COUNTRY: U.S.A.
21P: 30071
COUNTRY: U.S.A.
21P: 30071
COUNTRY: U.S.A.
21P: 30071
COMPUTER: SEADABLE FORM:
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb
MEDIUM TYPE: 3.7 Diskette, 1.995
APPLICATION NUMBER: 0.7/98/313.124A
FILING DATE: December 7, 1992
APPLICATION NUMBER: 0.7/98/422
ATDORNEY AGENT INFORMATION:
APPLICATION NUMBER: 3.2, 327
REFERENCE/DOCKET WUMBER: 26, 1992
APPLICATION NUMBER: 26, 1992
APPLICATION NUMBER: 27, 327
REFERENCE/DOCKET WUMBER: 26, 1992
ATDORNEY AGENT INFORMATION:
TELEFAX: 67-1510
TELEFAX: 67-1510
INFORMATION FOR SEQ ID NO: 1058:
SEGUENCE CHARACTERISTICS:
LENGTH: 17 Dase pairs
TYPE: nucleic acid ; TOPOLOGY: linear US-08-373-124A-1058

DB 1; Length 17; Indela 1.4%; Score 14.4; D: Best Local Similarity 93.8%; Pred. No. 94; Matches 15; Conservative 0; Mismatches

1811 TGTATATATATATA 1826

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RESULT 96
US-08-709-235
US-08-709-235
Sequence 235, Application US/08709209
FREEDT No. 5762938
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
TITLE OF INVENTION: STRAIN
NUMBER OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 462
CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, Morris & Safford
ADDRESSEE: CURTIS, Morris & Safford
ADDRESSEE: COMMILIAM S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY

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ô
 DB 1; Length 17;
 Sequence 1058, Application US/08435628
Sequence 1058, Application US/08435628
Batent No. 5817366
GENERAL INFORMATION:
APPLICANT: Brinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: Draper, James
APPLICANT: Draper, James
APPLICANT: Jarvis, Thale
APPLICANTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTERNOIS
ADDRESSES: Lyon & Lyon
STREET: Galgences: 2627
CORRESPONDENCE ADDRESS:
ADDRESSES: Lyon & Lyon
STREET: Galfornia
CONTRY: U.S.A.
ZIP: 90071
COMPUTER: Edhable FORM:
MEDIUM TYPE: Storage
CONGUTER: IBM Compacible
CONGUTER: IBM Compacible
CONGUTER: IBM Compacible
CONGUTER: Delay DATA:
MEDIUM TYPE: Galgences: 08/08/435,628
FILING DATE: Galgences: 08/08/435,628
FILING DATE: MAY 18, 1995
APPLICATION NUMBER: 08/08/435,466
FILING DATE: MAY 18, 1994
APPLICATION NUMBER: 08/192,943
APPLICATION NUMBER: 08/192,943
APPLICATION NUMBER: 07/936,422
ATTORNEY/AGENT INFORMATION:
NAME: WARDLE: RADLEC 26, 1992
 Indels
SOFTWARE: Patentin Release #1.0, Version #1.25

CURERNY APPLICATION DATA:
APPLICATION NUMBER: US/08/458,101
FILING DATE: 01-01-1995
GIASSIFCATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
NAME: Frommer, William S.
FREGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2740
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 840-0712
INPORMATION FOR SEQ ID NO: 235:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
105-08-458-101-235
 Query Match 1.4%; Score 14.4; I
Best Local Similarity 93.8%; Pred. No. 94;
Matches 15; Conservative 0; Mismatches
 1777 TITATATIGIAATAT 1792
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 Ouery Match
1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 94;
Matches 15; Conservative 0; Mismatches 1; Indels
 US-08 +58#-101-225

1 Sequence 235, Application US/08458101

Patent No. 5766599

GENERAL INFORMATION

APPLICANT: Perkus, Marion E.

APPLICANT: Taxlor, Jill

APPLICANT: Taxlor, Jill

APPLICANT: No. 576599ton, Elizabeth K.

APPLICANT: Inmbach, Keith J.

APPLICANT: Limbach, Keith J.

APPLICANT: Johnson, Gerard P.

APPLICANT: Johnson, Gerard P.

APPLICANT: Audonner, Jean-Christophe Francis

APPLICANT: STRAIN

NUMBER OF INVENTION: STRAIN

NUMBER OF SUCUENCES: 467

CORRESSES: C/o William S. Frommer

CITY: New York

STRAIE: NY

COUNTRY: NS

STRAIE: NS

COUNTRY: NS

COUNTRY: USA
 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,209
FILING DATE: 21-AUG-1996
CLASSIFFCATION: 424
PRIOR APPLICATION NUMBER: US 08/105,483
FILING DATE: 12-AUG-1993
APPLICATION NUMBER: US 08/105,483
FILING DATE: 12-AUG-1993
APPLICATION NUMBER: US 07/847,951
FILING DATE: 12-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
FILING DATE: (25,506
REFERENCE/DOCKET NUMBER: 45,4310-2400
FELEPHONE: (212) 840-3333
TELEPHONE: (212) 840-0712
INFORMATION FOR SEQ ID NO: 235:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: single
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 1777 TITATATIGIAATAT 1792
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 셤
 US-US-486-969-52
| Sequence 52, Application US/08486969
| Patent No. 584346
| GENERAL INFORMATION:
| APPLICANT: PAOLECTION:
| APPLICANT: Maki, Joanne
| TITLE OF INVENTION: RECOMBINANT POXVIEUS - RABIES
| TITLE OF INVENTION: COMPOSITIONS AND COMBINATION COMPOSITIONS AND USES
| TITLE OF INVENTION: COMPOSITIONS AND COMBINATION COMPOSITIONS AND USES
| TITLE OF INVENTION: COMPOSITIONS AND COMBINATION COMPOSITIONS AND USES
| TITLE OF INVENTION: COMPOSITIONS AND COMPOSITIONS AND USES
| CORRESPONDENCE ADDRESS: 55 COMPOSITION OF THE AVENDED OF THE A
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 DB 1; Length 17
 DB 1; Length 17;
 Indels
 Indels
 Score 14.4; D
Pred. No. 94;
0; Mismatches
 Query Match 1.4%; Score 14.4; Dest Local Similarity 93.8%; Pred. No. 94; Matches 15; Conservative 0; Mismatches
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMUNICATION INFORMATION:
TELEPAN: (213) 489-1600
TELEFAX: (213) 955-0440
TELER: 67-3510
INFORMATION FOR SEQ ID NO: 1058:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
 1811 TGTATATATATATA 1826
 TELEFAX: (212) 840-0712
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
 1.4%;
 Query Match
Best Local Similarity 93.84
Matches 15; Conservative
 LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 MOLECULE TYPE: CDNA
US-08-486-969-52
 linear
 US-08-435-628-1058
 US-08-486-969-52
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1777 TITATATIGIAATAT 1792

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Sequence 4155, Application US/0854040

PRIEMEAL INCORPUTE AT PAYOR, Demela APPLICANT: Machine Month Machine Ma
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Sequence 436, Application US/0822177A;
Sequence 436, Application US/0822177A;
Sequence 436, Application US/0822177A;
Septent No. S58239;
GENERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH FOLYMORPHISMS IN
TITLE OF INVENTION: (dG-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dewitt Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: Wisconsin
COUNTY: USA
COUNTY: USA
COMPUTER READABLE FORM:
MEDIUTER READABLE FORM:
COMPUTER FRADABLE FORM:
 Gaps
 APPLICANT: C. Frank Bennett
APPLICANT: C. Frank Bennett
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Lex M. Coweart
TITLE OP INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
FILE REPERENCE: 158H-0439
CURRENT APPLICATION NUMBER: US/09/496,694B
CURRENT FILING DATE: 2000-02-02
PRIOR FILING DATE: 1999-04-05
PRIOR FILING DATE: 1998-09-29
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 249
SEQ ID NO 235
LENGTH: 20
 Query Match 1.4%; Score 14.4; DB 1; Length 17; Best Local Similarity 81.2%; Pred. No. 94; Matches 13; Conservative 2; Mismatches 1; Indels
 Length 20;
 Indels
 Query Match
1.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3;
 ; OTHER INFORMATION: Antisense Oligonucleotide US-09-496-694B-235
 Sequence 235, Application US/09496694B Patent No. 6335194
GENERAL INFORMATION:
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 1814 ATATATATATATATGTACA 1832
 1 ACATATATATATAAACA 19
 1750 GCCTGTAACAAGCCAG 1765
 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
 PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
SEQ ID NO 6656
LENGTH: 17
 1 GCCUGUACCAAGCCAG 16
 TYPE: RNA
CRGANISM: Homo sapiens
US-09-371-772B-6656
 US-08-222-177A-436/c
 RESULT 104
US-09-496-694B-235
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 patent No. 6566127

| Patent No. 6566127
| Patent No. 6566127
| Patent No. 6566127
| Patent No. 6566127
| Patent No. 6566127
| Patent No. 6566127
| Patent No. Patent
 APPLICANT: Pavco, Pam
APPLICANT: Pavco, Pam
APPLICANT: Pavco, Pam
APPLICANT: Stinchcoub, Dan
APPLICANT: Stinchcoub, Dan
APPLICANT: Stinchcoub, Dan
APPLICANT: Escobedo, Jame
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MEHBOO, 876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1995-10-26
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 Gaps
 Gaps
 TYPE: DNA
ORGANISM: Artificial
FETURES
OTHER INFORMATION: Hypothetical Sequence for Exemplary Purposes
Fatent No. 6503710
US-09-321-005A-13
 Query Match
1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 94;
Matches 12; Conservative 3; Mismatches 1; Indels
 1.4%; Score 14.4; DB 1; Length 17;
93.8%; Pred. No. 94;
tive 0; Mismatches 1; Indels
 RESULT 103
US-09-371-772B-6656
; Sequence 6656, Application US/09371772B
; Parent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 1749 TGCCTGTAACAAGCCA 1764
 PatentIn version 3.0
 1891 ATATITCAATGITAGC 1906
 2 UGCCUGUACCAAGCCA 17
 16 ATATTTCAATGTCAGC 1
 Query Match
Best Local Similarity 93.8°
Matches 15; Conservative
 TYPE: RNA
CORGANISM: Homo sapiens
US-09-371-772B-1926
 RESULT 102
US-09-371-772B-1926
SOFTWARE: P
SEQ ID NO 13
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APPLICANT: SUNAWACHI, Hiroki
APPLICANT: TAKAHASHI, Michiaki
APPLICANT: TAKAHASHI, Michiaki
APPLICANT: TAKAHASHI, Michiaki
APPLICANT: TAKAHASHI, Michiaki
TITLE OF INTENTION: Wethod for Quality Control of an Attenuated Varicella Live Vaccine
FILE REPERENCE: 0216-0454P
CURRENT APPLICATION NUMBER: 0209-013,514
CURRENT FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: PCT/JP01/0678
PRIOR APPLICATION NUMBER: D2000-62734
PRIOR APPLICATION NUMBER: J2000-62734
PRIOR APPLICATION NUMBER: J2000-01-31
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 14
 ö
 Gaps
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0
 Sequence 27, Application PC/TUS9200282
GENERAL INFORMATION:
APPLICANT: OWENS, 105EPH K.
TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION
TITLE OF INVENTION: THEREIN.
NUMBER OF SEQUENCES:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
 Length 15;
 DB 1; Length 14;
81;
 0; Indels
 CORRESPONDENCES:
CORRESPONDENCES:
CORRESPONDENCES:
COUNTY: WASHINGTON
STATE:
D.C.
COUNTRY: U.S.A.
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00282
FILING DATE: 1992010
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26581
REFERENCE/DOCKET NUMBER: 26581
REFERENCE/DOCKET NUMBER: 26581
RELEFAX: 2020-202-0944
TELLEFAX: 202-861-3000
TELLEFAX: 202-861-3000
TELLEFAX: 202-861-3000
 DB 1;
89;
 Mismatches
 Query Match 1.3%; Score 14;
Best Local Similarity 100.0%; Pred. No.
 Score 14;
Pred. No.
 Ouery Match
Best Local Similarity 100.0%; P
Matches 14; Conservative 0;
 1813 TATATATATATA 1826
 14 rárarararara 1
 TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
 TYPE: DNA
, ORGANISM: Varicella virus
US-09-913-514-27
 STRANDEDNESS: single
 GOMI, Yasuyuki
 MOLECULE TYPE: CDNA PCT-US92-00282-27
 RESULT 108
PCT-US92-00282-27
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 g
 patence 4., Application Us/Usylsb14
Patent No. 6653069
GENERAL INPORMATION:
APPLICANT: SUNAMACHI, Hiroki
APPLICANT: TAKHASHI, Michiaki
FILE OF INVENTION: Method for Quality Control of an Attenuated Varicella Live Vaccin
FILE REFERENCE: 2016-0454P
CURRENT APPLICATION NUMBER: Us/09/913,514
CURRENT FILING DATE: 2001-12-07
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27

LEADTH: 14
 0
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 Gaps
 .;
0
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 Length 14;
 DB 1; Length 14;
81;
 0; Indels
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/22,177A
FILING DATE:
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REFERENCE/DOCKET NUMBER: 09865.601
TELEPHONE: (608) 831-2106
TELEPHONE: (608) 831-2106
TELEPHONE: (608) 831-2106
TELEPHONE: (608) 831-2106
TELEPHONE: GOOD SALASIES
INFORMATION FOR SEQ ID NO: 436:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
 Score 14; DB 1; Pred. No. 81; 0; Mismatches
 Mismatches
 Sequence 27, Application US/09913514
Patent No. 6653069
GENERAL INFORMATION:
 Application US/09913514
 Query Match
Best Local Similarity 100.0%; P
Matches 14; Conservative 0;
 Query Match
1.3%; Sc
Best Local Similarity 100.0%; P
Matches 14; Conservative 0;
 TYPE: nucleic acid

"TRANDENNES: double

"TOPOLOGY: linear

" MOLECULE TYPE: DNA (genomic)
US-08-222-177A-436
 1813 TATATATATATA 1826
 1794 GTGTGTGTGTGT 1807
 1 rararararara 14
 ; TYPE: DNA
; ORGANISM: Varicella virus
US-09-913-514-27
 US-09-913-514-27/c
 US-09-913-514-27
 à
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0; Gaps

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Query Match 1.3%; Score 14; DB 1; Length 16; Best Local Similarity 71.4%; Pred. No. 96; Matches 10; Conservative 4; Mismatches 0; Indels
 TELEFAX: (213) 955-0440
TELEX: 67-2310
INFORMATION FOR SEQ ID NO: 1060:
SEQUENCE CHARACTERISTICS:
 NUMBER OF SEQ ID NOS: 1208
SOFTWARE: Patentin version 3.0
SEQ ID NO 336
LENGTH: 16
 1392 GTTAAGACTTGACA 1405
PRIOR FILING DATE: 1997-09-22
 |::|||||::|||||
1 GUUAAGACUUGACA 14
 LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 TYPE: RNA
CORGANISM: Homo sapiens
US-09-479-005A-336
 US-08-373-124A-1060
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 Gaps
 Gaps
 Sequence 336, Application US/09479005A
Batent No. 6656731
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
FILE REFERENCE: MBHB00-884-C
CURRENT FILING DATE: 2000-01-07
PRIOR PILING DATE: 1999-11-19
PRIOR FILING DATE: 1999-11-19
PRIOR FILING DATE: 1999-11-19
PRIOR FILING DATE: 1999-12-1998-09-22
PRIOR PLING DATE: 1999-12-1998-09-22
PRIOR APPLICATION NUMBER: US 60/059,473
 ö
 PCT-US92-00282-27/c

| Sequence 27, Application PC/TUS9200282
| GENERAL INFORMATION:
| APPLICANT: RITTER, JOSEPH K. |
| TILLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION TITLE OF INVENTION: THEREIN. |
| TITLE OF INVENTION: THEREIN. |
| CORRESPONDENCES: 40 |
| CORRESPONDENCES: 40 |
| CORRESPONDENCES: TUSHWAN DARRAY & CUSHWAN STREET: 1615 L STREET; N.W. |
| CITT: WASHINGTON |
| COUNTRY: U.S.A. |
| COUNTRY: U.S.A. |
 Query Match
1.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 14; Conservative 0; Mismatches 0; Indels
 Indels
 CCUMTRY: U.S.A.
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00282
FILLING DATE: 19920110
CLASSIFICATION: 435
 ;
 Mismatches
 CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: SCOTT, WATSON I.
REGISTRATION NUMBER: 26581
TREECOMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEPHONE: 202-861-3000
 ö
 TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: NUCLEIC ACID
 1813 TATATATATATA 1826
 1813 TATATATATATA 1826
 1 rararararara 14
 14 TATATATATATA 1
 Matches 14; Conservative
 STRANDEDNESS:
 JS-09-479-005A-336
 RESULT 109
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Gaps
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 Ouery Match 1.3%; Score 14; DB 1; Length 17; Best Local Similarity 57.1%; Pred. No. 1e+02; Matches 8; Conservative 6; Mismatches 0; Indels
 GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Braper, Kenneth
APPLICANT: Draper, Kenneth
APPLICANT: Drayer, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENCIS AND
TITLE OF INVENTION: TREATMENT OF RESTENCIS AND
TITLE OF INVENTION: TREATMENT OF RESTENCIS
ANDRESSONDENCES.2627
CORRESPONDENCE ADDRESS.
ANDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: 633 West Fifth Street
CITY: Los Angeles
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER REAABABLE FORM:
MEDIUM TYPE: Storage
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER REAABABLE FORM:
MEDIUM TYPE: Storage
COMPUTER REAABABLE FORM:
MEDIUM TYPE: Storage
COMPUTER REAABABLE FORM:
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATION SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/997,132
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/997,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/997,132
FILING DATE: AUGUST 26, 1992
ATTING DATE: AUGUST 26, 1992
ATTING DATE: MAY 18, 1994
APPLICATION NUMBER: 07/936,422
 Sequence 1859, Application US/08373124A Patent No. 5646042 GENERAL INFORMATION:
 Sequence 1857, Application US/08373124A Patent No. 5646042
 32,327
ER: 209/035
 NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209,
TELEPHONE: (213) 489-1600
TELEFRAX: (213) 955-0440
 Stinchcomb, Dan T
Draper, Kenneth
McSwiggen, James
Jarvis, Thale
 1763 CAGATTTTTAAAA 1776
 3 CAGAUUUUUUAAAA 16
 TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
 nucleic acid
EDNESS: single
 linear
 STRANDEDNESS:
 ,
US-08-373-124A-1857
 US-08-373-124A-1859
 APPLICANT:
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 ö
 Gaps
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0
 Query Match 1.3%; Score 14; DB 1; Length 17; Best Local Similarity 57.1%; Pred. No. 1e+02; Matches 8; Conservative 6; Mismatches 0; Indels
1.3%; Score 14; DB 1; Length 17; 100.0%; Pred. No. 1e+02; tive 0; Mismatches 0; Indels
 VS-08-313-124A-1855

/ Sequence 1855, Application US/08373124A

/ Patent No. 5646042

/ APPLICANT: Stinchcomb, Dan T.

APPLICANT: Draper, Kenneth

APPLICANT: McSwiggen, James

APPLICANT: McSwiggen, James

/ APPLICANT: McSwiggen, James

/ APPLICANT: McSwiggen, Danes

/ APPLICANT: McSwiggen, James

/ APPLICANT: McSwiggen, Ja
 COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: 1BM Compatible
CURRENT APPLICATION DATA:
FILING DATE: January 13, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: PEDTUARY 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: DECEMBER 7, 1992
APPLICATION NUMBER: 07/986,132
FILING DATE: AUGUST 7, 1992
APPLICATION NUMBER: 07/986,132
FILING DATE: AUGUST 7, 1992
ATTORNEY/AGENT INFORMATION:
RESTRENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
TELECOMMUNICATION INFORMATION:
TELESPHONE: (213) 955-0440
 TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1855:
SEQUENCE CHARACTERISTICS:
IENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 1763 CAGATTTTTTAAAA 1776
 1811 TGTATATATATA 1824
 4 CAGAUTUTUTAAAA 17
 0.0 Ouery Match
Best Local Similarity 100.0
Matches 14; Conservative
 15 rGrarararara 2
 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
 ; TOPOLOGY: linear
US-08-373-124A-1855
```

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Ouery Match 1.3%; Score 14; DB 1; Length 17; Best Local Similarity 57.1%; Pred. No. 1e+02; Matches 8; Conservative 6; Mismatches 0; Indels
 US-08-435-528-1060/C

Sequence 1060, Application US/08435628
Patent No. 5817796
GENERAL INFORMATION:
APPLICANT: StinchComb, Dan T.
APPLICANT: StinchComb, Dan T.
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen
ITILE OF INVENTION: CANCER USING RIBOZYMES
ITILE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEB: Lyon & Lyon
STREET: Suite 4700
CORPUTER: Stitch Street
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER: Storage
COMPUTER: IBM Compatible
COMPUTER: Mord Perfect 5.1
 1763 CAGATTTTTAAAA 1776
 ||||::::::||||
1 CAGAUUUUUUAAAA 14
 U.S.A.
 RESULT 116
US-08-435-628-1060/c
STATE: CCCOUNTRY: U.S
COUNTRY: U.S
90071
 à
 g
 Gaps
 Query Match 1.3%; Score 14; DB 1; Length 17; Best Local Similarity 57.1%; Pred. No. 1e+02; Matches 8; Conservative 6; Mismatches 0; Indels
 RESULT 115
US-08-373-124A-1861
US-08-373-124A-1861
Sequence 1861, Application US/08373124A
Patent No. 5646042
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: Draper, Kenneth
APPLICANT: Drayis, Thale
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: S13 West Fifth Street
STREET: S111E 4700
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND TITLE OF INVENTION: CANCER USING RIBOZYMES NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STREET: California
COUNTRY: U.S.A.
 CCUNTRY: U.S.A.

ZIF: 90071

ZIF: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: Storage
CCMPUTER: 18 Carage
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION NUMBER: US/08/373,124A
FILING DATE: 40 1994
APPLICATION NUMBER: 08/29,943
FILING DATE: FEBRUARY 7, 1994
APPLICATION NUMBER: 07/991,132
FILING DATE: December 7, 1994
APPLICATION NUMBER: 07/992,943
FILING DATE: December 7, 1994
APPLICATION NUMBER: 07/991,132
FILING DATE: May 18, 1992
APPLICATION NUMBER: 07/991,132
FILING DATE: May 18, 1992
APPLICATION NUMBER: 20/9035
FILING DATE: May 18, 20, 30, 37
FILING DATE: May 18, 20, 30, 37
FILING DATE: MAUGHT 100:
FELERATION NUMBER: 20, 1992
APPLICATION NUMBER: 30, 337
FELEFRAX (213) 955-0440
FELEFR
 1763 CAGATTTTTTAAAA 1776
 2 CAGAUUUUUUAAAA 15
 CITY: Los Angeles
 ò
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FILING DATE: January 13, 1990
APPLICATION NUMBER: 08/25,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/102,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/986,422
APTORNEY/AGENT INFORMATION:
NAME: WALDURY, RICHARD
REGISTAATION NUMBER: 32,327
ATORNEY/AGENT NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 26,99/035
FILEROMMUNICATION INFORMATION:
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: TELEX: 67-3510
INFORMATION FOR SEQ ID NO: LEGGEN CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: NUCLEIC acid
STRANDENESS: single
 0; Gaps
 Query Match 1.3%; Score 14; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 16+02; Matches 14; Conservative 0; Mismatches 0; Indels
 APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: Moswiggen, James
APPLICANT: Moswiggen, James
APPLICANT: Moswiggen, James
APPLICANT: Moswiggen, James
APPLICANT: Marylow: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADORESS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
CITY: Los Angeles
STREET: California
COUNTRY: U.S.A.
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,08/435,628
FILING DATE: 05-MAY-1995
CIASSIFICATION: 5.4
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/33,124
FILING DATE: January 13, 1995
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/92,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/987,132
FILING DATE: AUGUST 7, 1992
APPLICATION NUMBER: 07/987,132
FILING DATE: AUGUST 7, 1992
APPLICATION NUMBER: 07/987,132
FILING DATE: AUGUST 7, 1992
APPLICATION NUMBER: 07/987,422
FILING DATE: AUGUST 7, 1992
APPLICATION NUMBER: 07/987,422
 NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
FELECOMMULICATION INFORMATION:
TELEPAK: (213) 489-1600
FELEPAK: (213) 489-1600
FELEPAK: (213) 955-0440
INFORMATION FOR SEQ ID NO: 1060:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDENNESS: single
STANDENNESS: single
GS-08-435-628-1060
 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
 UNIVERSITY APPLICATION DATA:
APPLICATION NUMBER: US/08/435,628
FILING DATE: 05-NAY-1995
FILING DATE: 05-NAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/373,124
 Sequence 1855, Application US/08435628; Patent No. 5817796; GENERAL INFORMATION:
 1811 TGTATATATATA 1824
 15 TGTATATATATA 2
 RESULT 117
US-08-435-628-1855
 90071
 g
```

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Query Match
1.3%; Score 14; DB 1; Length 17;
Best Local Similarity 57.1%; Pred. No. 1e+02;
Matches 8; Conservative 6; Mismatches 0; Indels
 RESULT IN SEATOR APPLICATION US/08435628

Sequence 1857, Application US/08435628

Sequence 1857, Application US/08435628

Sequence 1857, Application US/08435628

Settling No. S817708

APPLICANT: Stinchcomb, Dan T. APPLICANT: McWaigen, James APPLICANT: Jarvis, Thale TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: METHODS AND CONFESSERIES ASSET SALE AND TITLE OF INVENTION: TANCER USING RIBOZYMES AND CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon STREET: SALE AT 100 CITY: Los Angeles STREET: Galifornia COUNTRY: U.S.A.

CONFUTER READABLE FORM:

MEDIUM TYPE: Storage COMPUTER READABLE FORM:

MEDIUM TYPE: STORAGE SOFT STORE SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/435,628

FILING DATE: January 13, 1995

APPLICATION NUMBER: 08/192,943

FILING DATE: FEBRUARY 7, 1994

 1763 CAGATITITAAAA 1776
 US-08-435-628-1855
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TELECOMMUNICATION INFORMATION:
TELEFHONE: (213) 489-1600
TELEFHONE: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 1859:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-435-628-1859
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 g
 Query Match 1.3%; Score 14; DB 1; Length 17; Best Local Similarity 57.1%; Pred. No. 1e+02; Matches 8; Conservative 6; Mismatches 0; Indels
 Sequence 1859, Application US/08435628
Sequence 1859, Application US/08435628
Baten No. 281736
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Brayer, Kenneth
APPLICANT: Maryis, Thale
IITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: TREATMENT OF RESTENSIS AND TITLE OF INVENTION: A Lyon & Lyon
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFRMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELERAX: (213) 489-1600
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1857:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: TOPOLOGY: linear
US-08-435-628-1857
F7.1%; Pred
 1763 CAGATITITIAAAA 1776
 3 CAGAUTUTUTAAAA 16
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ö
Query Match 1.3%; Score 14; DB 1; Length 17; Best Local Similarity 57.1%; Pred. No. 1e+02; Matches 8; Conservative 6; Mismatches 0; Indels
 1763 CAGATTTTTAAAA 1776
 2 CAGAUUUUUUAAAA 15
```

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Sequence 80.5 1418. Splication US/08373124A

Patent No. 5646042

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: Draper, Kenneth
APPLICANT: Drayis, Thale
APPLICANT: McSwiggen, James
APPLICANT: Drayis, James
APPLICANT: Drayis, James
APPLICANT: McSwiggen, James
APPLICANT: Stinches
APPLICANT: James
APPL
 ઠે
 Query Match
1.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels
 Query Match
1.3%; Score 14; DB 1; Length 17;
Best Local Similarity 57.1%; Pred. No. 1e+02;
Matches 8; Conservative 6; Mismatches 0; Indels
 STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25
CURRENT APPLICATION DATA:
RILANG DATE:
FILANG DA
 US-08-84-021-16/c

Sequence 16, Application US/0849021

Sequence 16, Application US/0849021

Patent No. 595276

GENERAL INFORMATION:
APPLICANT: WORGANTE, MICHELE
APPLICANT: WORGANTE, MICHELE
TITLE OF INVENTION: PRIMERS FOR THE
TITLE OF INVENTION: PRIMERS FOR THE
TITLE OF INVENTION: PRIMERS FOR THE
TITLE OF INVENTION: POLYMORPHISMS
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: COMPANY
ADDRESSEE: COMPANY
STREET: 1007 MARKET STREET
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,456
FILING DATE: 28 NOVEMBER 1994
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1064-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
 TELEFAX: 302-992-7949
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
 , MOLECULE TYPE: DNA (genomic) US-08-849-021-16
 1763 CAGATITITIAAAA 1776
 ||||::::::||||
1 CAGAUUUUUUAAAA 14
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-628-1861
 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
```

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Gaps
 ö
 Query Match 1.3%; Score 13.8; DB 1; Length 17; Best Local Similarity 88.2%; Pred. No. 1.1e+02; Matches 15; Conservative 0; Mismatches 2; Indels
CONDESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: 813 West Fifth Street
CITY: Los Angeles
CITY: Los Angeles
CONDUTRY: U.S.A.
ZIP: 90071
COMPUTER: Galifornia
COMPUTER: 15.8" Diskette, 1.44 Mb
MEDIUM TYPE: 8.5.8" Diskette, 1.44 Mb
MEDIUM TYPE: 10.8 Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: Usmuary 13, 1995
APPLICATION NUMBER: 08/192,943
FILING DATE: Pebruary 7, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: Becember 7, 1992
APPLICATION NUMBER: 07/987,132
APPLICATION NUMBER: 07/987,132
FILING DATE: August 26, 1992
ATORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
RESISTRATION NUMBER: 20/935
TELEGRANDIN CONTACT NUMBER: 209/035
 RESULT 123
18-08-435-628-874/c
18-quence 874, Application US/08435628
Patent No. 5817796
 1765 GATTTTTAAAATTTAT 1781
 TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 874:
SEQUENCE CHARACTERISTICS:
 GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: MCSWiggen, James
APPLICANT: Jarvis, Thale
 17 GATTTTTAAAATATAT 1
 LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 ;
US-08-373-124A-874
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```
;
 Length 17;
 Indels
 Sequence 132, Application US/08851843A

Sequence 132, Application US/08851843A

Patent No. 603809

GENERAL INFORMATION:

APPLICANT: Cach, Thomas R.

APPLICANT: Lingner, Joachim

APPLICANT: Chapman, Karen B.

APPLICANT: Maraney, Toru

APPLICANT: Andrews, William H.

TITLE OF INVENTION: No. 6093809el Telomerase

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LIP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United To
 CORRESPONDENCE ADDAESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STARET: California
CONNTRY: U.S.A.
ZIP: 190071-2066
CONPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.3" Diskette, 3.3" Di
 Query Match
1.3%; Score 13.8; DB 1;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2;
 STATE: California
COUNTRY: United States of America
ZIP: 94111
 1537 GTGTAATTGAGAAGGAA 1553
 17 GGGTAATAGAGAAGGAA 1
 COMPUTER READABLE FORM
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & LY
 ; TOPOLOGY: linear
US-08-292-620A-1988
 ઠે
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 Gaps
 ö
 Length 17;
 Indels
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND TITLE OF INVENTION: CANCER USING RIBOZYMES CORRESPONDENCE ADDRESS: 2627
CORRESPONDENCE ADDRESS: ADDRESSE Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700
 Query Match
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2;
 RESULT 124
US-08-292-620A-1988/C
Sequence 1988, Application US/08292620A
Sequence 1988, Application US/08292620A
Sequence 1088, Application US/08292620A
Sequence 1088, Application US/08292620A
Septicant: Susan Grimm
APPLICANT: Susan Grimm
APPLICANT: Sean Sulivan
APPLICANT: Kenneth G. Draper
ITLE OF INVENTION: RIBOZYME TREATMENT OF
ITLE OF INVENTION: DISEASES OR COUNTIONS
ITLE OF INVENTION: RELATED TO LEVELS OF
ITLE OF INVENTION: INTRACELLULAR APHRSION
ITLE OF INVENTION: INTRACELLULAR APHRSION
ITLE OF INVENTION: INTRACELLULAR APHRSION
ITLE OF INVENTION: MOLECULE-1 (1-CAM-1)
 COUNTY: 0.0.0.0.

ZIF: 90071

COMPUTER READABLE FORM;
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: storage
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PETECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,628
FILING DATE: 05-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/73,124
FILING DATE: January 13, 1995
APPLICATION NUMBER: 08/25,466
FILING DATE: MAY 119,1994
APPLICATION NUMBER: 08/192,943
FILING DATE: DECEMBER 7, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: DECEMBER 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: DECEMBER 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: WAEDLEGY RICHARY 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
TELECOMMUTCATION INFORMATION:
THE COUNTY AGENT NUMBER: 32,327
 TELEPHONE: (213) 489-1600
TELEFA: (213) 955-0440
TELEX: 67-3510
INPORMATION FOR SEQ ID NO: 874:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 1765 GATTTTTAAAATTTAT 1781
 17 GATTTTTAAAAATATAT
 CITY: Los Angeles
STATE: California
 linear
 U.S.A.
 US-08-435-628-874
 COUNTRY:
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Word Perfect 5.1

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US-002-250-075-5

US-02-250-075-5

Sequence 5, Application US/09250075

Sequence 5, Application US/09250075

Patent No. 6207819

GENERAL INFORMATION:

APPLICANT: Maier, Martin A

TITLE OF INVENTION: Compounds Processes And Intermediates For Synthesis Of

TITLE OF INVENTION: Compounds Processes And Intermediates For Synthesis Of

TITLE OF INVENTION: Mixed Backbone Oligomeric Compounds

FILE REFERENCE: ISIS3299

CURRENT PAPLICANTON UMBER: US/09/250,075

CURRENT FILING DATE: 1999-02-12

NUMBER OF SEQ ID NOS: 12

SEQ ID NO 5

LENGTH: 17
 NAME/KEY: misc_feature

LOCATION: (1). (17)

COTHER INFORMATION: 2'-methoxyethoxy (MOE); modified linkage

OTHER INFORMATION: Description of Artificial Sequence: No. 6207819e1

OTHER INFORMATION: Sequence

US-09-250-075-5
 .
0
 Query Match
1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
 Query Match
1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
 FILING DATE:
CLASSIFICATION:
PRICE APPLICATION:
PRICE APPLICATION NUMBER: US/08/292,620
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/008,995
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRX: (213) 499-1600
TELEFX: (7-3510
TELEFY (213) 955-0440
TELES: 67-3510
TELEFY (213) 955-0440
TELER: 67-3510
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,845
 1537 GTGTAATTGAGAAA 1553
 17
 17 GGGTAATAGAGAAGGAA 1
 TYPE: DNA
ORGANISM: Artificial Seguence
 US-09-071-845-1988
 RESULT 128
 g
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 g
 Gaps
 Score 13.8; DB 1; Length 17; Pred. No. 1.1e+02; 0; Mismatches 2; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
 Sequence 1988, Application US/09071845
; Sequence 1988, Application US/09071845
; Patent No. 6122967
; GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: James MCSWiggen
APPLICANT: James MCSWiggen
APPLICANT: Sean Sullivan
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: MOLECULE-1 (1-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESSE:
ADDRESSEE: LYON & INVENTION
STATEMENTION: ADDRESSES
 015389-002930US
 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
APPLICATION NUMBER: 36,429
FILING DATE: 01-OCT-1996
CLASSIFICATION:
APPLICATION NUMBER: 36,429
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: 36,429
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: 36,429
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: 36,429
FILING DATE: 01-OCT-1996
TELEFRAY (415) 576-0200
TELEFRAY (415) 576-0200
TELEFRAY (415) 576-0300
TELEFRAY (415) 576-
 ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
 COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0
 E: Lyon & Lyon
633 West Fifth Street
Suite 4700
 1865 TTTTTTTTTTTTT 1881
 Query Match
Best Local Similarity 88.2%;
Matches 15; Conservative
 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
 US-08-851-843A-132
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mcgarry191-19.rni
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ö
 1.3%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 1.1e+02; vative 0; Mismatches 2; Indels
 CLABMENT, KATEN B.

MOTIN, Gregg B.

HARLEY, Calvin
Andrews, william H.

TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCES: 225
CORRESPONDENCE ADDRESS:
REFET: Two Embarcadero Center, 8th Floor
STREET: Two Embarcadero Center, 8th Floor
STREET: Canifornia
CONTYRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: PLOPBY disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
SOFTWARE: PETENTION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PETENTION NATURE ADDRESSE #1.0, Version #1.30
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CILASSIFICATION: «UNKNOWN»
PRIOR APPLICATION AUMBER: US 08/854,050
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 10-OCT-1996
ATTORNEY AGENT INFORMATION:
NAME: Apple: Nandolph T.
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
 GENERAL INFORMATION:
APPLICANT: Parco, Pamela
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Scoobed, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 132: US-09-430-323-132
 RESULT 130
12.08-584-040-2550
; Sequence 2550, Application US/08584040
; Patent No. 6346398
 INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
 1865 TITITATITITATI 1881
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
 Query Match
Best Local Similarity 88.23
Matches 15; Conservative
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 Query Match 1.3%; Score 13.8; DB 1; Length 17; Best Local Similarity 88.2%; Pred. No. 1.1e+02; Matches 15; Conservative 0; Mismatches 2; Indels
 APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANTION NUMBER:
APPLICAN
 US-08-854-050-132
; Sequence 132, Application US/08854050
; Patent No. 6261836
 1865 TTTTTTTTTTTTT 1881
 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-854-050-132
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US-09-430-323-132 ; Sequence 132, Application US/09430323 ; Patent No. 6309867

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ö
 Query Match
1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 1.1e+02;
Matches 10; Conservative 5; Mismatches 2; Indels
 RESULT 132
US-08-584-040-6049
Sequence 6049, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: BScobedo, Jaimes
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: Galifornia
COUNTRY: Los Angeles
STATE: Galifornia
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OSPERATING SYSTEM: IBM COMPATION
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: ENCOMPATIBLE
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION NUMBER: 61/05,974
FILING DATE: OCCODER 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: MATCHEY/AGENT INFORMATION:
NAME: MATCHEY/AGENT INFORMATION:
NAME: MATCHEY/AGENT INFORMATION:
NAME: MATCHEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
 1639 TGTTCCTTAAGTCAGAA 1655
 1 UGUGCCUUAAUUCAGAA 17
 TELEFAT: (213) JULIARIES TELEFAT: (713) JULIARIES 67-3510
INFORMATION FOR SEQ ID NO: 60 SEQUENCE CHARACTERISTICS: LENGTH: 17 base pairs TYPE: nucleic acid STRANDEDNESS: single TOOLOGY: linear
 TOPOLOGY: J
US-08-584-040-6047
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 Gaps
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 DB 1; Length 17;
 Indele
 RESULT 131

US-08-584-040-6047

Sequence 6047, Application US/08584040

Patent No. 6346398

GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: Pavco, Pamela
APPLICANT: Bacobedo, James
APPLICANT: Bacobedo, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
AUMBER OF SEQUENCES: 8502

CORRESPONDENCE ADDRESS:
ADDRESSER: LYON & LYON

STREET: SULE 4700
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SECURCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSE: 1400 & LyON
STREET: 631 West Fifth Street
STRANDENDER: 61 West Fifth Street
STRANDENDESS: SINGle
STRANDENESS: SINGle
 .1e+02;
2;
 Query Match 1.3%; Score 13.8; E Best Local Similarity 5.9%; Pred. No. 1.1e+ Matches 1; Conservative 14; Mismatches
 1864 CTITITATITITIT 1880
 1 connoconomical 17
 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
 US-08-584-040-2550
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Gaps

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RESULT 135
US-09-371-772B-1074

i Sequence 1074, Application US/09371772B

i Sequence 1074, Application US/09371772B

i Sequence 1074, Application US/09371772B

i Septent No. 6566127

i GENERAL INFORMATION:

i APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Rocobedo, Jaime

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

FILE REPERBNCE: MEHBOO, 876-J (237/198)

CURRENT ILING DATE: 1999-08-10.

FRICR APPLICATION NUMBER: US 60/005,974

FRICR FILING DATE: 1995-01-08

NUMBER OF SEQ ID NOS: 14225

SEQ ID NO: 1074

LENGTH: 17
 Sequence 2884, Application US/09371772B

Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REPERENCE: MGHB00, 376-J (2377/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
 Gaps
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0
 ; Score 13.8; DB 1; Length 17;
Pred. No. 1.18+02;
14; Mismatches 2; Indels
 Query Match 1.3%; Score 13.8; DB 1; Length 17; Best Local Similarity 88.2%; Pred. No. 1.1e+02; Matches 15; Conservative 0; Mismatches 2; Indels
 FRATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Oligonucleotide
NAME/KEY: misc_feature
LOCATION: (1)..(19)
COTHER INFORMATION: 2'-methoxyethoxy (MOE); phosphorothioate
OTHER INFORMATION: internucleoside linkage
 1864 CTTTTTATTTTTT 1880
 1865 TITITATITITITI 1881
 1 COUNTYUNDUNUUUUUUUU 17
 1 TTTTTTTTTTTTTTT 17
 TYPE: DNA ORGANISM: Artificial Sequence
 Query Match 1.3%;
Best Local Similarity 5.9%;
Matches 1, Conservative
 TYPE: RNA
CRGANISM: Homo sapiens
US-09-371-7728-1074
 RESULT 136
US-09-371-772B-2884
 US-09-726-096A-5
 SEQ ID NO 5
LENGTH: 17
 g
 ò
 ઠે
 Sequence 5, Application US/09726096A
Patent No. 6462184
GENERAL INFORMATION:
APPLICANT: Manoharan, Muthiah
APPLICANT: Manoharan, Muthiah
APPLICANT: Manoharan, Muthiah
APPLICANT: Maier, Martin A.
TITLE OF INVENTION: Compounds Processes And Intermediates For Synthesis Of Mixed Back
TITLE OF INVENTION: Oligomeric Compounds
FILE REFERENCE: ISIS4528
CURRENT APPLICATION NUMBER: US/09/726,096A
CURRENT FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.0
 ô
 ; OTHER INFORMATION: designed sequence for nucleic acid purification US-09-619-103-23
 Ouery Match
1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
 Query Match 1.3%; Score 13.8; DB 1; Length 17; Best Local Similarity 70.6%; Pred. No. 1.1e+02; Matches 12; Conservative 3; Mismatches 2; Indels
 APPLICANT: Kurz, Markus
APPLICANT: Lohse, Peter
APPLICANT: Lohse, Peter
APPLICANT: Lohse, Peter
TITLE OF INVENTION: Peptide Acceptor Ligation Methods
FILE REPERENCE: 50036/031002
CURRENT APPLICATION NUMBER: US/09/619,103
CURRENT FILING DATE: 2000-07-19
PRIOR PELLING DATE: 2007-27
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 17
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEFONE: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: (7-3510 NO: 6049:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: muclaic acid
LENGTH: 17 base pairs
TYPE: muclaic acid
TYPE: muclaic acid
STRANBEDNESS: single
 Sequence 23, Application US/09619103; Patent No. 6429300; GENERAL INFORMATION:
 1643 CCTTAAGTCAGAACAGC 1659
 1865 TITITATITITIT 1881
 1 CCUUAAUUCAGAACACC 17
 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
 linear
 ; TOPOLOGY:]
US-08-584-040-6049
 US-09-619-103-23/c
 RESULT 134
US-09-726-096A-5
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Sequence 386, Application US/09827998

| Sequence 386, Application US/09827998
| Patent No. 6656700
| Patent No. 6656700
| APPLICANT: Gu. Yizhong
| APPLICANT: Shannon, Mark
| APPLICANT: Shannon, Mark
| TITLE OF INVENTION: NOVEL ISOPORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
| FILE REFERENCE: MDHMORF-8
| CURRENT APPLICATION NUMBER: US/09/827,998
| CURRENT FILING DATE: 2001-04-06
| PRIOR FILING DATE: 2000-05-26
| PRIOR FILING DATE: 2000-09-27
| WUMBER OF SEQ ID NOS: 1881
| SOFTWARR: Abomica Sequence Listing Engine
| Patent No. 6656700
 GENERAL INFORMATION:

APPLICANT: GU, YIZIDON:

APPLICANT: GU, YIZIDON:

APPLICANT: GL, YIZIDON:

APPLICANT: GL, YIZIDON:

APPLICANT: GL, YIZIDON:

TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E

TITLE PEPERENENCE:

CURRENT APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,359

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 Gaps
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 1.3%; Score 13.8; DB 1; Length 17; 88.2%; Fred. No. 1.1e+02; tive 0; Mismatches 2; Indels
 Length 17;
 Indels
 1.3%; Score 13.8; DB 1;
88.2%; Pred. No. 1.1e+02;
tive 0; Mismatches 2;
SOPTWARE: Aeomica Sequence Listing Engine
Patent No. 6656700
SEQ ID NO 384
 Sequence 385, Application US/09827998
Patent No. 6656700
 1793 TGTGTGTGTGTGTGT 1809
 1794 GIGIGIGIGIGIGIG 1810
 11
 Query Match
Best Local Similarity 88.2
Matches 15; Conservative
 15; Conservative
 ORGANISM: Homo sapiens
 TYPE: DNA
CRGANISM: Homo sapiens
US-09-827-998-384
 Query Match
Best Local Similarity
Matches 15; Conserv
 ; TYPE: DNA
; ORGANISM: Homo
US-09-827-998-386
 JS-09-827-998-386
 US-09-827-998-385
 Patent No. 6656
SEO ID NO 386
LENGTH: 17
 TYPE: DNA
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 g
 US-09-371-772B-2886

Sequence 2886, Application US/09371772B

Sequence 2886, Application US/09371772B

Patent No. 6566127

GENERAL INPORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Bescobedo, Jaime

APPLICANT: Stinchcomb, Dan

APPLICANT: Bescobedo, Jaime

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: 1990-08-10

FILE REFERENCE: MBHB00, 876-J (237/198)

CURRENT FILING DATE: 1996-01-08

PRIOR FILING DATE: 1996-01-08

NUMBER OF SEQ ID NOS: 14225

SOFTWARE: PatentIn version 3.0

LENGWARE: PatentIn version 3.0

LENGWARE: PatentIn version 3.0
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 Sequence 384, Application US/09827998

Patent No. 6656700

GENERAL INFORMATION:
APPLICANT: GLAY YIZAONG
APPLICANT: Shannon, Mark
TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
FILE REFERENCE: MDHMORF-8
CURRENT PELING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/205-26
PRIOR APPLICATION NUMBER: US 60/205-26
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
 Gaps
 ô
 Score 13.8; DB 1; Length 17; Pred. No. 1.18+02; 3; Mismatches 2; Indels
 Query Match
1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 1.1e+02;
Matches 10; Conservative 5; Mismatches 2; Indels
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1395-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
EDG ID NO 2884
 1639 TGTTCCTTAAGTCAGAA 1655
 1643 CCTTAAGTCAGAACAGC 1659
 1 UGUGCCUUAAUUCAGAA 17
 1.3%;
 Query Match
Best Local Similarity 70.6
Matches 12; Conservative
 ; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-2884
 ; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-2886
 US-09-827-998-384
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APPLICATION NUMBER: US/08/153,051B
FILING DATE: No. 5645986ember 12, 1993
PRIOR APPLICATION DATA:
 STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Storage
MEDIUM TYPE: Storage
 Sequence 52, Application US/08153051B
Patent No. 5645986
GENERAL INFORMATION.
APPLICANT: Jerry W. Shay
 COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
 Michael D. West
Jerry W. Shay
Woodring E. Wright
Elizabeth Blackburn
 Catherine Strahl
Michael J. McEachern
 ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700
 1799 TGTGTGTGTGTGTAT 1815
 Nam Woo Kim
Calvin B. Harley
Scott L. Weinrich
 17
 Query Match 1.3%;
Best Local Similarity 88.2%;
Matches 15; Conservative
 Homayoun Vaziri
 1 rerrrereasteratar
 APPLICANT: Homayoun Vaz
TITLE OF INVENTION: THE
TITLE OF INVENTION: CON
TITLE OF INVENTION: LEN
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
 TYPE: DNA
ORGANISM: Homo sapiens
 US-09-827-998-389
 APPLICANT:
APPLICANT:
APPLICANT:
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 ## Sequence 387, Application US/09827998

Sequence 387, Application US/09827998

Patent No. 6656700

GRERAL INFORMATION:

APPLICANT: Gu, Yizhong

TILE OF INVERTION: NOVEL ISOFORMS OF HUMAN PRECNANCY-ASSOCIATED PROTEIN E

CURRENT APPLICATION: NUMBER: US/09/827,998

CURRENT APPLICATION: NUMBER: US 60/236,359

PRIOR PILING DATE: 2000-09-27

NUMBER: OF SEQ ID NOS: 1881

SOFTWARE: Aeomica Sequence Listing Engine

SEC ID NO 387

INVERTION: APPLICATION: SEQUENCE LISTING ENGINE

SEC ID NO 387

INVERTION: APPLICATION:
 USO-05-02/096-050

Sequence 388, Application US/09827998

Patent No. 6656700

GENERAL INFORMATION:
APPLICANT: Gu, Yizhong
APPLICANT: Gu, Vizhong
TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
FILE REFERENCE: MOMORE-8
CURRENT APPLICATION NUMBER: US/09/827,998

CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PRILING DATE: 2000-05-26
PRIOR PRILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 1881
PRICE APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 1881
PATENT NOS: 1881
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 Gaps
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 Score 13.8; DB 1; Length 17;
Pred. No. 1.1e+02;
0; Mismatches 2; Indels
 Length 17;
Score 13.8; DB 1; Length 17; Pred. No. 1.1e+02; 0; Mismatches 2; Indels
 Indels
 Query Match
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2;
 1794 GIGIGIGIGIGIGIG 1810
 1793 TGTGTGTGTGTGTGT 1809
 1 reretriereAsrerer 17
 1 GIGIGITIGICAGIGIG 17
 Query Match
Best Local Similarity 88.2%;
Matches 15; Conservative C
 1.3%;
Local Similarity 88.2%;
nes 15; Conservative
 ORGANISM: Homo sapiens
US-09-827-998-388
 TYPE: DNA
CORGANISM: Homo sapiens
US-09-827-998-387
 US-09-827-998-388
 JS-09-827-998-387
 Query Match
 Best Locar
Matches
```

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1798 GIGTGTGTGTGTGTA 1814

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;
0
 Length 17;
 THERAPY AND DIAGNOSIS OF CONDITIONS RELATED TO TELEOMERE LENGTH AND/OR TELOMERASE ACTIVITY
 Score 13.8; DB 1;
Pred. No. 1.1e+02;
0; Mismatches 2;
1 GTGTTTGTGAGTGTGTA 17
```

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Gaps
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 Query Match
1.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
 Query Match
1.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
 Sequence 52, Application US/08151477A

Sequence 52, Application US/08151477A

Patent No. 5830644

GENERAL INFORMATION:
APPLICANT: Michael D. West
APPLICANT: Modring E. Wright
APPLICANT: Modring E. Wright
APPLICANT: Calvin B. Harley
APPLICANT: Calvin B. Harley
APPLICANT: Catherine Strahl
APPLICANT: Catherine Strahl
APPLICANT: Michael J. McEachen
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: LENGTH AND/OR TELOMEREE
TITLE OF INVENTION: LENGTH AND/OR TELOMEREE
TITLE OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
CARRESPONDENCE ADDRESS:
CARSESPONDENCE ADDRESS:
CAUCHER CARSESPONDENCE ADDRESS ADDRES
 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATIOS SYSTEM: IBM PC. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/151,477A
FILING DATE: No. 5330644ember 12, 1993
PRIOR APPLICATION NUMBER: 08/038,766
FILING DATE: March 24, 1993
ATTORNEY/AGENT INPORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
RELEPHONE: (213) 955-0440
TELEPHONE: (213) 955-0440
TELEPHONE: (213) 955-0440
TELEPHONE: (213) 955-0440
TELEPHONE: SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
LENGTH: 15 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
 ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700 CITY: Los Angeles STRIE: California COUNTRY: U.S.A. ZIP: 90071
 1792 TIGIGIGIGIGIG 1806
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 linear
 US-08-151-477A-52
 ;
TOPOLOGY:
US-08-060-952C-51
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 Gaps
 ;
 Sequence 51, Application US/08060952C

Sequence 51, Application US/08060952C

RENERAL INFORMATION:
APPLICANT: Michael D. West
APPLICANT: Moding E. Wright
APPLICANT: Woodring E. Wright
APPLICANT: Woodring E. Wright
APPLICANT: Woodring E. Wright
APPLICANT: Elizabeth Blackburn
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
ITILE OF INVENTION: TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: 632 West Fifth Street
 Query Match
1.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
 CITY: LOS ADGELES
CITY: LOS ADGELES
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: Extraction
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATE:
APPLICATION NUMBER: US/08/060,952C
FILING DATE: MAY 13, 1993
ATTORNEY/AGENT INFORMATION:
NAME: WATDIN INFORMATION:
MEDITY MATORNER: 202/045
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (213) 955-0440
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
 AFPLIATION NUMBER: Various, VETILING DATE: March 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: WAZDHIG, MICHAEL
REGISTRATION NUMBER: 204/195
REFERENCE/DOCKET NUMBER: 204/195
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: (7-3510
TELEFA
 08/038,766
 1792 TTGTGTGTGTGTG 1806
 APPLICATION NUMBER:
 ; TOPOLOGY: linear
US-08-153-0518-52
 US-08-060-952C-51
 RESULT 145
```

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-011B-51

1792 TIGIGIGIGIGIG 1806

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Sequence 51, Application US/08464011B
Sequence 51, Application US/08464011B
Patent No. 6168789
GENERAL INFORMATION:
Michael D. West
Applicant: Michael D. West
Woodring E. Wright
Woodring E. Wright
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF TELOMERE LENGTH AND/OR
TELOMERASE ACTIVITY
 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
 g
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 ö
 Gaps
 ..
0
 DB 1; Length 15;
e+02;
 Indels
 GENERAL INFORMATION:
APPLICANT: Michael D. West
APPLICANT: Galvin B. Harley
APPLICANT: Scott L. Weinrich
APPLICANT: Scott L. Weinrich
APPLICANT: Scott L. Weinrich
APPLICANT: Michael J. Weachern
APPLICANT: Michael J. Mceachern
APPLICANT: Michael J. Weachern
APPLICANT: Michael J. Weachern
APPLICANT: Blizabeth H. Blackburn
APPLICANT: Homayoun Vaziri
TITLE OF INVENTION: TEOLOMERE LENGTH AND/OR
TITLE OF INVENTION: TELOMERESE ACTIVITY
NUMBER OF SEQUENCES: 80
 COKRESCEE: Lyon & Lyon
STREET: 633 Weet Fifth Street
STREET: 801te 4700
CITY: Los Angeles
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.05"
COMPUTER: IBM COMPATIBLE C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
FILING DATE: Work 14, 1997
APPLICATION NUMBER: BATTORNEY AGENT INFORMATION:
NAME: CHAMBER: 224/232
TELECOMMUNICATION INFORMATION:
TELEFRAX: (213) 955-0440
 Ouery Match 1.3%; Score 13.4; D
Best Local Similarity 93.3%; Pred. No. 1e+0
Matches 14; Conservative 0; Mismatches
 3-08-819-867-79
Sequence 79, Application US/08819867
Patent No. 6007989
 TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 1 redrerererere 15
 US-08-819-867-79
```

```
Gaps
 .
0
 Query Match 1.3%; Score 13.4; DB 1; Length 15; Best Local Similarity 93.3%; Pred. No. 1e+02; Matches 14; Conservative 0; Mismatches 1; Indels
 RESULT 149
US-09-475-947A-83/C
US-09-475-947A-83/C
Sequence 83, Application US/09475947A
Patent No. 6472154
GENERAL INFORMATION:
APPLICANT: Garner, Harold R.
APPLICANT: Wren, Jonathan D.
APPLICANT: Minna, John D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes
ECOMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,011B
FILING DATE: 05-701-1995
CLASSIFICATION - CURCOWN-
PRIOR APPLICATION NUMBER: 07/882,438
FILING DATE: May 13, 1993
APPLICATION NUMBER: 08/06,952
FILING DATE: May 13, 1993
APPLICATION NUMBER: 08/06,952
FILING DATE: May 13, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
 ;
TOPOLOGY: linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-08-464-0118-51
 TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
 1792 TIGIGIGIGIGIG 1806
 TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 51:
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1792 TIGIGIGIGIGIG 1806

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RESULT 151
US-09-371-772B-6067
i Sequence 6067 Application US/09371772B
sequence 6067 Application US/09371772B
sequence 6067 Application US/09371772B
sequence 6067 Application US/09371772B
sequence 6067 Application
US/0937172B
sequence 6067 Application
sequence 6067 Application Sequence 6067 Sequence
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 RESULT 152
US-09-479-005A-185/c
US-09-479-005A-185/c
US-09-479-005A-185/c
Sequence 185, Application US/09479005A
Fatent No. 6656731
GENERAL INFORMATION Pharmaceuticals, Inc.
TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
FILE REFERENCE: BHBH00-884-C
CURRENT APPLICATION NUMBER: US/09/479,005A
CURRENT FILING DATE: 2000-01-07
FRIOR FILING DATE: 1999-11-19
FRIOR FILING DATE: 1999-11-19
FRIOR FILING DATE: 1999-11-19
FRIOR FILING DATE: 1999-09-22
FRIOR FILING DATE: 1997-09-22
 Gaps
 ö
 Query Match
Best Local Similarity 46.7%; Pred. No. 1.1e+02;
Matches 7; Conservative 7; Mismatches 1; Indels
 1.3%; Score 13.4; DB 1; Length 15; 93.3%; Pred. No. 1e+02; ive 0; Mismatches 1; Indels
TOPOLOGY: linear sequence DESCRIPTION: SEQ ID NO: 79: US-09-378-535-79
 1791 ATTGTGTGTGTGT 1805
 1792 TIGIGIGIGIGIG 1806
 | :|:|:|:|:|:
2 Acugugugugugu 16
 Query Match
Best Local Similarity 93.3%
Matches 14, Conservative
 TYPE: RNA
ORGANISM: Homo sapiens
 TYPE: RNA
CRGANISM: Homo sapiens
US-09-371-772B-6067
 US-09-479-005A-18
 LENGIH: 16
 ઠે
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 Gaps
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0
 Query Match
1.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
 Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
 CONDITIONS RELATED TO
TECLOMERE LENGTH AND/OR
TELOMERASE ACTIVITY
 COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTESEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/378,535
FILING DATE: 20-Aug-1-999
CLASSIFICATION TOWNER: 08/819,867
FILING DATE: WINKNOWN>
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/819,867
FILING DATE: WINKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: CLABMDER: DATA
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/232
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
 PILE REFERENCE: UTSD0667
CURRENT PELLING DATE: 1999-12-31
UUMBER OF SEQ ID NOS: 346
SOFTHARE: Patentin Ver. 2.1
SEQ ID NO B1
LENGTH: 15
 NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 Weet Fifth Street
Suite 4700
 Jerry Shay
Woodring E. Wright
Elizabeth H. Blackburn
Nam Woo Kim
 APPLICANT: Michael D. West
Calvin B. Harley
Scott L. Weinrich
Catherine M. Strahl
Michael J. Mceachern
 FELEPHONE: (213) 489-1600
 US-09-378-535-79; Sequence 79, Application US/09378535; Sequence 79, Application US/09378535; Patent No. 6551774
GENERAL INFORMATION:
 TELEX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
 1811 TGTATATATATAT 1825
 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
 15 irraiarararar 1
 TYPE: DNA
CRGANISM: human
US-09-475-947A-83
```

APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: Draper, Kenneth
APPLICANT: Dravis, Thale
APPLICANT: Marvis, Thale
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF SEQUENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENTES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles

Sequence 1060, Application US/08435628 Patent No. 5817796 GENERAL INFORMATION:

```
STATE: SALES AND STATES AND STATE
```

Query Match
1.3%; Score 13.4; DB 1; Length 17;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 7; Conservative 7; Mismatches 1; Indels

1813 TATATATATATAT 1827

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mcgarry191-19.rni
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Gaps
 Gaps
 ö
 NAME/KEY: misc binding
LOCATION: (1)...(13)
OTHER INPORMATION: synthesized test oligonucleotide for binding
OTHER INFORMATION: studies
US-09-393-783A-41
 CURRENT FILING DATE: 1990-10.

APPLICANT: Schrott, Thomas Wayne
APPLICANT: Schrott, Thomas Wayne
APPLICANT: Suh, Young J.

APPLICANT: Suh, Young J.

TILE OF INVENTION: Nucleic Acid Ligand Interaction Assays
FILE REFERENCE: 4600-0128.30
CURRENT APPLICATION NUMBER: US/09/393,783A
CURRENT APPLICATION NUMBER: US 09/151,890
PRIOR APPLICATION NUMBER: US 09/151,890
PRIOR FILING DATE: 1998-09-11
NUMBER OF SEQ ID NOS: 80
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 41
LENGTH: 13
 Query Match
1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 13; Conservative 0; Mismatches 0; Indels
 Length 13;
 0; Indels
MEDIUM TYPE: FLOPPY DISA
COMPUTER: IBM PC COMPATIBLE
COMFUTER: IBM PC COMPATIBLE
CORFRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,021
FILING DATE: US/08/846,456
FILING DATE: 28 NOVEMBER 1994
ATPOLICATION NUMBER: US/346,456
FILING DATE: 28 NOVEMBER 1994
ATPOLICATION NUMBER: 33,692
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AZAMETHY
REGISTRATION NUMBER: 33,692
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-8112
TELEFRAX: 302-992-7949
 Query Match 1.2%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 96; Matches 13; Conservative 0; Mismatches
 US-09-393-783A-41
; Sequence 41, Application US/09393783A
Patent No. 635545B
; GENERAL INFORMATION:
 TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-849-021-15
 TYPE: DNA ORGANISM: Artificial Sequence
 1794 GIGIGIGIGIGIG 1806
 INFORMATION FOR SEQ ID NO: 1. SEQUENCE CHARACTERISTICS: LENGTH: 13 base pairs TYPE: nucleic acid STRANDEDNESS: single
 1793 TGTGTGTGTGT 1805
 1 rererererer 13
 RESULT 158
 ઠે
 ò
 g
 Length 13;
 Indels
 APPLICANT: VOGEL, JULIE M.

TITLE OF INVENTION: COMPOUND MICROSATELLITE
TITLE OF INVENTION: DEPRETED FOR THE
TITLE OF INVENTION: POLYMORPHISMS
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND
ADDRESSEE: COMPANY
STREET: 1007 NARKET STREET
CITY: WILMINGTON
STREET: U.S.A.
ZIP: 19898
COMPUTER READABLE PORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OFFWARE: PATENT IN RELEASE #1.0, VERSION 1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,021
 RESULT 156
US-08-049-021-15
Sequence 15, Application US/08849021
Facture No. 595276
GENERAL INFORMATION:
APPLICANT: WORGL, JULIE M.
TITLE OF INVENTION: PRIMERS FOR THE TITLE OF INVENTION: DETECTION OF GENETIC NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESSE: B. I. DU PONT DE NEMOURS AND ADDRESSEE: COMPANY
STREET: 1007 MARKET STREET
CITY: MILMINGTON
STREET: DELAMARE
COUNTRY: U.S.A.
 Query Match 1.2%; Score 13; DB 1; Best Local Similarity 100.0%; Pred. No. 96; Matches 13; Conservative 0; Mismatches (
 REDERENCE/DOCKET NUMBER: BB-1064-A TELECOMUNICATION: TELEPHONE: 302-892-8112
 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,456
FILING DATE: 28 NOVEMBER 1994
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
 TELEPHONE: 302-892-8112
TELEPHONE: 302-892-9449
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGHH: 13 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
 MORGANTE, MICHELE
 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
 1793 TGTGTGTGTGT 1805
 ZIP: 19898
COMPUTER READABLE FORM:
 US-08-849-021-13
```

```
(213) 489-1600
(213) 955-0440
 2152 TCACCTGGAAGCA 2164
 Query Match 1.2
Best Local Similarity 100.
Matches 13; Conservative
 TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
 TYPE: nucleic acid
STRANDEDNESS: single
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US-08-291-932A-121
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 Gapa
 0
 .
0
 TYPE: DNA
CRGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc binding
LOCATION: (1)...(13)
COTHER INFORMATION: synthesized test oligonuclectide for binding
US-09-151-890B-41
 GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Thomas Wayne Bruice
APPLICANT: Thomas Wayne Bruice
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICANTON NUMBER: US/09/151,890B
CURRENT FILLS DATE: 1998-09-11
NUMBER OF SEQ ID NOS: 80
SOFTWARE: FASTEEQ FOR WINGOWS Version 3.0
IENGTH::13
 Length 15;
 Query Match
1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 13; Conservative 0; Mismatches 0; Indels
 US-09-475-947A-83

US-09-475-947A-83

Sequence 83, Application US/09475947A

Patent No. 6472154

GENERAL INFORMATION:

APPLICANT: Wren, John D.

APPLICANT: Wren, John D.

APPLICANT: Wren, John D.

APPLICANT: Wren, John D.

TITLE OF INVENTION: POLYMORPHIC Repeats in Human Genes
FILE REFERENCE: UTS0067

CURRENT TILING DATE: 1999-12-31

NUMBER OF SEQ ID NOS: 346

SEQ ID NO 83

LENGTH: 15
 Score 13; DB 1; Le
Pred. No. 1.1e+02;
 Sequence 121, Application US/08291932A

Sequence 121, Application US/08291932A

GENERAL No. 5658780

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth G.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: RELATED TO LEVELS OF
 100.0%; Prec. ...
 Seguence 41, Application US/09151890B
 1814 ATATATATATA 1826
 1794 GIGIGIGIGIG 1806
 1 ATATATATATA 13
 Query Match
Best Local Similarity 100.
Matches 13; Conservative
 TYPE: DNA
ORGANISM: human
 US-09-475-947A-83
US-09-151-890B-41
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.
0
 Length 15;
 CCASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
ATTORNEY, ADENT INFORMATION:
NAME: Warburg, Richard J.
REGISTATION NUMBER: 32,327
REGISTATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/157
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
 1.2%; Score 13; DB 1; Lt
100.0%; Pred. No. 1.1e+02;
tive 0; Mismatches 0;
 RESULT 161
US-08-291-932A-194/C

Sequence 194, Application US/08291932A

Patent No. 5638780
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: NF-KB

STREET: Signer Electrone Along
TITLE OF INVENTION: NR-KB
NUMBER OF SEQUENCES: 830
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 631 Weet Fifth Street
STREET: Suite 4700
CITY: Los Angeles
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE PORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 9.5" Diskette, 1.44 Mb
MEDIUM TYPE: 9.5" Diskette, 1.44 Mb
MEDIUM TYPE: 150 COMPUTER: 1500 S.0
SOFTWARE: MEDION PATA:
APPLICATION NUMBER: US/08/291,932A
FILING DATE: ANGUSET 15, 1994
```

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```
Sequence 1, Application US/08812951B

Sequence 1, Application US/08812951B

Parent No. 6297066

GENERAL INFORMATION:
APPLICANT: Drmanac, Radoje T.
APPLICANT: Drmanac, Radoje T.
APPLICANT: Hou, Aaron
APPLICANT: Hou, Aaron
APPLICANT: Brian
TITLE OF INVENTION: Detection or Quantification of Nucleic Acid Species
NUMBER OF SEQUENCES 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: McCucchen, Doyle, Brown & Enersen LLP
STREET: Three Embarcadero Center
CITY: San Francisco
STATE: CA.
 Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels
 COUNTRY: USA

ZIP: 94111
COMPUTER READABLE FORM:
COMPUTER: LEM Compatible
OOMPUTER: IEM Compatible
OOMPUTER: IEM Compatible
OOMPUTER: TEM Compatible
OOMPUTER: TEM Compatible
OOMPUTER: TEM COMPATION
SOFTWARE: TEMSCREED FOR Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,951B
FILING DATE: 04-MAR-1997
CLASSIFICATION ATA:
APPLICATION NUMBER: US08/784747
FILING DATE: 16-CAN-1997
ATTORNEY/AGENT INFORMATION:
 including application described below:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER:
APPLICATION WURBER:
FILING DATE:
MAY 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/157
RELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
TELESAX: (214) 955-0440
TELESAX: (215) 955-0440
TELESAX: (215) 955-0440
TELESAX: (215) 955-0440
TELESAX: (215) 955-0440
TELESAX: (217-9510)
TELENTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
 NAME: Kumamoto, Andrew A
REGISTRATION NUMBER: 40,690
REFERENCE, POCKET NUMBER: 20
TELECOMUNICATION INFORMATION
TELEPHONE: 415-393-2000
 2152 TCACCTGGAAGCA 2164
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 ;
US-08-291-932A-310
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 d
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 Gaps
 J
W
D
 .
0
 Length 15;
 0; Indels
 MEDIUM TIPE: BLOTAGE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Berfect 5.1
CURRENT APPLICATION DATA:
PRING DATE: AUGUST 15, 1994
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08/245,466
APPLICATION NUMBER: 07/994
APPLICATION NUMBER: 07/997
ATTORNEY/AGENT INFORMATION:
NAME: WAIDING, RICHARD 32,327
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATIO
 DB 1; Le
1.1e+02;
 Sequence 310, Application US/08291932A

Patent No. 5688780

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth G.
APPLICANT: Draper, Kenneth G.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: BLEATED TO LEVELS OF
TITLE OF INVENTION: PRELATED TO LEVELS OF
TITLE OF INVENTION: NF-KB
NUMBER OF SEQUENCES: 830
CORRESPONDENCE ADDRESSS:
ADDRESSEB: Lyon & Lyon
STREET: Suite 4700
CITY: Los Angeles
STREET: Suite 4700
CITY: Los Angeles
STREET: California
 Query Match 1.2%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 1.1 Matches 13; Conservative 0; Mismatches
 ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 35" Diskette, 1.44 Mb
MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
OPREATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/291,932A
FILING DATE: August 15, 1994
CLASSIFICATION: 514
 OMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
 TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 194:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleate acid
STRANDEDNESS: single
TOPOLOGY: linear
 2152 TCACCTGGAAGCA 2164
 15 rcaccrecaadca 3
 RESULT 162
US-08-291-932A-310/c
 TOPOLOGY: 1
US-08-291-932A-194
```

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Query Match
 ઠ
 g
 RESULT 164
US-08-812-951B-2/C
i Sequence 2, Application US/08812951B
i Patent No. 6297006
i GENERAL INFORMATION:
APPLICANT: Drmanac, Radoje T.
APPLICANT: Drmanac, Snezana
APPLICANT: Bruser, Brian
i APPLICANT: Hou, Aaron
i APPLICANT: Hou, Aaron
i APPLICANT: Houser, Brian
ITILE OF INVENTION: Methods and Compositions for
ITILE OF INVENTION: Detection or Quantification of Nucleic Acid Species
NUMBER OF SEQUENCES:
ADDRESSEE: McCutchen, Doyle, Brown & Enersen LLP
STREET: Three Embarcadero Center
CITY: San Francisco
STATE: CA
COUNTRY. ...
 ö
 ö
 ö
 1.2%; Score 13; DB 1; Length 15; 92.9%; Pred. No. 1.1e+02;
 Query Match 1.2%; Score 13; DB 1; Length 15; Best Local Similarity 92.9%; Pred. No. 1.18+02; Matches 13; Conservative 0; Mismatches 1; Indels
 i, Indels
 COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
OFBRATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,951B
FILING DATE: 04-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: AND DATA:
APPLICATION NUMBER: US/08/784747
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
 NAME: Kumamoto, Andrew A
REGISTRATION NUMBER: 40,690
REFERENCE/DOCKET NUMBER: 20411-701
TELECOMMUNICATION INFORMATION:
 1863 CCTTTTTATTTTG 1876
 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTER.STICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 Best Local Similarity 92.9
Matches 13; Conservative
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-812-9518-1
 94111
 US-08-812-951B-2
 Query Match
```

RESULT 165 US-08-784-747-2

```
COTHER INFORMATION: Exemplary oligonucleotide primer used in sequence assembly process:
NAMES/KEY: misc_feature
NAMES/KEY: mis
 ö
 Sequence 117, Application US/09479005A

Patent No. 6656731

Gegrance 117, Application US/09479005A

Patent No. 6656731

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity

FILE REPERENCE: MBH800-884-C

CURRENT FILING DATE: 2000-01-07

PRIOR PILICATION NUMBER: US 09/444,209

PRIOR FILING DATE: 1999-11-19

PRIOR FILING DATE: 1999-11-19

PRIOR FILING DATE: 1998-09-22

PRIOR FILING DATE: 1997-09-22

NUMBER OF SEQ ID NOS: 1206

SOFTWARE: Patentin version 3.0

SEQ ID NO 117

LENGTH: 16
 Gaps
 ö
 GENERAL INFORMATION:
APPLICANT:
APPLICANT:
Pord, John
APPLICANT:
Ford, John
APPLICANT:
Ford, John
APPLICANT:
FOR JOHN
TITLE OF INVENTION: A CONA LIBRARY OF FETAL LIVER-SPLEEN
TITLE OF INVENTION: A CONA LIBRARY OF FETAL LIVER-SPLEEN
TITLE OF INVENTION: A CONA LIBRARY OF FETAL LIVER-SPLEEN
TITLE OF INVENTION: A CONA LIBRARY OF FETAL LIVER-SPLEEN
TITLE OF INVENTION: A CONA LIBRARY OF FETAL LIVER-SPLEEN
CURRENT FILING DATE: 1999-09-22
CURRENT FILING DATE: 1999-06-29
PRIOR PILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: US 09/106,800
PRIOR APPLICATION NUMBER: US 09/106,800
PRIOR PILING DATE: 1999-06-26
PRIOR FILING DATE: 1999-06-26
SPRIOR FILING DATE: 1999-06-26
INVENER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
 .
0
 Query Match
1.2%; Score 13; DB 1; Length 16;
Best Local Similarity 38.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 8; Mismatches 0; Indels
 Query Match
1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels
sequence 10, Application US/09409778
 1863 CCTTTTTATTTTG 1876
 ORGANISM: Artificial Sequence
 2268 TITITICIATAAA 2280
 1 UUUUUUCUAUAAA 13
 15 ccriririniriris 2
 ; ORGANISM: Homo sapiens US-09-479-005A-117
 RESULT 169
US-09-479-005A-117
 RESULT 170
US-07-971-978-36
 TYPE: RNA
 TYPE: DNA
 ò
 g
 ठ
 g
 FEATURE:
OTHER INFORMATION: Exemplary oligonuclectide primer used in sequence assembly proces
NAME/KBY: misc.feature
LOCATION: (8)...(8)
 ; OTHER INFORMATION: n = A, T, C, G or 1-(2-deoxy-D-ribfuranosyl)-3-nitropyrrole US-09-409-778-9
 ö
 ö
 GENERAL INVORMATION:

APPLICANT:
POIG, John
APPLICANT:
POIG, John
APPLICANT:
POIG, John
APPLICANT:
POIG, JOHN
AND GEOFGE
TITLE OF INVENTION: A NOVEL CHEMOKINE RECEPTOR OBTAINED FROM
TITLE OF INVENTION: A CDNA LIBERAY OF FETAL LIVER-SPLEEN
TITLE OF INVENTION: A CDNA LIBERAY OF FETAL LIVER-SPLEEN
FILE REFERENCE: 20411-742CON2 (now 28110/360578)
CURRENT FELING DATE: 1999-02-2
PRIOR APPLICATION NUMBER: DCT/US99/12829
PRIOR FILING DATE: 1999-01-2
PRIOR PR
 Length 15;
 1; Indels
 Length 15;
 1; Indels
 Query Match 1.2%; Score 13; DB 1; I Best Local Similarity 92.9%; Pred. No. 1.1e+02; Matches 13; Conservative 0; Mismatches 1.
 Score 13; DB 1;
Pred. No. 1.1e+02;
0; Mismatches 1
 US/08/784,747
 5-09-409-778-9
Sequence 9, Application US/09409778
Patent No. 6472173
GENERAL INFORMATION:
APPLICANT: Ford, John
 FILING DATE: 16-7AN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KUMMMOCO, ANDREW:
REFERENCE/DOCKET NUMBER: 2041)
TELECHONICATION INFORMATION:
TELECHONE: 415-393-2286
 Query Match
1.2%; Sc
Best Local Similarity 92.9%; Pr
Matches 13; Conservative 0;
 1863 CCTTTTTATTTTG 1876
 1863 CCTTTTTATTTTG 1876
 TELEX:
INFORMATION FOR SEQ ID NO: 3:
 CCTTTTTNTTTTG 14
 15 CCTTTTTNTTTTG 2
 SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 APPLICATION NUMBER:
 , TOPOLOGY: linear
US-08-784-747-3
 RESULT 168
US-09-409-778-10/c
 Best Loca
Matches
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NESOLI 1978-42

Sequence 42, Application US/07971978

Sequence 42, Application US/07971978

Sequence 42, Application US/07971978

Sequence 42, Application US/07971978

Patent No. 5614617

TITLE OF INVENITION: Nuclease Resistant, Pyrimidine

TITLE OF INVENITION: Modified Oligonucleotides that Detect and Modulate

TITLE OF INVENITION: Gene Expression

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 5614617ris

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

COUNTRY: U.S.A.

ZIP: 19103
 Gaps
 ..
0
 Length 16;
 Indels
 FEATURE:

NAME/KEY: Modified-site
LOCATION: Substitution
OTHER INFORMATION: S-fluoro-2'-deoxyuridine
 Query Match
1.2%; Score 12.8; DB 1;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 2;
 LOCATION: 14
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
PEATURE:
 LOCATION: 15
CTHER INFORMATION: S-fluoro-2'-deoxyuridine
CTHER INFORMATION: substitution
US-07-971-978-36
 5-fluoro-2'-deoxyuridine
substitution
 LOCATION: 7
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
 1865 TITITATITITI 1880
 1 rrrrrrrrrrrrrrrrr 16
 FACTURE:
NAME/KEY: Modified-site
LOCATION: 13
OTHER INFORMATION: 5-fluo:
POTHER INFORMATION: substit
POTHER INFORMATION: MASELIE
NAME/KEY: MODIfied-site
 NAME/KEY: Modified-site LOCATION: 15
 Modified-site
 RESULT 171
 ò
Sequence 36, Application US/07971978

Patent No. 5614617

GENERAL INFORMATION:
APPLICANT: Coan and Sanghvi
TITLE OF INVENTION: Modified Oligonuclectides that Detect and Modulate
TITLE OF INVENTION: Modified Oligonuclectides that Detect and Modulate
TITLE OF INVENTION: Gene Expression
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
ADDRESSEE: One Liberty Place - 46th Floor
CITY: Philadelphia
 **RATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
FRATURE:
 LOCATION: 5
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
 LOCATION: 1
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
 OTHER INFORMATION: 5-fluoro-2'-deoxyuridine OTHER INFORMATION: substitution EATURE:
 LOCATION: 4
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
EATURE:
NAME/KEY: Modified-site
 OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
RATHUR:
NAME/KEY: Modified-site
 COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Dispy disk
COMPUTER: Wordberfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/971,978
FILING DATE: February 18, 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/558,806
FILING DATE: Dispy disk
REJESTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: 1515-0333
TELEPAX: 215-568-3100
TELEPAX: 215-568-310
 ### Addition in Ad
 NAME/KEY: Modified-site
 NAME/KEY: Modified-site
 U.S.A.
 CITY: Phila
STATE: PA
COUNTRY: U
```

NAME/KEY: Modified-site

```
CHERN INFORMATION: S-LOCATION: 0

PRANTER: PROMOTION: substitution
OTHER INFORMATION: S-LOCATION: 0

PRANTER: PROMOTION: substitution
OTHER INFORMATION: S-LOCATION: S-LOCATIO
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PEATURE:
DOCATION:
LOCATION:
COTHER INFORMATION: 5-iodo-2'-deoxyuridine
OTHER INFORMATION: substitution
PEATURE:
NAME/KEY:
MODIFIED:
LOCATION:
OTHER INFORMATION: 5-iodo-2'-deoxyuridine
OTHER INFORMATION: substitution
PEATURE:
NAME/KEY:
MODIFIED:
NAME/KEY:

 NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: 5-iodo-2'-deoxyuridine
OTHER INFORMATION: substitution
 OTHER INFORMATION: 5-iodo-2'-deoxyuridine
OTHER INFORMATION: substitution
FRATURE:
 5-iodo-2'-deoxyuridine
substitution
 5-iodo-2'-deoxyuridine
substitution
 5-iodo-2'-deoxyuridine
substitution
 5-iodo-2'-deoxyuridine
substitution
 5-iodo-2'-deoxyuridine
substitution
 5-iodo-2'-deoxyuridine
substitution
 LOCATION: 6
CTHER INFORMATION: 5-iodo-2'-deoxyuridine
OTHER INFORMATION: substitution
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEPAX: 215-568-319
INFORMATION FOR SEQ ID NO: 60: SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
 PEATURE:
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: 5-iodo
OTHER INFORMATION: substi
 FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: 5-iodo
OTHER INFORMATION: substil
FEATURE:
NAME/KEY: Modified-site
 LOCATION: 12
OTHER INFORMATION: 5-10do
OTHER INFORMATION: Suberi
FEATURE:
NAME/KEY: Modified-site
LOCATION: 13
 NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: 5-loc
OTHER INFORMATION: subst
 'EATURE:
NAME/KEY: Modified-site
LOCATION:
 NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: 5-100
OTHER INFORMATION: subst
 NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: 5-iod
OTHER INFORMATION: Subst
 NAME/KEY: Modified-site LOCATION: 1
```

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 Gaps
 Gaps
 WESULT 173
UG-08-415-370-2
is Gauence 2, Application US/08415370
is Sequence 2, Application US/08415370
is Gaurent No. 5801155
is Gaurent Intervention of December 1 applicant: Kutyavin, Igor V.
APPLICANT: Lukhtanov, Eugeny A.
APPLICANT: Gamper, Howard B.
APPLICANT: Gamper, Howard B.
ITILE OF INVENTION: COVALENTLY LINKED OLIGONUCLECTIDE MINOR TITLE OF INVENTION: GROOVE BINDER CONJUGATES
INUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
STREET: 4199 Campus Drive, Suite 700
CITY: Irvine
STATE: CA
COUNTRY: USA
ZIP: 92715
COMPUTER PROFES
 ·
0
 ö
 Ouery Match
1.2%; Score 12.8; DB 1, Length 16;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
 Length 16;
 Indels
 Query Match
1.2%; Score 12.8; DB 1;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 2;
OTHER INFORMATION: 5-iodo-2'-deoxyuridine CTHER INFORMATION: substitution NAME/KEY: Modified-site LOCATION: 14 OTHER INFORMATION: 5-iodo-2'-deoxyuridine OTHER INFORMATION: substitution FEATURE:
 NAME/KEY: Modified-site
LOCATION: 15
COTHER INFORMATION: 5-iodo-2'-deoxyuridine
COTHER INFORMATION: Substitution
US-07-971-978-60
 1865 TTTTTTTTTTT 1880
 1865 TITITATITITE 1880
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Sequence 15, Application US/08687551
Patent No. 2856435
GENERAL INFORMATION:
APPLICANT: BAZIE, Didier
APPLICANT: BAZIE, Didier
APPLICANT: BAZIE, Carcle
APPLICANT: SPENIEHAUER, Gilles
ITILE OF INVENTION: UNCLEIC ACID-CONTAINING COMPOSITION, ITS
ITILE OF INVENTION: PREPARATION AND USE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: SOO Arcola Rd. 3C43
CITY: Collegeville
 ö
 1.2%; Score 12.8; DB 1; Length 16; 87.5%; Pred. No. 1.3e+02; tive 0; Mismatches 2; Indels
 ZIP: 19426

ZIP: 19426

COMPUTER READABLE FORM:

MEDIUM TYPE: Flopy disk

COMPUTER: IEM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOPTWARE: PARENTH Release #1.0, Version #1.30

APPLICATION NUMBER: US/08/687,551
 APPLICATION NOBER: US/08/68/551
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/01381
FILING DATE: 08-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PUT/FR95/00098
FILING DATE: 27-JAM-1995
ATOMNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: 38,619
REGISTRATION NUMBER: 38,619
REGISTRATION NUMBER: 38,619
REGISTRATION NUMBER: 38,619
REGISTRATION INFORMATION:
TELEPHONE: (610)454-3809
INFORMATION FOR SEQ 1D NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
 MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
US-08-687-551-15
 1865 TTTTTTTTTTTT 1880
 Query Match
Best Local Similarity 87.5
Matches 14; Conservative
 linear
 USA
 PA
RESULT 174
US-08-687-551-15
 COUNTRY:
 ద
```

US-08-893-614-1

Sequence 1, Application US/08893614

Patent No. 5936077

GENERAL INFORMATION:

APPLICANT: PFLEIDERR, Wolfgang
APPLICANT: BEIER, Markus
TITLE OF INVENTION: SOLID PHASE SYNTHESIS OF

TITLE OF INVENTION: OLIGONUCLECTIDES
NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

```
Gaps
 ö
 Sequence 2, Application US/09141764

| Sequence 2, Application US/09141764
| Patent No. 6084102
| GENERAL INFORMATION:
| APPLICANT: Kutyavin, Igor V. APPLICANT: Lukhtanov, Bugany A. APPLICANT: Gover, Jr., Rich B. TITLE OF INVENTION: GOVERNING BINDER CONJUGATES
| TITLE OF INVENTION: GROOVE BINDER CONJUGATES
| NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: 2 CORRESPONDENCE ADDRESS: 3 ADDRESSE: KLEIN & SZEKERES
| STREET: A199 Campus Drive, Suite 700 CITY: Irvine
 Length 16;
 2; Indels
 COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/893,614

FILING DATE: 11-UTL-1997

CLASSIFICATION NUMBER: DE 19627898.8

FILING DATE: 11-UTL-1996

ATTORNEY/AGENT INFORMATION:

NAME: SANDERCOCK, Colin G.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 11,298

REFERENCE/DOCKET NUMBER: 13,298

REFERENCE/DOCKET NUMBER: 13,298

REFERENCE/DOCKET NUMBER: 118748/343/HOCE

TELEPEPAN: (202)672-5300
 COUNTRY: USA
ZIP: 92715
COMPUTER FEBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRETION TAPLICATION DATA:
APPLICATION NUMBER: US/09/141,764
 Ouery Match
1.2%; Score 12.8; DB 1;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 2;
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
 1836 ATCTAAGTTAATTTAA 1851
 1 ArriaArriaArriaA 16
 TELERAX: (202)672-5399
TELEX: 90416
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
 ; TOPOLOGY: linear
US-08-893-614-1
 US-09-141-764-2
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ö
 Length 16;
 COMPARESTORDING AND MERSES:

STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZUNP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: OF-MAY-1997
CLASSIFICATION NUMBER: US 08/846,017
FILING DATE: 12-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 13-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 10-OCT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 10-OCT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 10-OCT-1996
CLASSIFICATION NUMBER: US 08/724,643
 Sequence 131, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Marania, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
 Query Match
1.2%; Score 12.8; DB 1;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 2;
 ATTCASSITION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INPORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 131:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INPORMATION FOR SEQ ID NO: 131:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-851-843A-131
 1865 TITITATITITI 1880
 RESULT 178
US-08-854-050-131/c
 ö
 Query Match
1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: US/08/851,843A
FLING DATE: 06-MAY-1997
FLING APPLICATION:
APPLICATION NUMBER: US 08/846,017
FLING DATE: 25-APR-1997
CCASSIFICATION:
 Sequence 131, Application US/08851843A
Sequence 131, Application US/08851843A
Sequence 131, Application US/08851843A
Sequence 131, Application US/08851843A
Sequence 131, Application US/08851843A
Sequence 131, Application:
GENERAL INFORMATION:
APPLICANT: Cachim APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
 ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
 APPLICATION NUMBER: US 08/415,370
FILING DATE: 03-APR-1995
ATTORNEY AGENT UNFORMATION:
NAME: STACKET SERVETON:
REGISTRATION NUMBER: 28,675
REFERENCE/DOCKET NUMBER: 491-09-PA
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-854-5502
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTER.STICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 PRICE APPLICATION DATA:
APPLICATION WNBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
 1865 TTTTATTTTTGTTT 1880
 1 rrrrrrrrrrrrrrrrrr
 CATION:
 US-09-141-764-2
 RESULT 177
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Length 16;

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RESULT 180
US-09-507-345A-2
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 Gaps
 STATE: California

COUNTRY: United States of America
2IF: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: THEW PC COMPATIBLE
COMPUTER: THEW PC COMPATIBLE
COMPUTER: THEW PC COMPATIBLE
COMPUTER: THEW PC COMPATIBLE
COMPUTER: PATENTON PC-DOS/NS-DOS
SOFTWARE: PATENTON PC-DOS/NS-DOS
CURRENT APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIPTCATION: CUNKNOWN>
PRIOR APPLICATION NUMBER: US 08/854,050
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 10-APPL-1997
APPLICATION NUMBER: US 08/344,419
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INPORMATION:
NAME: AAPPLE
REPERVENCE/DOCKET NUMBER: 36,429
REPERRENDE/DOCKET NUMBER: 01-38,429
REPERRENDE/DOCKET NUMBER: 01-38,429
 Query Match
1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
 ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
 APPLICANT: Cech, Thomas R.
Lingner, Joachim
Makamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
 TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 131:
US-09-430-323-131
 US-09-430-323-131/c
; Sequence 131. Application US/09430323
Patent No. 6309867
; GENERAL INFORMATION:
 TELECOMMUNICATION INFORMATION
 TELEPHONE: (415) 576-02(
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 131:
SEQUENCE CHARACTERISTICS:
 1865 TTTTATTTTTT 1880
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-854-050-131
```

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Gaps
 Query March 1.2%; Score 12.8; DB 1; Length 16; Best Local Similarity 87.5%; Pred. No. 1.3e+02; Matches 14; Conservative 0; Mismatches 2; Indels
 COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

CLASSIFICATION NUMBER: US 09/141, 764

FILING DATE: 27-AUG-1998

ATTORNEY AGENT INFORMATION:

NAME: Reader: Milliam B.

REGISTRATION NUMBER: 37, 369

uery Match
1.2%; Score 12.8; DB 1; Length 1
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
 CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
 Sequence 2, Application US/09507345A
Sequence 2, Application US/09507345A
Patent No. 6426408
GENERAL INFORMATION:
APPLICANT: KULYAVIN, Igor V.
Lukhtanov, Eugeny A.
Gamper, Howard B.
Meyer Jr., Rich B.
TITLE OF INVENTION: Covalently Linked Oligonu
Groove Binder Conjugates
 RESULT 181
US-09-619-103-22/c
| Sequence 22, Application US/09619103
| Patent No. 6429300.
 1865 TTTTTTTTTTT 1880
 INFORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 Dase pairs
 1865 TTTTTTTTTTTTT 1880
 NUMBER OF SEQUENCES: 12
 16 rrrrrrrrrrrrrr
 GENERAL INFORMATION
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 g
 셤
 ö
 Gaps
 , OTHER INFORMATION: designed sequence for nucleic acid purification US-09-619-103-22
 Sequence 2, Application US/09739928
Patent No. 6486308
GENERAL INFORMATION:
APPLICANT: Kittyavin, Igor V.
Lukhtanov, Eugeny A.
Gamper, Howard B.
Meyer Jr., Rich B.
TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
 ö
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/739,928

FILING DATE: 11-May-201

CLASSIFICATION DATA:

APPLICATION NUMBER: US 08/415,370

FILING DATE: 03-APR-1995

APPLICATION NUMBER: US 09/141,764

FILING DATE: 27-AGU-1996

APPLICATION NUMBER: US 09/141,764

FILING DATE: 27-AGU-1996

ATTORNEY/AGENT INFORMATION:

ATTORNEY/AGENT INFORMATION:
 Length 16;
 2; Indels
 APPLICANT: LOLDS, PREER APPLICANT: Magner, Richard APPLICANT: Wagner, Richard TITLE OF INVENTION: Peptided Acceptor Ligation Methods; FILE REFRENCE: 50036/031002 CURRENT APPLICATION NUMBER: US/09/619,103 CURRENT FILING DATE: 2000-07-19 PRIOR APPLICATION NUMBER: 60/145,834 PRIOR FILING DATE: 1999-07-27 NUMBER OF SEQ ID NOS: 26 SOFTWARE: FastSEQ for Windows Version 4.0 LENGTH: 16
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
 NAME: Kezer, William B.
REGISTRATION NUMBER: 37,369
REFERENCE/DOCKET NUMBER: 17682A-003510US
 Query Match
1.2%; Score 12.8; DB 1;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 2;
 TELECOMMUNICATION INFORMATION
 1865 TITITATITITI 1880
 TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS
 16 rririririririri
 NUMBER OF SEQUENCES:
Kurz, Markus
 q
```

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Sequence 6072, Application US/09371772B
; Sequence 6072, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: Bacobedo, Jaim
 APPLICANT: Stinchcomb, Dan
 APPLICANT: Scobedo, Jaime
 ITILE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
 ITILE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
 ITILE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
 ITILE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
 ITILE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
 ITILE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
 TILE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
 TILE OF INVENTION: Method 80/00/3/1/7/2B
 CURRENT APPLICATION NUMBER: US 60/005, 974
 PRIOR FILING DATE: 1995-01-08
 NUMBER OF SEQ ID NOS: 14225
 SEQ ID NO 6072
 LENGTH: Le
 gequence 6074; Application US/09371772B

gequence 6074; Application US/09371772B

gequence 6074; Application US/09371772B

general No. 6566127

general No. 666127

general No. 666107

general N
 Gaps
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 Length 16;
 Indels
 Indels
 Query Match
1.2%; Score 12.8; DB 1;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 2;
 Score 12.8; DB 1;
Pred. No. 1.3e+02;
6; Mismatches 2;
TOPDIOGY: linear MOLECULE TYPE: DNA SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-09-739-928-2
 1794 GTGTGTGTGTGTGT 1809
 1865 TITITATITITI 1880
 1 GUGUGUGGGUGUGGGU 16
 Query Match
Best Local Similarity 50.0%;
Matches 8; Conservative
 ; ORGANISM: Homo sapiens
US-09-371-772B-6072
 RESULT 184
US-09-371-772B-6074
```

Fri Apr

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mcgarry191-19.rni
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FAULULANT NO. 281/10.

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: Jaryis, Thale
TITLE OF INVENTION: TREATMENT OF RESTRACSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: A27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 Weet Fifth Street
STREET: 105 Angeles
STREET:
 Query Match
1.2%; Score 12.8; DB 1;
Best Local Similarity 43.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 7; Mismatches 2;
 SUFERNALE.

SUFERNALE.

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/373,124A

FILING DATE: January 13, 1995

PRIOR APPLICATION NUMBER: 08/245,466

FILING DATE: May 18, 1994

APPLICATION NUMBER: 08/192,943

FILING DATE: December 7, 1994

APPLICATION NUMBER: 07/980,132

FILING DATE: December 7, 1992

APPLICATION NUMBER: 07/936,422

FILING DATE: August 26, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard

REGISTRATION NUMBER: 22, 1992

ATTORNEY/AGENT INFORMATION:

REFERENCE/DOCKET NUMBER: 209/035

TELEFRONG: (213) 489-1600

TELEFRONG: (213) 489-1600
YSTEM: IBM P.C. DOS 5.0
Word Perfect 5.1
 RESULT 187
US-08-435-628-1058
; Sequence 1058, Application US/08435628
; Patent No. 581796
 TELERA: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR ESC ID NO: 1058:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
1 TOPOLOGY: linear
US-08-373-124A-1058
 1811 TGTATATATATATA 1826
 2 UUUAUAUAUAUAUACA 17
 US-09-479-005A-522

Sequence 522, Application US/09479005A

Sequence 522, Application US/09479005A

Sequence 522, Application US/09479005A

Sequence 522, Application US/09479005A

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

TITLE OF INFORMATION: Nucleic Acid Catalysts with Endonuclease Activity

FILE REPERENCE: MBHB00-884-C

CURRENT FILING DATE: 1900-01-07

PRIOR PELICATION NUMBER: US 09/444,209

PRIOR APPLICATION NUMBER: US 09/159,274

PRIOR PELLING DATE: 1999-11-19

PRIOR PILING DATE: 1999-09-22

NUMBER OF SEQ ID NOS: 1208

SOFTWARE: Patentin version 3.0

SEQ ID NO 522

LENGTH: 16
 Query Match
1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 43.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 7; Mismatches 2; Indels
 Query Match
1.2%; Score 12.8; DB 1; Length 1
Best Local Similarity 43.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 7; Mismatches 2; Indels
 RESULT 186
US-08-373-124A-1058
US-08-373-124A-1058
Sequence 1058, Application US/08373124A
FREEDRICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Danger, Kenneth
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: TREATHENT OF RESTENCESS
TITLE OF INVENTION: TREATHENT OF RESTENCESS
NUMBER OF SEQUENCES: 2627
CORRESCONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 Weet Fitch Street
STREET: 631 Weet Fitch Street
STREET: 631 Weet Fitch Street
STREET: Galifornia
CUNTRY: Los Angeles
STATE: California
CUNTRY: U.S.A.
 ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM COMPATIBLE
 1794 GTGTGTGTGTGTGT 1809
 1832 AGTTATCTAAGTTAAT 1847
 1 GUGGGUGUAUGUGUGU 16
 TYPE: RNA
CAGANISM: Homo sapiens
US-09-479-005A-522
 ; SEQ ID NO 6074
; LENGTH: 16
; TYPE: RNA
; OKGANISM: Homo sapiens
US-09-371-772B-6074
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Gaps

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mcgarry191-19.rni
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```
Query Match
1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 204/195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAK: (213) 955-0440
TELEFAK: (213) 955-0440
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
STRANDEDNESS: single
 1793 TGTGTGTGTGTG 1806
 ઠે
 ö
 Query Match
1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 43.8%; Pred. No. 1.46+02;
Matches 7; Conservative 7; Mismatches 2; Indels
 GENERAL INTURMATION:

APPLICANT: Michael D. West
APPLICANT: Michael D. West
APPLICANT: Gerry W. Shay
APPLICANT: Woodring E. Wright
APPLICANT: Elizabeth Blackburn
APPLICANT: Elizabeth Blackburn
APPLICANT: Calvin B. Harley
APPLICANT: Geott L. Weinrich
APPLICANT: Geott L. Weinrich
APPLICANT: Achael J. MeBachern
APPLICANT: Michael J. MeBachern
APPLICANT: Los Angeles
STREET: 631 West Fifth Street
STREET: Callifornia
STREET: Callifornia
STREET: Callifornia
 ZIP: 20071
ZIP: 20071
ZIP: 20071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 8torage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ Veraion 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,051B
FILING DATE: No. 5645966miber 12, 1993
PRIOR APPLICATION NUMBER: 08/038,766
FILING DATE: MATCH 24, 1993
ATTORNEY/AGENT INFORMATION:
 APPLICATION NOMBER: 06/11/100

FILING DATE: Way 18, 1994

APPLICATION NUMBER: 07/98/112, 943

FILING DATE: February 7, 1994

APPLICATION NUMBER: 07/98/112, 943

FILING DATE: December 7, 1992

APPLICATION NUMBER: 07/986, 422

FILING DATE: December 7, 1992

ATORNEY/AGENT INFORMATION:
NAME: WATORNEY, BACATOR CASTOR REFERENCE/DOCKET NUMBER: 209/035

TELECOMMUNICATION INFORMATION:
TELEFAX: (213) 489-1600

TELEFAX: (213) 489-1600

TELEFAX: (213) 955-0440

INFORMATION FOR SEQ ID NO: 1058: SEQUENCE CHARACTERISTICS:
LENGTH: 17 Dase pairs

TYPE: INClear acid

STRANDEDNESS: single
 RESULT 188
US-08-153-051B-57
; Sequence 57, Application US/08153051B
; Patent No. 5645986
; GENERAL INFORMATION:
 08/245,466
 1811 TGTATATATATATA 1826
 2 UUUAUAUAUAUAUACA 17
```

1 TGGGTGTGTGTG 14

; TOPOLOGY: linear US-08-060-952C-56

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CORRESPONDENCE ADJANCE ADJANCE ADDRESSEE: Lyon & Lyon STREET: Sulte 4700 CITY: Los Angeles STREET: Sulte 4700 CITY: Los Angeles STREET: Sulte 4700 CITY: Los Angeles STATE: California COUNTRY: U.S.A. ZIP: 90071-2066 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: Batsof for Windows 2.0 COMPUTER: EMACOMPATA: PREJICATION NUMBER: US/08/819,867 FILING DATE: March 14, 1997 CLASSIFICATION NUMBER: 08/153,051 FILING DATE: No. 6007989ember 12, 1993 APPLICATION NUMBER: 34,561 FILING DATE: No. 6007989ember 12, 1993 APPLICATION NUMBER: 34,561 FILING DATE: ATTING DATE: ATT
 APPLICANT: Nam Woo Kim
APPLICANT: Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: CONDITIONS RELATED TO
TITLE OF INVENTION: TECLOMERE LENGTH AND/OR
TITLE OF INVENTION: TECLOMERE LENGTH AND/OR
TITLE OF INVENTION: TECLOMERES ACTIVITY
CORRESPONDENCES: 80
CORRESPONDENCES: 80
 APPLICANT: Jerry Shay
APPLICANT: Woodring E. Wright
APPLICANT: Elizabeth H. Blackburn
APPLICANT: Nam Woo Kim
 Sequence 78, Application US/08819867
Patent No. 6007989
 APPLICANT: Michael D. West
APPLICANT: Calvin B. Harley
APPLICANT: Scott L. Weinrich
APPLICANT: Catherine M. Strahl
APPLICANT: Michael J. Mceachern
 linear
 US-08-819-867-78
 US-08-819-867-78
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 Gaps
 Query Match 1.2%; Score 12.4; DB 1; Length 14; Best Local Similarity 92.9%; Pred. No. 1.2e+02; Matches 13; Conservative 0; Mismatches 1; Indels
Query Match
1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels
 APPLICANT: Michael D. West
APPLICANT: Michael D. West
APPLICANT: Woodring E. Wright
APPLICANT: Woodring E. Wright
APPLICANT: Nam Woo Kim
APPLICANT: Calvin B. Harley
APPLICANT: Catherine Birahl
APPLICANT: Michael J. Meachern
APPLICANT: Michael J. Me
 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 5.0 Separate
COMPUTER: 1BM Compatible
OPERATING SYSTEM: 1EM PC. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/151,47A
PILING DATE: No. 5330644ember 12, 1993
PRIOR APPLICATION NUMBER: 08/036,766
FILING DATE: March 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRAITON NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/189
TELEPPONE: (213) 489-1600
TELEPPONE: (213) 489-1600
TELEPPONE: (213) 955-0440
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
 E: Lyon & Lyon
633 West Fifth Street
Suite 4700
 1793 TGTGTGTGTGTG 1806
 LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
 linear
 ;
TOPOLOGY:
US-08-151-477A-57
 JS-08-151-477A-57
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..
 1.2%; Score 12.4; DB 1; Length 14; 92.9%; Pred. No. 1.2e+02; tive 0; Mismatches 1; Indels
 1793 TGTGTGTGTGTG 1806
 Query Match 1.2
Best Local Similarity 92.9
Matches 13; Conservative
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 RESULT 192
US-08-998-099-351
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1793 TGTGTGTGTGTG 1806

Gaps

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Query Match
1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels
 Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
CONDITIONS RELATED TO
 TEOLOMERE LENGTH AND/OR TELOMERASE ACTIVITY
 COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FRASEBO for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/378,535
FILING DATE: 20-Aug-1999
CLASSIFICATION: «UNROWENDED DATA:
PRIOR APPLICATION: «UNROWENDED DATA:
OFFICE OFFICE DATA:
OFFICE OFFICE OFFICE DATA:
OFFICE OFFICE
 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: CLambers, Daniel M.
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/232
TELECOMMUNICATION INFORMATION:
 TOPOLOGY: linear ; SEQUENCE DESCRIPTION: SEQ ID NO: 56: US-08-464-011B-56
 APPLICATION NUMBER: 08/819,867
 NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEs: Lyon & Lyon
STREET: 633 West Fifth Street
Sulte 4700
 Jerry Shay
Woodring E. Wright
Elizabeth H. Blackburn
Nam Woo Kim
 Catherine M. Strabl
Michael J. Mceachern
 TELECOMMUNICATION INFORMATION:
 Sequence 78, Application US/09378535
Patent No. 6551774
GENERAL INFORMATION:
APPLICANT: Wichael D. West
Calvin B. Harley
Scott i. Weinrich
 3: (213) 489-16
(213) 955-0440
 INFORMATION FOR SEQ 1D NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 storage
 1793 TGTGTGTGTGTGTG 1806
 CITY: LOS Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
 TELEFAX:
 09-378-535-78
 ઠ
 셤
 ö
 Gaps
 GENERAL INFORMATION:
APPLICANT: STARVIS.
APPLICANT: STARVIS.
APPLICANT: STINCHCORB, JAMES A.
APPLICANT: STINCHCORB, JAMES A.
APPLICANT: STINCHCORB, JAMES A.
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF C-FOS
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF C-FOS
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF C-FOS
CURRENT APPLICATION NUMBER: 60/037,658
EARLIER FILING DATE: 1997-01-23
EARLIER FILING DATE: 1997-01-13
EARLIER FILING DATE: 1995-01-13
EARLIER FILING DATE: 1995-01-13
EARLIER FILING DATE: 1994-05-18
SEALIER FILING DATE: 1994-05-18
NUMBER OF SEQ ID NOS: 375
SOFTWARE: FASTESEQ for Windows Version 3.0

FEWENTY OF THE PRINCE OF THE PRINCE OF THE PARTIES FILING DATE: 1994-05-18
TOWNERS OF SEQ ID NOS: 375
TENERAL OF THE PARTIES FILING DATE: 1994-05-18
TOWNERS OF SEQ ID NOS: 375
TENERAL OF THE PARTIES FILING DATE: 1994-05-18
TOWNERS OF SEQ ID NOS: 375
TENERAL OF THE PARTIES FILING DATE: 1994-05-18
TOWNERS OF SEQ ID NOS: 375
TENERAL OF THE PARTIES FILING DATE: 1994-05-18
TOWNERS OF THE PARTIES FILING DATE: 1994-05-18
 ö
 APPLICANT: "ALCHOUT STATE AND DIAGNOSIS OF CONDITIONS TITLE OF INVENTIONS TELEMAPY AND DIAGNOSIS OF CONDITIONS RELATED TO TELOMERE LENGTH AND/OR TELOMERASE ACTIVITY
 Query Match 1.2%; Score 12.4; DB 1; Length 14; Best Local Similarity 71.4%; Pred. No. 1.2e+02; Matches 10; Conservative 3; Mismatches 1; Indels
 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,011B
FILING DATE: 05-Unn.1995
CLASSIFICATION AUKINOWN.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/082,438
FILING DATE: May 13, 1992
APPLICATION NUMBER: 08/038,766
FILING DATE: MAY 13, 1993
APPLICATION NUMBER: 08/038,766
FILING DATE: MAY 13, 1993
APPLICATION NUMBER: 08/038,766
FILING DATE: MAY 13, 1993
APPLICATION NUMBER: 08/050,952
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
Sequence 351, Application US/08998099A Patent No. 6103890
 US-08-464-011B-56
; Sequence 56, Application US/08464011B
; Patent No. 6368789
; GENERAL INFORMATION:
 NAME: Warburg, Richard J.
 1567 TCACTGACCTGCCT 1580
 ATTORNEY/AGENT INFORMATI
 1 ucacceaeccueccu 14
 TYPE: RNA
CORGANISM: Homo sapiens
US-08-998-099-351
 Best Loca
Matches
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Length 15;
 Indels
1; Indels
 COMPACTER: IEM COMPACTED COMPACTER: CONTRACT COMPACTED COMPACTER: MOTO PERFOCT 5.1

SOFTWARE: MOTO PERFOCT 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,492B

FILING APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/006,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
 1.3e+02;
 APPLICANT: Sullivan, Sean M.
APPLICANT: Sullivan, Sean M.
APPLICANT: Draper, Kenneth G.
APPLICANT: Stanchoomb, Dan T.
TITLE OF INVENTION: RIBOZYME TREATMENT OF DIS
TITLE OF INVENTION: OR CONDITIONS RELATED TO
TITLE OF INVENTION: OF IL-5
NUMBER OF SEQUENCES: 751
CORRESSEDE: Lyon & Lyon
STREET: G13 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: G21ifornia
COUNTRY: U.S.A.
ZIP: 90071
ZIP: 90071
ZIP: 90071
ZIP: SOUTHY: S.A.
ZIP: SOUTHY: S.A.
ZIP: SOUTHY: S.A.
MEDIUM TYPE: 35" Diskette, 1.44 Mb
MEDIUM TYPE: Street
COMPUTER READABLE FORM:
 0uery Match 1.2%; Score 12.4; D
Best Local Similarity 35.7%; Pred. No. 1.3e
Matches 5; Conservative 8; Mismatches
 2; Mismatches
 Sequence 491, Application US/08319492B Patent No. 5616488 GENERAL INFORMATION:
 // Sequence 335, Application US/08334847
// Patent No. 5693532
 TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
 1284 TIATITAAATCIGT 1297
 1956 AAAGCATGAAATGG 1969
 1 AAAGCAUAAAAUGG 14
 TELEX: 67.3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
 11; Conservative
 TYPE: nucleic acid
STRANDEDNESS: single
 ;
US-08-319-492B-491
 Matches
 DD
 Score 12.4; DB 1; Length 15; Pred. No. 1.3e+02;
 tch 1.2%; Score 12.4; DB 1; Length 14; al Similarity 92.9%; Pred. No. 1.2e+02; 13; Conservative 0; Mismatches 1; Indels
 Sequence 474, Application US/08319492B
; Patent No. 561648
; Patent No. 561648
; GENERAL INFORMATION:
APPLICANT: Sullivan, Sean M.
APPLICANT: McSwiggen, James
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF IL-5
; NUMBER OF SEQUENCES: 751
; CORRESPONDENCE ADDRESS:
 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Gradelible
COMPUTER: 18M Compatible
OPERATING SYSTEM: 18M P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
PRICH APPLICATION NUMBER: US/08/319,492B
FILING DATE: October 7, 1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
APPLICATION NUMBER: 32,327
MAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
 SEQUENCE CHARACTERISTICS:

LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 78:
US-09-378-535-78
 REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/276
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3=1
 E: Lyon & Lyon
633 West Fifth Street
Suite 4700
 TELERA: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 474:
SEQUENCE CHARACTERISTICS:
 1.2%;
 INFORMATION FOR SEQ ID NO: 78
 1793 TGTGTGTGTGTG 1806
 TYPE: nucleic acid
STRANDEDNESS: sing
 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
 Query Match
Best Local Similarity
Matches 13; Conserva'
 Query Match
Best Local Similarity
 ADDRESSEE:
STREET: 633
STREET: Sui
 .08-319-492B-474
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APPLICANT: Combates, N.
APPLICANT: Pardinas, J.
APPLICANT: Stenn, K.
TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
FILE REFERENCE: UBP-382, CURRENT APPLICATION NUMBER: US/08/832,021
CURRENT PILING DATE: 1997-04-02
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
 ; OTHER INFORMATION: Description of Artificial Sequence: primer US-08-832-021-20
 Length 15;
 1.2%; Score 12.4; DB 1; Length 15;
42.9%; Pred. No. 1.3e+02;
trive 7; Mismatches 1; Indels
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
2IP: 90071-2066
COMPUTER: EACABLE FORM:
MEDIUM TYPE: Storage
COMPUTER: IBM COMPACIBLE
COMPUTER: TBM COMPACIBLE
APPLICATION DATA: GBGCTIBED BEILGALION DATA: GBGCTIBED BEILGATION NUMBER: O8/008, 895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/899, 849
FILING DATE: DECEMBER: 07/899, 849
FILING DATE: DECEMBER: 07/899, 849
FILING DATE: DECEMBER: 32,327
ATTORNY/AGENT INFORMATION:
NAME: WARDING: MICHARATION:
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFX: 67-3510
INFORMATION FOR SEQ ID NO: 331:
SEQUENCE CHARACTERISTICS:
LENGTH: LS base pairs
TYPE: mucleic acid
STRANDEDNESS: Single
 1.2%; Score 12.4; DB 1; 92.9%; Pred. No. 1.3e+02;
 Sequence 20, Application US/08832021
Patent No. 6045998
GENERAL INFORMATION:
 TYPE: DNA
ORGANISM: Artificial Sequence
 1801 TGTGTGTGTGTA 1814
 0.0 Ouery Match
Best Local Similarity 42.9%
Matches 6, Conservative
 Query Match
Best Local Similarity
 US-08-292-620A-331
 RESULT 199
US-08-832-021-20
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 1.2%; Score 12.4; DB 1; Length 15; 92.9%; Pred. No. 1.3e+02; tive 0; Mismatches 1; Indels
 Sequence 331, Application US/08292620A; Sequence 331, Application US/08292620A; Parent No. 5837542.

GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: San Sullivan
APPLICANT: Sean Sullivan
APPLICANT: Reneeth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: DISEASES OF
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESSER: LYON & LYON
STREET: 633 West File:
 APPLICANT: MCSAWAGGEN, James APPLICANT: Draper, Vames APPLICANT: Pavco, Pam APPLICANT: MCHIBITING RESPIRATORY TITLE OF INVENTION: SNCKTIAL VIRUS NUMBER OF SEQUENCES: 909
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Lyon & Lyon STREET: Suite 4700
CITY: Los Angeles STREET: Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: STREET: ST
 ATTORNEY AGENT INFORMATION:
NAME: WARDING, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/(
TELECOMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
TELER: 67-3510
INFORMATION FOR SEQ ID NO: 335:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDENESS: single
 1784 TGTAAATATTGTGT 1797
 Query Match
Best Local Similarity 92.9%
Matches 13; Conservative
 linear
 ;
TOPOLOGY:
US-08-334-847-335
 ઠે
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Sequence 203, Application US/08444818

Patent No. 6150087
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Chien, David Y.
APPLICANT: Chien, William J.
TILES OF INVENTION: NANBY Diagnostics and Vaccines NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSE: Chiron Corporation STREET: 4560 Horton Street
CITY: Emeryville
STREET: 4560 Horton Street
CITY: Emeryville
CONTYRY: USA
ZIP: 94608-2916
COMPUTER: BENDALLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BENDALLE FORM:
MEDIUM TYPE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE: 14-WAR-1995
ATTORNAY AGENT INFORMATION:
REGISTRATION NUMBER: US/08/403,590
FILING DATE: 14-WAR-1995
ATTORNAY AGENT INFORMATION:
NAME: HAZDIN, Alica A.
REGISTRATION NUMBER: 0.110.002
TELECOMMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMMUNICATION I
 TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 203:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
 1801 TGTGTGTGTGTA 1814
 TYPE: nucleic acid
STRANDEDNESS: single
 -08-444-818-203
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 g
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 Gaps
Gaps
 RESULT 200
US-08-832-021-64

| Sequence 64, Application US/08832021
| Patent No. 604598
| GENERAL INFORMATION:
| APPLICANT: Combates, N. |
| APPLICANT: Pardinas, J. |
| TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
| TITLE OF INVENTION NUMBER: US/08/832,021 |
| CURRENT APPLICANT: 1997-04-02 |
| NUMBER OF SEQ ID NOS: 64 |
| SOFWARE: PatentIN Ver. 2.0 |
| SEQ ID NO 64 |
| LENGTH: 15 |
| TYPE: DNA |
| ORGANISM: Artificial Sequence |
| ORGANISM: Artificial Sequence |
ö
 ; FEATURE;
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-64
 Query Match
1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels
Indels
 Sequence 311, Application US/09071845

Patent No. 6132867

GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Guean Grimm
APPLICANT: James McSwiggen
APPLICANT: Gean Sullivan
APPLICANT: Gean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: NOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Sulfe 4700
STREET: Sulfe 4700
 Mismatches
 ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
 COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,845
FILING DATE:
 TTGTT 1878
 1871 TTTTTGTTTTAAT 1884
 Matches 13; Conservative
 STREET: 633 West Fi
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
 1865 TTTTTATT
 RESULT 201
US-09-071-845-331
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 Query Match
1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 42.9%; Pred. No. 1.3e+02;
Matches 6; Conservative 7; Mismatches 1; Indels
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/08,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-044
TELEPHONE: (213) 955-0440
TELEPHONE: (213) 955-044
TELEFAK: (213) 955-0440
TELEFAK: (213) 9
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REGISTRATION NUMBER: 30,492
REFERENCE/COCKET WINGER: 09865.601
TELECOMUNICATION INFORMATION:
TELEPRONE: (608) 831-2100
TELEFX: (608) 831-2106
 INFORMATION FOR SEQ ID NO: 433:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
 TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
 1794 GTGTGTGTGT 1805
 12 Grerererer 1
 US-08-222-177A-433
 RESULT 206
US-09-164-249B-2/c
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 엄
 ô
 ò
 Sequence 1, Application US/08875710

Patent No. 6326139

GENERAL INFORMATION:
APPLICANT: Soreq, Hermona
APPLICANT: Soreq, Hermona
APPLICANT: Soreq, Hermona
APPLICANT: Soreq, Hermona
ANTICHE OF INVENTION: MATHOD OF SCREENING FOR GENETIC PREDISPOSITION TO
TITLE OF INVENTION: MATHOD OF SCREENING FOR GENETIC PREDISPOSITION TO
TITLE OF INVENTION: MATHOD OF SCREENING FOR GENETIC PREDISPOSITION TO
TITLE OF INVENTION: UNMER: 105/0076
CURRENT APPLICATION NUMBER: DS/0076
CURRENT APPLICATION NUMBER: PC/0056
EARLIER FILING DATE: 1997-10-06
EARLIER FILING DATE: 1996-01-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0

LENGTH. 15
 Gaps
 Gapв
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 1.2%; Score 12.4; DB 1; Length 15; 92.9%; Pred. No. 1.3e+02; tive 0; Mismatches 1; Indels
 Query Match
1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels
 Query Match 1.2%; Score 12.4; DB 1; Length 15; Best Local Similarity 86.7%; Pred. No. 1.3e+02; Matches 13; Conservative 0; Mismatches 2; Indels
 RESULT 204
US-09-475-947A-158

Sequence 158, Application US/09475947A

Patent No. 6472154

GENERAL INFORMATION:

APPLICANT: Garner, Harold R.

APPLICANT: Mren, John D.

TITLE OF INVENTION: Polymorphic Repeats in Human Genes

FILE REFERENCE: UTSD0667.

CURRENT APPLICATION NUMBER: US/09/475,947A

CURRENT FILING DATE: 1999-12-31

NUMBER OF SEQ ID NOS: 346

SOFTWARE: Patentin Ver. 2.1

SEQ ID NOS: 346
; TOPOLOGY: linear; MOLECULE TYPE: other nucleic acid; DESCRIPTION: /desc = "primer based on clone 11b." US-08-444-818-203
 OTHER INFORMATION: n signifies a, t, c or g
US-09-475-947A-158
 1865 TTTTATTTTGTTT 1879
 1378 CIGGITIGAAGAAT 1391
 2174 ACTITGATATGACT 2187
 1 CTGGCTTGAAGAAT 14
 2 ACTITIGCIATGACT 15
 Query Match
Best Local Similarity 92.94
Matches 13; Conservative
 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-875-710-1
 TYPE: DNA
ORGANISM: human
 RESULT 203
US-08-875-710-1
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US-08-222-177A-433/c

Sequence 433, Application US/08222177A

Sequence 433, Application US/08222177A

Sequence 433, Application US/08222177A

GENERAL INFORMATION:

APPLICANT: Weber, James L.

TITLE OF INVENTION: (GC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME TITLE OF INVENTION: (GC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME NUMBER OF SEQUENCES: 460

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dewitt Ross & Stevens, S.C.

STREET: 3000 Excelsior Drive, Suite 401
 Sequence 2, Application US/09164249B
Patent No. 6322971
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chetverin, Alexander B.
APPLICANT: Kramer, Fred Russel
TITLE OF INVENTION: NOVEL OLIGONUCLECTIDE ARRAYS AND THEIR USE FOR SORTING,
TITLE OF INVENTION: ISOLATING, SEQUENCING, AND MANIPULATING NUCLEIC ACIDS
FILE REPERENCE: 0.765-004003
CURRENT APPLICATION NUMBER: US 09/164,249B
CURRENT FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: US 08/473,010
PRIOR APPLICATION NUMBER: US 08/475,010
PRIOR FILING DATE: 1994-05-23
 Query Match
1.1%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels
 ALDESOES: DEFLICE NOSE & SCEVELLY, STREET: 8000 Excelsior Drive, Suite 401

CITY: Madison
STATE: Wisconsin
COUNTRY: USA
ZIP: $3717-1914
COMPUTER REABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible.
OURRATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
FILING DATE: 21-APR-1989
ATTORNEY/AGATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGATION NUMBER: 30,431,562
FILING DATE: 21-APR-1989
ATTORNEY/AGATION NUMBER: 30,431,562
FILING DATE: AMPRATION: AMPRE: SATA, Charles S.
REGISTRATION NUMBER: 30,400666,601
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 .
0
 Query Match 1.1%; Score 12; DB 1; Length 12; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 12; Conservative 0; Mismatches 0; Indels
 Query Match
1.1%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: US 07/838,607

PRIOR FILING DATE: 1992-02-19

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 2

LENGTH: 1.2

TYPE: DNA

PRATURE: DNA

PRATURE:

PRATURE:

COMBANISM: Artificial Sequence

PRATURE:

COMBANISM: Artificial Sequence

 1794 GTGTGTGTGT 1805
 12 base pairs
 TYPE: nucleic aci
 US-09-281-481A-21
 US-09-281-481A-21
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0
M
H
 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: primer US-09-958-221A-1
 Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels
Sequence 1, Application US/09958221A; Sequence 1, Application US/09958221A; Sequence 1, Application US/09958221A; Sequence 1, Application US/09958221A; Sequence 1, Application; Millem A.; APPLICANT: Haeringen van, Willem A.; APPLICANT: Haeringen van, Hendrik; TITLE CAPITION: UNIVERSAL VARIABLE FRAGMENTS; FILE REFRENCE: 92750/64
CURRENT APPLICATION NUMBER: US/09/958,221A; CURRENT FILING DATE: 2001-10-03
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 27
SEQ ID NOS: 27
SEQ ID NO 1.
LENGTH: 12
 including application described below:
 NEGULI 209

US-08-201-932A-120/C
Sequence 120, Application US/08291932A
Sequence 120, Application US/08291932A
Sequence 120, Application US/08291932A
Settle Color Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth G.
APPLICANT: Draper, Kenneth G.
APPLICANT: MCAWIGGEN, James
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: NF-KB
NUMBER OF SEQUENCES: 830
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: G13 West Fifth Street
STREET: G11fornia
COUNTRY: U.S.A.
COUNTRY: U.S.A.
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/291,932A
FILING DATE: August 15, 1994
CLASSITCATION: 514
FRIOR APPLICATION DATA: including appli
PRIOR APPLICATION DATA: described below
 COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1
 TYPE: DNA ORGANISM: Artificial Sequence
 1793 TGTGTGTGTG 1804
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 Query Match 1.1%; Score 12; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 12; Conservative 0; Mismatches 0; Indels
 US-08-291-392A-309/C

Sequence 309, Application US/08291932A

Patent No. 5668/30

Patent No. 5668/30

Patent INPORMATION:

APPLICANT: Stinchcomb, Dan T.

APPLICANT: Stinchcomb, Dan T.

APPLICANT: Borner, Kenneth G.

APPLICANT: McSwiggen, James TREATMENT OF TITLE OF INVENTION: RELATED TO LEVELS OF TITLE OF INVENTION: RELATED TO LEVELS OF TITLE OF INVENTION: NF-KB

UNMBER OF SEQUENCES: 830

CORRESSONDENCE ADRERS: 1830

CORRESSONDENCE ADRERS: 1840

CORRESSONDENCE ADRERS: 1840

CORRESSONDENCE ADRERS: 1840

CORRESSONDENCE ADRERS: 1840

COUNTRY: U.S.A.

COUNTRY: U.S.A.

CONPUTER: Solie 4700

CITY: LOS ANGELS: 1950

CORPUTER: SOLIE ADRERS: 1950

CORPUTER: SOLIE ADRERS: 1950

CORPUTER: IBM Compatible

COMPUTER: SOLIE ADRERS: 1950

CORPUTER: Mord Perfect 5.1

CURRENT APPLICATION DATA: described below:

REDIOM TYPE: 3.5" Diskette, 1.44 MD

MEDIOM TYPE: 3.5" Diskette, 1.44 MD

MEDIOM TYPE: 3.5" Diskette, 1.49 MD

MARE: Addust's Mord Perfect 5.1

CURRENT APPLICATION DATA: described below: 7, 1992

ATTORNEY/AGENT INPORMATION: 1.40 MD

MAMBE: MARDING, 1.40 MD

MAMBE: MARDING, 1.40 MD

MAMBE: MARDING, 1.40 MD

MAMBE: MARDING, 1.40 MD

MARE: MARDERS MD

MARE: MARDING, 1.40 MD

MARE: MARDING, 1.40 MD

MARE: MARDERS MD

MARE: MARDING, 1.40 MD

MARC: MARDING, 1.40 MD

MARC: MARDING, 1.40 MD

MARC: MARDING, 1.40 MD

MARC: MARDING, 1.40 MD
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: mucleic acid
TYPE: mucleic acid
STRANDEDNESS: single
 2153 CACCTGGAAGCA 2164
 (213) 955-0440
 linear
 ;
US-08-291-932A-309
 ;
US-08-291-932A-193
 g
 ò
 Gaps
 Score 12; DB 1; Length 15;
Pred. No. 1.5e+02;
 Indels
 COUNTER, EAST-SORGE
COMPUTER, READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM DATE: 18M P.C. DOS 5.0
SOFTWARE: WANDER: 1.994
PRIOR APPLICATION DATA: 10.101ding application
PRIOR APPLICATION DATA: 10.101ding application
PRIOR APPLICATION DATA: 466
FILING DATE: May 18, 1.994
APPLICATION NUMBER: 0.7/987,132
PLING DATE: MAY 18, 1.992
ATTORNEY/AGENT INPORMATION:
NAME: WALDING, RICHARD J.
SPERDENNER, 10.1014,157
 Sequence 193, Application US/08291932A

Batent No. 5658780

GENERAL INFORMATION:
APPLICANT: Stinholomb, Dan T.
APPLICANT: Brayer, Kenneth G.
APPLICANT: MCSW49Gen, James
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: NELATED TO LEVELS OF
TITLE OF INVENTION: NELATED TO LEVELS OF
TITLE OF SEQUENCES: 830
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
 Query Match
1.1%; Score 12; DB
Best Local Similarity 100.0%; Pred. No. 1.5
Matches 12; Conservative 0; Mismatches
 FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: WAADEL 32,327
REFERENCE/DOCKET NUMBER: 20,327
REFERENCE/DOCKET NUMBER: 20,327
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 120: SEQUENCE CHARACTERICIES:
 2153 CACCTGGAAGCA 2164
 TYPE: nucleic acid
STRANDEDNESS: single
 APPLICATION NUMBER:
 CITY: Los Angeles
STATE: California
 ; TOPOLOGY: linear
US-08-291-932A-120
 -08-291-932A-193/c
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US-08-334-847-32 ઠે d ö Gaps ö RESULT 212
US-08-143-219-16
Sequence 16, Application US/08143219
Sequence 16, Application US/08143219
Sequence 16, Application US/08143219
Sequence 16, Application US/08143219
Septent No. 2670330
APPLICANT: Sonemberg, Nahum
APPLICANT: Koromilas, Antonis E.
APPLICANT: Koromilas, Antonis E.
APPLICANT: Koromilas, Antonis E.
APPLICANT: Barber, Glen N.
TITLE OF INVENTION: TUMOR-CELL ASSAY METHOD AND KIT
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Loy & Lyon
CITY: Los Angeles
STAFE: CA
COUNTRY: USA
ZIP: 90017 INDIVIDUAL ISOLATE: COMPLEMENTARY TO THE RNA PROBE FOR INDIVIDUAL ISOLATE: PR-IV, FIGURE 5 Query Match
1.1%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels Length 15; 0; Indels COUNTER, USAS

ZIP: 90017

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5." Diskette, 1.44 Nb

COMPUTER: 1BM compatible
OPERATING SYSTEM: PC-DOS (Version 5.0)
SOFTWARE: Worderfect (Version 5.1)
CURRENT APPLICATION DATA:
RILING DATE: October 25, 1993
CLASSIFICATION DATA: Including application
PRIOR APPLICATION DATA: Hosting application
PRIOR APPLICATION NUMBER: 08/141,24
FILING DATE: September 22, 1993
APPLICATION NUMBER: 07/93,681
FILING DATE: September 22, 1992
APPLICATION NUMBER: 22,798
REFERENCE FORCER INUMBER: 204/139
TELEPHONE: (213) 489-1600
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERICS:
LENGTH: 15 base pairs
WVDP: MICHAEL ACCIDITATION
WVDP: MICHAEL ACCIDITATION
PRIOR MICHAEL ACCIDITAT Query Match
1.1%; Score 12; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE: TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear US-08-143-219-16

Query Match
1.1%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels RESULT 213
US-08-34-847-32/C

US-08-34-847-32/C

J Sequence 32, Application US/08334847

J PAPLICANT: Draper, Kenneth
APPLICANT: Draper, Kenneth
APPLICANT: Pavoo, Pam
APPLICANT: Pavoo, Pam
APPLICANT: Woolf, Tod
TITLE OF INVENTION: INHIBITING RESPIRATORY
TITLE OF INVENTION: INHIBITING RESPIRATORY
TITLE OF INVENTION: SYNOYTIAL VIRUS
NUMBER OF SEQUENCES: 909
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STREET: California
COUNTRY: U.S.A.
ZIF: 90071-206

COMPUTER: READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: BLORGAGE

COMPUTER: HEM COMPUTER: IBM COMPATA:
APPLICATION NUMBER: US/08/334,847

FILING DATE: NO. 5693532ember 4, 1994

PRICORARY APPLICATION DATA:
ATTORNEY APPLICATION NUMBER:
FILING DATE: ... RESULT 214
US-08-34-647-33/C
Sequence 33, Application US/08334847
Patent No. 569532
GENERAL INFORMATION:
APPLICANT: MoSwiggen, James
APPLICANT: Parco, Pam
APPLICANT: Woolf, Tod
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING RESPIRATORY
TITLE OF INVENTION: SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 909
CORRESPONDENCE ADDRESS: ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGIESTRATION NUMBER: 32,32/
REFERENCE/DOCKET 32,209/(
TELECOMMUNICATION INFORMATION:
TELEFAM: (213) 955-0440
TELEFAM: (213) 955-0440
TELEFAM: 67-3510
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDENESS: single 1347 TGTCAAACAAT 1358 TOPOLOGY: linear

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1784 TGTAAATATTGT 1795

APPLICATION NUMBER: US/08/877,418

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 Length 15;
 ALLOWALT AND ALL AND AND ALL AND AND AND AND AND AND AND AND A
 Query Match
1.1%; Score 12; DB 1; I
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0;
 FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
 1521 AIGCCIGCTATT 1532
 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGHH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 13 ArGCCTGCTATT 2
 US-09-340-798A-51
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 Gaps
 Sequence 51, Application US/09340798A

Sequence 51, Application US/09340798A

Sequence 51, Application US/09340798A

Sequence 51, Application US/09340798A

Sequence 51, Application US/09340798A

SERRAL INFORMATION:

BERRY, HELEN C.

PATTLE OF INVENTION: VACCINES COMPRISING SYNTHETIC GENES NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSE: J. MARK HAND - MERCK & CO., INC. STREET: 126 B. LINCOLN AVE., P.O. BOX 2000

CITY: RAHAN

STATE: NEW JERSEY
 ;
 Length 15;
 0; Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURREN APPLICATION DATA: 28-Jun-1999
FILING DATE: 28-Jun-1999
CLASSIFICATION DATA:
 1.1%; Score 12; DB 1; Le
100.0%; Pred. No. 1.5e+02;
tive 0; Mismatches 0;
 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5. Diskette, 1.44 Mb
MEDIUM TYPE: 3.5. Diskette, 1.44 Mb
MEDIUM TYPE: 3.5. Diskette, 1.44 Mb
MEDIUM SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION UNITS: 18/08/334,847
FILING DATE: NO. 5693532ember 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFRENCE/DOCKET NUMBER: 209/C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: (77-33) 955-0440
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
 1347 TGTCAAACAAAT 1358
 Best Local Similarity 100.
Matches 12; Conservative
 COUNTRY: US
ZIP: 07065-0907
DDRESSEE: Lyon & Lyon
TREET: 633 West Fifth
TREET: Suite 4700
 linear
 ADDRESSEE:
 US-08-334-847-33
 Query Match
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 Gaps
 0; Gaps
 Query Match 1.1%; Score 11.4; DB 1; Length 13; Best Local Similarity 92.3%; Pred. No. 1.4e+02; Matches 12; Conservative 0; Mismatches 1; Indels
 Sequence 5, Application US/08476614

Patent No. 5618673

GENERAL INFORMATION:
APPLICANT: MARANG HARASH K
TITLE OF INVENTION: OLIGONUCLEOTIDES AND THEIR USE IN AN ITLE OF INVENTION: ASSAY
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 8TH FLOOR, 1100 NORTH GLEBE ROAD
CITY: MALINGTON
 Length 22;
 Query Match
1.1%; Score 12; DB 1; Length 22;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 5; Indels
 CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
Z1P: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPRAATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/476,614
FILING DATE: 07-UN-1995
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
NAME: MITCHARD, LEONARD C
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 604-349
TELEPHONE: (703) 816 4100
TYPE: MULCIAL SAGE PAIRS
TYPE: MULCIAL SAGE PAIRS
TYPE: MULCIAL SAGE PAIRS
TYPE: MULCIAL SAGE SAGE
MOLGOLY: LINEAR
MOLGOLOGY: LINEAR
MOLECULE TYPE: NO
MUTI-SENSE: NO
 RESULT 218
US-08-153-0518-51
Sequence 51, Application US/081530518
Fatent No. 564596
GENERAL INFORMATION:
APPLICANT: Michael D. West
APPLICANT: Jerry W. Shay
APPLICANT: Woodring E. Wright
 1813 TATATATATATATGTACA 1832
 1 TATATATACACACACA 20
/ TOPOLOGY: linear
// MOLECULE TYPE: DNA (genomic)
US-08-849-021-88
 1818 ATATATATATGTA 1830
 1 ATATATATACGTA 13
 ; ANTI-SENSE: NO
US-08-476-614-5
 RESULT 217
US-08-476-614-5
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 g
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APPLICANT: Elizabeth Blackburn
APPLICANT: Num Woo Kim.
APPLICANT: Calvin is Maria
APPLICANT: Higher and Discosts of Elizabeth
APPLICANT: Higher and Discosts of Elizabeth
APPLICANT: Higher and Discosts of Elizabeth
APPLICANT: Calvin is Earth ANI/ON TELOGRAMSE ACTIVITY
COUNTRY: Calvin is Earth ANI/ON ANI/ON TELEGRAMSE ACTIVITY
COUNTRY: Calvin is Earth ANI/ON ANI/ON TELEGRAMSE ACTIVITY
COUNTRY: Calvin is Earth ANI/ON TELEGRAMSE ACTIVITY
COUNTRY: Calvin is Earth ANI/ON TELEGRAMSE ACTIVITY
CALVIN INCIDENT INCIDENT INCIDENT INCIDENT
CALVIN INCIDENT INCIDENT
CALVIN CALVIN INCIDENT
CALVIN CALVIN CALVIN CALVIN
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Query Match
1.1%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 1.46+02;
Matches 12; Conservative 0; Mismatches 1; Indels
 GENERAL INFORMATION:

APPLICANT:

HATORNEY/AGENT INFORMATION:

NAME: PERKER, David L.

REGISTRATION NUMBER: 32,165

REFERENCE/DOCKET NUMBER: ARCD:155/PAR

TELECOMMUNICATION INFORMATION:

TELEFROME: (713) 789-2679

TELERA: 79-0924

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 base pairs

TYPE: nucleic acid

TYPE: nucleic acid

TYPE: nucleic acid

TOPOLOGY: linear

US-08-431-080-2
 RESULT 221
US-08-151-477A-51
Sequence 51, Application US/08151477A
Patent No. 5830644
GENERAL INFORMATION:
 TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 51:
 1794 GIGIGIGIGIG 1806
 ö
 US-08-431-USD-08-2

US-08-431-USD-08-2

Patent No. 5698686

| Patent No. 5698686
| Patent No. 5698686
| Patent No. 5698686
| Patent No. 5698686
| Patent No. 5698686
| Patent No. 5698686
| Patent No. 5698686
| Patent No. 5698686
| Patent No. 5698686
| Patent Singer, Miriam S.
| Patent Additional Singer Sing
 Query Match
1.1%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels
 CCUNTY: Us.A.

CUNTY: Us.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM COMPATIBLE
COPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/060,952C
FLING DATE: May 13, 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/882,438
FILING DATE: May 13, 1992
APPLICATION NUMBER: 07/882,438
FILING DATE: May 13, 1992
APPLICATION NUMBER: 08/038,766
FILING DATE: May 13, 1993
APPLICATION NUMBER: 08/038,766
APPLICATION NUMBER: 08/038,766
APPLICAT
 1792 TIGIGIGIGIG 1804
 ;
US-08-060-952C-50
```

Application US/08819867

```
GENERAL INFORMATION:

APPLICANT: Michael D. West
APPLICANT: Calvin B. Harley
APPLICANT: Scott L. Weinrich
APPLICANT: Wichael J. Weachern
APPLICANT: Wand Wook in
APPLICANT: Blizabeth H. Blackburn
APPLICANT: Nam Woo Kim
APPLICANT: Nam APPLICANTON: TELOMERASE ACTIVITY
NUMBER OF SCQUENCES: B.
COUNTRY: Los Angeles
STREET: Suite 470
CITY: Los Angeles
STREET: Suite 470
CITY: Los Angeles
STREET: Suite 470
CITY: Los Angeles
STREET: Suite 470
COUNTRY: US A.
ZIP: BOOTI-2066
COMPUTER: EBM Compatible
COMPUTER: IBM Compatible
COMPUTER: TEM Compatible
COMPUTER: TEM Compatible
COMPUTER: TEM COMPATION: 435
APPLICATION NUMBER: 14, 1997
CLASSITICATION NUMBER: 08/153,051
FILING DATE: March 14, 1997
CLASSITICATION NUMBER: 34,561
APPLICATION NUMBER: 34,561
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 Gaps
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 US-06-938-534-2

US-06-938-534-2

JEGUREAL INCRMATION:

APPLICANT: Singer, Miriam S.

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: ATOIG, White & Durkee

STREET: P.O. Box 4433

CITY: HOUSENEES ARTOIG, White & Durkee

CITY: HOUSENEES ARTOIG, White & Durkee

STREET: P.O. Box 4433

CITY: HOUSENEES ARTOIG, White & Durkee

CITY: HOUSENEES ARTOIG, White & Durkee

STREET: P.O. Box 4433

COMPUTER: TEXAS

COMPUTER: TEXAS

COMPUTER: TEXAS

COMPUTER: ELPOPY disk

COMPUTER: ELPOPY disk

COMPUTER: PATABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: PATABLE FORM:

MEDIUM TYPE: PATENTION DATE:

APPLICATION NUMBER: US/08/938,534

FILING DATE: 26-SEP-1997

CLASSIERCATION: 536

PRIOR APPLICATION NUMBER: SN 08/326,781

FILING DATE: PATKER: DAVIG L.

APPLICATION NUMBER: 32,165

FILING DATE: PATKER: DAVIG L.

REGISTRAATION NUMBER: 32,165

REFERENCE/DOCKET NUMBER: 32,165

REFERENCE/DOCKET NUMBER: 32,165

REFERENCE/DOCKET NUMBER: 32,165

REFERENCE CHARACTERISTICS:

LEBNOTH: 13 Dase pairs

TELENATH: 13 Dase pairs

TTELEX: 79-0924

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LEBNOTH: 13 Dase pairs

TYPE: nucleic acid

STREET: 19-0924

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LEBNOTH: 13 Dase pairs

TYPE: nucleic acid

STREET: 79-0924

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LEBNOTH: 13 Dase pairs

TYPE: nucleic acid

STREET: TOWN OF SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LEBNOTH: 13 Dase pairs

TYPE: Number: SINGle
 Query Match 1.1%; Score 11.4; DB 1; Length 13; Best Local Similarity 92.3%; Pred. No. 1.46+02; Matches 12; Conservative 0; Mismatches 1; Indels
 Query Match
1.1%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 1.40+02;
Matches 12; Conservative 0; Mismatches 1; Indels
 1792 TIGIGIGIGIG 1804
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-151-477A-51
 1 regrerererere 13
```

ö ö 1.1%; Score 11.4; DB 1; Length 13; 92.3%; Pred. No. 1.4e+02; ative 0; Mismatches 1; Indels RESULT 224
US-08-464-011B-50
; Sequence 50, Application US/08464011B
; Patent No. 6388789
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
Jerry W. Shay 1792 TIGIGIGIGIGIG 1804 Query Match Best Local Similarity 92.3 Matches 12, Conservative TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear ; US-08-819-867-77

. 0

1794 GIGIGIGIGIG 1806

RESULT 223 US-08-819-867-77

```
Sequence 10, Application US/09922445
; Sequence 10, Application US/09922445
; Patent No. 6528268
; GENERAL INFORMATION:
APPLICANT: Aderson, Maria K.
APPLICANT: Reneland, Lars G. T.
APPLICANT: Reneland, Rikard H.
APPLICANT: Reneland, Rikard H.
APPLICANT: Reneland, Rikard H.
APPLICANT: Reneland, Rikard H.
APPLICANT: Repland, Lars G. T.
APPLICANT: Reneland, Rikard H.
APPLICANT: Repland H. R.
APPL
 Gaps
 Gaps
 ;
0
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PILNG DATE: 30-Jun-1999
CLASSIFICATION: CURROWN-
PRIOR APPLICATION NUMBER: 08/431,080
PRIOR APPLICATION NUMBER: 08/431,080
PRIOR APPLICATION NUMBER: 08/431,080
ATTORNEY/AGENT INFORMATION:
NAME: PARKET CATION NUMBER: 32,165
REGISTRATION NUMBER: 32,165
REGISTRATION NUMBER: 32,165
REGISTRATION NUMBER: 37,165
REGISTRATION NUMBER: 37,165
RETERMORM (512) 418-3000
TELEPHONE: (713) 789-2679
INFORMATION: FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 Dase pairs
 Length 13;
 Query Match
1.1%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels
 Indels
 Query Match
Best Local Similarity 92.3%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 1;
 TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 TYPE: nucleic acid
STRANDEDNESS: single
 1794 GIGIGIGIGIG 1806
 1319 TICCCACCCAATT 1331
 1 Treceacerati 13
 ; ORGANISM: synthetic US-09-922-445-10
 RESULT 227
US-09-922-445-35/c
 US-09-922-445-10
 US-09-345-294-2
 TYPE: DNA
 셤
 à
 a
a
 ઠે
 Gaps
 APPLICANT: Gottschling, Daniel E.
Singer, Mirlam S.
TILLE OF INVENTION: Telomerase Compositions and Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESSE: ADDRESSE: ADDRESSE: ALOUGH, White & Durkee
STREET: P.O. Box 4433
 Woodring E. Wright
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
RELATED TO TELOMERE LENGTH AND/OR
TELOMERASE ACTIVITY
 Indels
 Query Match

1.1%; Score 11.4; DB 1;
Best Local Similarity 92.3%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 1;
 COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
PILLING DATE: 05-JUL-1995
CLASSIFICATION NUMBER: 07/862,438
APPLICATION NUMBER: 07/862,438
APPLICATION NUMBER: 07/802,438
FILLING DATE: MAY 13, 1992
APPLICATION NUMBER: 08/038,766
FILLING DATE: MARCH 24, 1993
APPLICATION NUMBER: 08/059
FILLING DATE: MAY 13, 1993
FILLING DATE: MAY 13, 1993
 CITY: Los Angeles
STATE: California
CCUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/045
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
 TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
 NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 Weet Fifth Street
Suite 4700
 Sequence 2, Application US/09345294
Patent No. 6387619
GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
 ATTORNEY/AGENT INFORMATION:
 1792 TIGIGIGIGIGIG 1804
 CITY: Houston
 US-08-464-011B-50
```

; Sequence 35, Application US/09922445; Patent No. 6528268; GENERAL INFORMATION: APPLICANT: Andersson, Maria K.

STATE: TEXAS COUNTRY: UNITED STATES OF AMERICA ZIP: 77210

JS-09-345-294-2

COMPUTER READABLE FORM:

ö

```
APPLICANT: Berglund, Lars G. T.
APPLICANT: Reneland, Rikard H.
APPLICANT: Adam, Gail I. R.
TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTION OF HEART FAILURE
FILE REPERENCE: GG126US
CURRENT APPLICATION NUMBER: US/09/922,445
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 51
SQOTWARE: Patentin version 3.1
SQOTWARE: Patentin version 3.1
TYPE: ...
 ö
 .
 1.1%; Score 11.4; DB 1; Length 13; 92.3%; Pred. No. 1.4e+02; tive 0; Mismatches 1; Indels
 Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
CONDITIONS RELATED TO
TECLOMERE LENGTH AND/OR
TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 80
 COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FRASESQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/378,535
FILING DATE: 20-Aug-1999
CLASSIPTCATION: <UNKnown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/819,867
 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 2071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ATTORNAY AGENT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
TELECOMMUNICATION:
TELEPHONE: (213) 489-1600
 APPLICANT: Michael D. West
Calvin B. Harley
Scott L. Weinrich
Catherine M. Strahl
Michael J. Meeachern
Jerry Shay
Woodring E. Wright
Blizabeth H. Blackburn
Nam Woo Kim
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
613 West Fifth Street
 US-09-378-535-77; Sequence 77, Application US/09378535; Patent No. 6551774; GENERAL INFORMATION:
 TELEFAX: (213) 955-0440
TELEX: 67-3510
 storage
 1319 TTCCCACCCAATT 1331
 Best Local Similarity 92.3
Matches 12; Conservative
 13 TICCCACCCTAIL 1
 ; TYPE: DNA
; ORGANISM: synthetic
US-09-922-445-35
 Query Match
 RESULT 228
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 g
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Journal May No. 1992 (1992)

Journal May No. 1992 (1992)

Journal May No. 1992 (1992)

JUTIE OF INVENTION: Human No. 5648464ch And Delta, Binding Domains TITLE OF INVENTION: Human No. 5648464ch And Methods Based Thereon NUMBER OF SEQUENCES: 34

CORRESPONDERCE ADDRESS: 34

CORRESPONDERCE ADDRESS: 14

CORRESPONDERCE Bedwords

STREET: 1155 Avenue of the Americas

JOURTY: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MADIUM TYPE: FLOUDEN GISK

COMPUTER TREADABLE FORM:

MADIUM TYPE: FLOUDEN GISK

COMPUTER: THE PO C
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 Gaps
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-377-497-56
 ö
 1.1%; Score 11.4; DB 1; Length 13; 92.3%; Pred. No. 1.4e+02; tive 0; Mismatches 1; Indels
 Ouery Match 1.1%; Score 11.4; DB 1; Length 13; Best Local Similarity 92.3%; Pred. No. 1.4e+02; Matches 12; Conservative 0; Mismatches 1; Indels
 US-09-377-497-56

"Sequence 56, Application US/09377497

"Return No. 6670119

"GENERAL INFORMATION:
APPLICANT: WORSHIXMA, YOSHIE
APPLICANT: MARAL, HIROYUKI
APPLICANT: RATO, IKUNOZO
APPLICANT: RATO, IKUNOSHIN
TITLE OF INVENTION: CANCER-ASSOCIATED GENES
FILE REFERENCE: 1422-388P
CURRENT APPLICATION NUMBER: US/09/377,497
CURRENT FILING DATE: 1999-08-20
NUMBER OF SEO ID NOS: 70
SOFTWARE: FALENTIN Ver. 2.0
 ; TOPOLOGY: BINGLE; SEQUENCE DESCRIPTION: SEQ ID NO: 77: US-09-378-535-77
 OTHER INFORMATION: any n or Xaa = unknown
 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERLSTICS:
LENGTH: 13 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 ORGANISM: Artificial Sequence
 1792 ITGIGIGIGIGIG 1804
 1871 TTTTGTTTTAA 1883
 Local Similarity 92.3%
nes 12, Conservative
 1 redrerererere 13
 1 rrrrrrrrrah 13
 US-08-264-534-28
 SEQ ID NO 56
LENGTH: 13
 Query Match
 TYPE: DNA
 Best Loca
Matches
 LENGTH:
 ઠે
 ઠે
 g
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mcgarry191-19.rni

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1 AGCAAGAAATGGA 13
 ADDRESSEE: Dike, Brons STREET: 130 Water StreCITY: Boston STATE: Massachusetts COUNTRY: USA ZIP: 02109
 Best Local Similarity 92.3
Matches 12; Conservative
 13 raagtraactraa 1
TYPE: nucleic acid
synthesis singlary TOPOLOGY: unknown
MOLECULE TYPE: CDNA
US-08-264-534-28
 RESULT 233
US-08-465-500-28
 US-08-268-799-6
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 GEOUR 264-534-28/C

Sequence 28, Application US/08264534

Fatent No. 5648464

Fatent No. 5648464

FATENCE INTORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: In Toporythmic Proteins, And Methods Based Thereon NUMBER OF SEQUENCES: 34

CITLE OF INVENTION: In Toporythmic Proteins, And Methods Based Thereon NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
FITEET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: FIORPY disk
COMPUTER: Ish PC Compatible
COMPUTER: LIBM PC COMPATION COMPUTER: LIBM PC COMPATION COMPUTER: LIBM PC COMPATION COMPAT
 Query Match
1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels
 PatentIn Release #1.0, Version #1.25
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,534
 FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/695,189
FILING DATE: 03-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MASTOCK, S. Leslie
REFERENCE/DOCKET NUMBER: 18,72
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 212 869864/9741
TELEFAX: 212 869864/9741
TELEFAX: 6141 PENNIE
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TERGH: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
US-08-264-534-28
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/695,189
FILING DATE: 03-MAY-1991
ATTORNEY/AGENT INFORMATION:
 NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REPERENCE/DOCKET NUMBER: 7326-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9990
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,534
 TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
 1839 TAAGTTAATTTAA 1851
 2 TAAGTTAACTTAA 14
 FILING DATE:
 SOFTWARE:
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 Sequence 6, Application US/08268799;
Patent No. 5654195
GENERAL INFORMATION:
APPLICANT: Scalcoski, Joseph
APPLICANT: Haseltine, William A.
APPLICANT: Letvin, No. 5654195man
APPLICANT: Li, John
TITLE OF INVENTION: Wectors Expressing Hybrid Viruses,
TITLE OF INVENTION: Methods of Use And No. 5654195el Assays
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
Query Match 1.1%; Score 11.4; DB 1; Length 14; Best Local Similarity 92.3%; Pred. No. 1.6e+02; Matches 12; Conservative 0; Mismatches 1; Indels
 1.1%; Score 11.4; DB 1; Length 14; 92.3%; Pred. No. 1.6e+02; tive 0; Mismatches 1; Indels
 COMPUTE: PLODY disk
MEDIUM TYDE: Plopy disk
COMPUTER: Plopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,799
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/887,505
PLING DATE: 22-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Elsentelly Romald I.
REGISTATION NUMBER: 30628
REPERENCE/DOCKET NUMBER: 41858
TELECOMMUNICATION INFORMATION:
TELEPRATION INFORMATION:
TELEPRATION INFORMATION:
TELEPRATION INFORMATION:
TELEPRATION INFORMATION:
TELEPRATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
 E: Dike, Bronstein, Roberts and Cushman
130 Water Street
 1839 TAAGTTAATTTAA 1851
 1958 AGCATGAAATGGA 1970
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mcgarry191-19.rni

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US-08-465-500-28
 RESULT 235
US-08-672-564-11
 Sequence 28, Application US/08465500
| Patent No. 5789195
| GENERAL INFORMATION: Artavanis-Tsakonas, Spyridon
| APPLICANT: Artavanis-Tsakonas, Spyridon
| APPLICANT: Rebay, Intervention, Marc A.T. APPLICANT: Belay, Intervention: APPLICANT: Belay, Intervention: Number OF Sequence Secute B. TITLE OF INVENTION: IN TOPORYTHMIC PROTEINS, AND METHODS BASED THEREON NUMBER OF SEQUENCES: ADDRESS:
 Patent No. 5789195
GENERAL INFORMATION
APPLICANT: Muskavitch, Marc A.T.
APPLICANT: Febon, Richard G.
APPLICANT: Rebay, Ilaxia
APPLICANT: Rebay, Ilaxia
APPLICANT: Shepard. Scott B.
TITLE OF INVENTION: IN TOPORYTHMIC PROTEINS, AND METHODS BASED THEREON
TITLE OF INVENTION: IN TOPORYTHMIC PROTEINS, AND METHODS BASED THEREON
NUMBER OF SEQUENCES. 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
 ö
 ö
 Query Match 1.1%; Score 11.4; DB 1; Length 14; Best Local Similarity 92.3%; Pred. No. 1.6e+02; Matches 12; Conservative 0; Mismatches 1; Indels
 ; Sequence 28, Application US/08465500
 1839 TAAGTTAATTTAA 1851
 2 raagiraacrraa 14
 12; Conservative
 USA
 RESULT 234
US-08-465-500-28/c
 COUNTRY:
 셤
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JOSEPHENCE 11, Application US/08672564

Patent No. 5824503

GENERAL INFORMATION:

APPLICANT: KUROWE,

APPLICANT: RAPO, INCOMING

CONTESSONDERSS:

ADDRESSED:

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 Query Match 1.1%; Score 11.4; DB 1; Length 14; Best Local Similarity 92.3%; Pred. No. 1.6e+02; Matches 12; Conservative 0; Mismatches 1; Indels
ZIP: 10036-2711

COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTES: IBM PC compatible
COMPOTES: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,500
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTOMNEY/AGENT INFORMATION:
NAME: MASTORE NUMBER: 18,872
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1326-034
TELEPHONE: (212) 790-9050
TELEPAR: (212) 790-9050
 ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC 8.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1422-0263P
TELECOMMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELEFAX: (703) 205-8000
 TELEX: 248345
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
 1839 TAAGTTAATTTAA 1851
 13 TAAGTTAACTTAA 1
 TOPOLOGY: unknown MOLECULE TYPE: CDNA
```

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
FILING DATE: 07/791,923
FILING DATE: 14-NOV-1991
ATTORNEY/AGENT INFORMATION:
 1839 TAAGTTAATTTAA 1851
 2 raagrraactraa 14
 TOPOLOGY: unknown;
MOLECULE TYPE: cDNA
US-08-346-126-28
 ; Patent No. 5849869
 ઠે
 ö
 Sequence 11 Application US/08672564

Patent No. 5824503

GENERAL INPORMATION:
APPLICANT: KUROME, Yoko
APPLICANT: IZUM, Yoshiya
APPLICANT: SANO, Mutsumi
APPLICANT: RATO, Ikunoshin
APPLICANT: RATO, Ikunoshin
APPLICANT: RATO, Ikunoshin
APPLICANT: SANO, Mutsumi
APPLICANT: RATO, Ikunoshin
APPLIC
 ö
 Ouery Match 1.1%; Score 11.4; DB 1; Length 14; Best Local Similarity 92.3%; Pred. No. 1.6e+02; Matches 12; Conservative 0; Mismatches 1; Indels
 1.1%; Score 11.4; DB 1; Length 14; 92.3%; Pred. No. 1.6e+02; tive 0; Mismatches 1; Indels
 TOPOLOGY: linear MOLECULE TYPE: other nucleic acid (synthetic DNA)
 TOPOLOGY: linear MOLECULE TYPE: other nucleic acid (synthetic DNA) US-08-672-564-11
 COUNTY: USA
ZIE: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,564
FILING DATE: 28 UNDE 1996
CLASSIFICATION: 435
ATTORNEY, AGENT INPORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 1422-0263P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATICATION INFORMATION:
TELECOMMUNICATION INFORMATICATION INFORMA
 RESULT 237
US-08-346-126-28
; Sequence 28, Application US/08346126
 TELEFAX: (703) 205-8050
TELEFAX: 488445
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 Dase pairs
TYPE: mucleic acid
TYPE: mucleic acid
 1839 TAAGTTAATTTAA 1851
 1839 TAAGTTAATTTAA 1851
 2 TAAGTTAACTTAA 14
 Query Match
Best Local Similarity 92.3
Matches 12; Conservative
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 13 TAAGTTAACTTAA 1
 RESULT 236
US-08-672-564-11/c
 US-08-672-564-11
 ò
 g
 g
```

```
GENERAL INFORMATION:
APPLICANT: Attavanis-Teakonas, Spyridon et al.
TITLE OF INVENTION: Human No. 5849869ch And Delta, Binding Domains
TITLE OF INVENTION: Human No. 5849869ch And Delta, Binding Domains
TITLE OF INVENTION: In Toporythmic Proteins, And Methods Based Thereon
NUMBER OF SEQUENCES: 30
CORRESONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
GITY: New York
COINTRY: U.S.A.
SITATE: New York
COUNTRY: U.S.A.
 MS-08-346-126-28/C

Sequence 28, Application US/08346126

Sequence 28, Application US/08346126

Patent No. 584984ATION:

APPLICANT: Arravanis-Teakonas, Spyridon et al.

APPLICANT: Arravanis-Teakonas, Spyridon et al.

TITLE OF INVENTION: Human No. 5849869ch And Delta, Binding Domains

TITLE OF INVENTION: In Toporythmic Proteins, And Methods Based Thereon NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

CONDITE: New York

CONDITE: US.A.
 Query Match 1.1%; Score 11.4; DB 1; Length 14; Best Local Similarity 92.3%; Pred. No. 1.6e+02; Matches 12; Conservative 0; Mismatches 1; Indels
 STATE: New York
COUNTRY: U.S.A.
ZIP: 10.036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,126
```

ö Query Match
1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels

1839 TAAGTTAATTTAA 1851

13 TAAGTTAACTTAA 1

VESCULT 28-28
VS-08-346-128-28
VS-08-346-128-28
VS-08-346-128-28
VS-08-346-128-28
VS-08-346-128-28
VS-08-346-128-28
VS-08-346-128-28
VS-08-346-120
VS-08-346

LENGTH: 14 base pairs TYPE: nucleic acid STRANDEDNESS: single

US-UB-14B-148-24 C

Sequence 28, Application US/08346128

Patent No. 5856441

GENERAL INFORMATION:
TITLE OF INVENTION: Human No. 5856441ch And Delta, Binding Domains
TITLE OF INVENTION: In Toporythmic Proteins, And Methods Based Thereon
TITLE OF INVENTION: In Toporythmic Proteins, And Methods Based Thereon
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSES: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
CUNTRY: US-X.

ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,128 APPLICATION NUMBER: US/US/STG/LEG
TILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879,038
FILING DATE: 30-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION INFORMATION:
TELEFAX: 212 869864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs 1839 TAAGTTAATTTAA 1851 2 TAAGTTAACTTAA 14 nucleic acid MOLECULE TYPE: CDNA US-08-346-128-28

1.1%; Score 11.4; DB 1; 92.3%; Pred. No. 1.6e+02; tive 0; Mismatches 1; RESULT 241
US-08-682-847-8
; Sequence 8, Application US/08682847
; Parent No. 5858989
; GENERAL INFORMATION: 1839 TAAGTTAATTTAA 1851 Query Match 1.1 Best Local Similarity 92.3 Matches 12, Conservative 13 raagrraacrraa 1

Gaps

.. 0

Length 14; Indels

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WESOUR 1443
US-08-544-381B-216/C

Sequence 216, Application US/08544381B
PEREME NO. 6027880

PEREME NO. 6027880

PEREMEAN: MYDRAW-ITON:
APPLICANT: MYDEAL, Earl A.
APPLICANT: Cronin, Mark
APPLICANT: Chee, Mark
APPLICANT: Chee, Mark
APPLICANT: Chee, Mark
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lobann, Peter E.
APPLICANT: Sheldon, Edward L.
TILLE OF INVENTION: Arrays of Nucleic Acid Probes for TITLE OF INVENTION: Arrays of Cystic Pibrosis
NUMBER OF SEQUENCES: 250

CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, 8th Floor
STREET: Two Embarcadero Center, 8th Floor
STREET: California
STREET: California
 CUDNIKY: USA

ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PatentlN Park:
APPLICATION NUMBER: US/08/544,381B
FILING DATE: 10-CCT-1995
CLASSIFICATION NUMBER: US 08/510,521
FILING DATE: 02-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12305
FILING DATE: C2-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: C3-CCT-1994
FILING DATE: 02-AUG-1994
 Query Match
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1;
 FILING DATE: 12-JUL-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: PARK, FREDDIE K.
REGISTRATION NUMBER: 35,636
RERERRENGCE/DOCKET NUMBER: 29310-20005.10
TELESTRENGCE/DOCKET NUMBER: 29310-20005.10
TELESTRINGCE/DOCKET NUMBER: 29310-20005.10
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE AND ASSESSION OF SEQ PAIRS
TYPE: NUCLEIC CACAG
STRANDEDNESS: single
TOPOLLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-682-847-8
 1839 TAAGTTAATTTAA 1851
 셤
 ò
 ö
 Gaps
 APPLICANT: VAN DEN HURK, SYLVIA
APPLICANT: ZAMB, TIM
APPLICANT: TIZZATRICK, DAVID
TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE 1
TITLE OF INVENTION: POLYPEPTIDES AND VACCINES
NUMBER OF SEQUENCES:
CORRESPONDENCES:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
 ö
 Query Match 1.1%; Score 11.4; DB 1; Length 14; Best Local Similarity 92.3%; Pred. No. 1.6e+02; Matches 12; Conservative 0; Mismatches 1; Indels
 COUNTEY: USA

ZIP: 94304-1018

ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,847
FILING DATE: 12-UL-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: PARK, FREDDIE: 35,636
REGISTRATION NUMBER: 35,636
REGISTRATION NUMBER: 35,636
TELEFRAM: (415) 813-5600
TELEFRAM: (415) 494-0792
TELEFRAM: INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: mucleic acid
TYPE: mucleic acid
TYPE: mucleic acid
 ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) US-08-682-847-8
 1839 TAAGTTAATTTAA 1851
 2 raagrraacrraa 14
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Gaps

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1; Indels

Length 14;

APPLICATION NUMBER:

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RESULT 247
US-08-724-466B-17
; Sequence 17, Application US/08724466B.
CURRENT FILING DATE: 1997-04-02
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 14
 Query Match 1.1%;
Best Local Similarity 92.3%;
Matches 12; Conservative
 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
 1865 TITITATITIGI 1877
 1865 TTTTTATTTTGT 1877
 2 rrrrrrrrrrrrrr 14
 rrrrrrrrrr
 LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 linear
 ;
US-08-724-466B-14
 RESULT 246
US-08-724-466B-14
 g
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 δ
 엄
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 Gaps
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 APPLICANT: Combates, N. APPLICANT: Combates, N. APPLICANT: Pardinas, J. APPLICANT: Pardinas, J. APPLICANT: Pardinoo, S. APPLICANT: Prouty, S. APPLICANT: Stenn, K. TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY FILE REFERENCE: JBP-382 CURRENT APPLICATION NUMBER: US/08/832,021
 TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY FILE REFERENCE: JBP-382
CURRENT APPLICATION WHERE: US/08/832,021
CURRENT FILING DATE: 1997-04-02
NUMBER OF SEQ ID NOS: 64
SOFWMARE: Patentin Ver. 2.0
SEQ ID NO SEQ ID NOT. 2.0
 ; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-5
 Length 14;
 Query Match
1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels
 Indels
 Query Match

1.1%; Score 11.4; DB 1;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1;
 HILDER DATE: 26-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Jos
REFERENCE/DOCKET NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 018547-004130US
TELEPHONE: 415-576-020
TELEPHONE: 415-576-0300
INPORMATION POR SEQ ID NO: 216:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
US-08-544-381B-216
 US 08/143,312
 Sequence 16, Application US/08832021
Patent No. 6045998
GENERAL INFORMATION:
 Sequence 5, Application US/08832021
Patent No. 6045998
 TYPE: DNA
ORGANISM: Artificial Sequence
 1871 TTTTTGTTTTAA 1883
 1564 TGCTCACTGACCT 1576
 13 recrearreacer 1
 APPLICANT: Combates, N. APPLICANT: Pardinas, J. APPLICANT: Parimoo, S. APPLICANT: Stenn, K.
 APPLICATION NUMBER:
 GENERAL INFORMATION
 US-08-832-021-16
 JS-08-832-021-5
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, OTHER INFORMATION; Description of Artificial Sequence; primer US-08-832-021-16
 Query March
1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.66+02;
Matches 12; Conservative 0; Mismatches 1; Indels
 Indels
 US-US-1/44-466B-14
Sequence 14, Application US/08724466B
Patent No. 6063606
GENERAL INFORMATION:
GENERAL INFORMATION:
FAPLICANT: Petkovich, P. Martin, White, Jay A.,
APPLICANT: Beckett, Barbara R., Jones, Glenville
TITIE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West
CITY: Toronto
ZIP: MSD 1AS
COUNTRY: Canada
COUNTRY: Canada
COUNTRY: CORRESPONDENCE DISKETCE, 3 1/2 inch, 1.4 Mb storage
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETCE, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPUTEN COMPUTEN COMPUTENCE CONTRY: COMPUTENCE CO
 1.4 Mb storage
 Score 11.4; DB 1;
Pred. No. 1.6e+02;
0; Mismatches 1;
 COMPUTER: COMPAQ, IEM PC COMPATIBLE
COMPUTER: COMPAQ, IEM PC COMPATIBLE
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,466B
RIING DATE: October 1, 1996
RIING DATE: OLOGOBER 1, 1996
RIING DATE: OLOFOR 1, 1996
APPLICATION NUMBER: 08/667,546
RIING DATE: JUMP 21, 1996
ATTORNEY/AGENT INFORMATION:
NAME: HUNT, JOHN C.
REGISTRATION NUMBER: 36,424
REFERENCE/POCKET NUMBER: 36,424
REFERENCE/POCKET NUMBER: 36,434
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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mcgarry191-19.rni

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ð
 Sequence 28, Application US/08893828

Patent No. 6990922

GENERAL INFORMATION:

APPLICANT: Muskavicch, Marc A.T.

APPLICANT: Muskavicch, Marc A.T.

APPLICANT: Rebay, Ilaria

APPLICANT: Shepard, Scott B.

ITTLE OF INVENTION: HUMAN NOTCH AND DELTA, BINDING DOMAINS

TITLE OF INVENTION: IN TOPORYTHMIC PROTEINS, AND METHODS BASED THEREON

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: PRINIE & EDMONDS

STREET: 1155 Avenue of the Americas

CITY: New York
 0; Gaps
 Query Match 1.1%; Score 11.4; DB 1; Length 14; Best Local Similarity 92.3%; Pred. No. 1.6e+02; Matches 12; Conservative 0; Mismatches 1; Indels
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
FULLCANT: BECKET, BATBATA R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADBRESS:
GORRESPONDENCE ADBRESS:
STREET: BOX 25, COMMERCE COURT West
CITY: TOYONG
STREET: BOX 25, COMMERCE COURT WEST
COUNTRY: Canada
COMPUTER: CAMPAQ, IBM PC COMPATIBLE FORM:
MEDILARY TO COMPAQ, IBM PC COMPATIBLE COMPUTER: COMPAQ, IBM PC COMPATIBLE COMPAG, IBM PC COMPATIBLE COMPAG, IBM PC COMPATIBLE COMPAG, IBM PC COMPAGE: MEDILARION NUMBER: MANAE: MANE: M
 COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
 1871 TITITGTTTTAA 1883
 2 rrrrrrrrraa 14
 US-08-893-828-28
 q
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Sequence 28, Application US/08893828

Sequence 28, Application US/08893828

Patent No. 609032

GENERAL INFORMATION:
APPLICANT: Artavanis-Teakonas, Spyridon
APPLICANT: Rebay, Ilaria G.
APPLICANT: Rebay, Ilaria G.
APPLICANT: Blaumenler, Cristine M.
APPLICANT: Shepard, Scott B.
TITLE OF INVEXTION: HUMAN NOTCH AND DELTA, BINDING DOMAINS
TITLE OF INVEXTION: IN TOPORYTHMIC PROTEINS, AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 34
CORRESPONDED ADDRESSE: PENNIE & EDNONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
CONNEM:
 1.1%; Score 11.4; DB 1; Length 14; 92.3%; Pred. No. 1.6e+02; tive 0; Mismatches 1; Indels
 COUNTRY: USA
ZTATE: NY
COUNTRY: USA
ZTATE: NY
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORPUTER: TEM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/893,828
FILING DATE: 11-JUL-1997
CLASSTFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leelie
REGISTRATION: VMBER: 18,735
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ 1D NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: MIGGIG acid
STRANDEDNES: single
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/893,828
FILING DATE: 11-ULL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REFERENCE/DOCKET NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 726-050
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 28:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 1839 TAAGTTAATTTAA 1851
 Query Match
Best Local Similarity 92.33
Matches 12; Conservative
 TOPOLOGY: unknown MOLECULE TYPE: CDNA
 ; MOLECULE TYPE: CDNA
US-08-893-828-28
 unknown
 TOPOLOGY
```

mcgarry191-19.rni

```
APPLICATION NUMBER: 08/724,466
FILING DATE: October 1, 1996
ATTORNEY/AGENT INFORMATION:
NAME: HUND. JOAN C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00010
TELECOMUNICATION INFORMATION:
TELECAX: (416) 863-434
TELECAX: (416) 863-434
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
 1865 TITITATITIGI 1877
 Query Match
Best Local Similarity 92.34
Matches 12, Conservative
 2 rrrrrrrrrrr 14
 TYPE: nucleic acid
STRANDEDNESS: single
 linear
 linear
 ; TOPOLOGY:
US-08-882-164D-14
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 Gaps
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 ASSULT 2019-095A-26
) Sequence 26, Application US/09019095A
Patent No. 628785B
) GENERAL INFORMATION:
) APPLICANT: D'Adrea, Alan D.
TITLE OF INVENTION:
) TITLE OF INVENTION: Deubiquitinating Enzymes That Regulate
TITLE OF INVENTION: Deubiquitinating Enzymes That Regulate
TITLE OF INVENTION: Deubiquitinating Enzymes That Regulate
TITLE OF INVENTION: Deubiquitinating Enzymes That Regulate
FILE REFERENCE: DFCT-43592A2.
CURRENT APPLICATION NUMBER: US/09/019,095A
CURRENT APPLICATION NUMBER: PCT/US96/12884
PRIOR FILING DATE: 1998-02-05
PRIOR FILING DATE: 1996-08-09
PRIOR FILING DATE: 1996-06-14
NUMBER OF SECIENCE STATE

NUMBER OF SECIENCE STATE
SOFTWARE: FastSEQ for Windows Version 3.0
 Query Match
1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels
 Query Match
1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels
 COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage COMPUTER: COMPAQ, IBM PC compatible COMPUTER: COMPAG, IBM PC compatible OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT CUREBUT APPLICATION DATA: APPLICATION NUMBER: US/08/882,164D
PILING DATE: Unne 25, 1997
PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/667,546
PILING DATE: Unne 21, 1996
 JOSEPH TO SEQUENCE 14, Application US/08882164D

| Patent No. 6306624
| APPLICANT: Beckett, Barbara R., Jones, Glenville
| TITLE OF INVENTION: Retinoid Metabolizing Protein
| NUMBER OF SEQUENCES: 43
| CORRESPONDENCE ADDRESS:
| ADDRESSE: Blake, Cassels & Graydon
| STREET: Box 25, Commerce Court West
| CITY: Toronto
 1839 TAAGTTAATTTAA 1851
 1865 TITITATITIGE 1877
 2 rrrrrrrrrgr 14
 13 TAAGTTAACTTAA 1
 STATE: Ontario
COUNTRY: Canada
ZIP: M5L 1A9
 TYPE: DNA ORGANISM: murine
 RESULT 251
US-08-882-164D-14
 US-09-019-095A-26
 US-08-893-828-28
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1.1%; Score 11.4; DB 1; Length 14; 92.3%; Pred. No. 1.6e+02; tive 0; Mismatches 1; Indels
 Query Match 1.1%; Score 11.4; DB 1; Length 14; Best Local Similarity 92.3%; Pred. No. 1.6e+02; Matches 12; Conservative 0; Mismatches 1; Indels
 RESULT 252

RESULT 252

RESULT 252

RESULT 252

RESULT 252

REGUREAL INFORMATION:

Patent No. 6306624

REPLICANT: Petkovich, P. Martin, White, Jay A., APPLICANT: Petkovich, P. Martin, White, Jay A., APPLICANT: Becket, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Protein NUMBER OF SEQUENCES: 43

CORRESPONDENCES: 43

CORRESPONDENCES: 143

COUNTY: Canada

ZITY: TOTOTO COUT West

COUNTY: Canada

ZITY: TOTOTO

COUNTY: Canada

ZITY: TOTOTO

COUNTY: Canada

ZITY: MSLIABS FORM:

MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage

COMPUTER: COMPACE: WORD PERFECT

COMPUTER: COMPACE: WORD PERFECT

COMPUTER: WORD PERFECT

COMPUTER: WORD PERFECT

CORPATION NUMBER: US/08/882,164D

FILING DATE: June 25, 1997

RILING DATE: June 21, 1996

APPLICATION NUMBER: 08/724,466

FILING DATE: June 21, 1996

APPLICATION NUMBER: 36,424

REFERENCE/DOCKET NUMBER: 50767/00010

TELEPRAX: (416) 863-263

INFORMATION FOR SEO ID NO: 17:

SEQUENCE: CHARACTERISTICS:

LENGTH: 14 base pairs

FUENCE: LENGTH: 14 base pairs

FUENCE: LENGTH: 14 base pairs
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1871 TITITGITTIAA 1883

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 1; Indels 0; Gaps
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 RESULT 254

US-09-375-673B-13

Sequence 13, Application US/09375673B

Patent No. 6605431

GENERAL INFORMATION:
APPLICANT: GOURE, RICHARD L.
APPLICANT: ESTERN, SHAWN T.
APPLICANT: ROSS, WILMA E.
APPLICANT: BOSS, WILMA E.
APPLICANT: BOSS, WILMA E.
CURRENT ROSS, WILMS E.
CURRENT APPLICATION NUMBER: US/09/375,673B

CURRENT APPLICATION NUMBER: US/09/375,673B

NUMBER OF SEQ ID NOS: 89

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 13

LENGTH: 14
 TYPE: DNA
CRGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Distal
COTHER INFORMATION: accessory promoter element
US-09-375-673B-13
 Query Match
1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels
 Query Match 1.1%; Score 11.4; DB 1; Length 14; Best Local Similarity 92.3%; Pred. No. 1.6e+02; Matches 12; Conservative 0; Mismatches 1; Indels
US-09475-947A-296

US-09475-947A-296

Sequence 226, Application US/09475947A

Patent No. 6472154

GARDERAL INFORMATION:
APPLICANT: Wren, Jonathan D.
APPLICANT: Mren, John D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes
FILE REFERENCE: UTSD0667

CURRENT APPLICATION NUMBER: US/09/475,947A

CURRENT FILING DATE: 1999-12-31

NUMBER OF SEQ ID NOS: 346

SEQ ID NO 296

LENGTH: 14
 Search completed: April 2, 2004, 14:34:11
Job time : 3 secs
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 1773 AAAATTTATATTG 1785
 1 GIGIGIGAGIGIG 13
 2 AAAATTTATTTIG 14
 ; TYPE: DNA
; ORGANISM: human
US-09-475-947A-296
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61, App 1
62, App 1
63, App 1
64, App 1
65, App 1
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US-10-006-191-93
US-10-006-191-93
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 9, Appli
10, Appl
601, App
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770, App
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 2, 2004, 14:38:01 ; Search time 3 Seconds (without alignments) 2.527 Million cell updates/sec
 us-10-006-191-19
1049
1 ttgaactgattcacatctca......gtgtatattttttctataaa 1049
 45,
 Description
 Sequence of sequen
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Sequence
Sequence
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Sequence
Sequence
 420
 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 US-10-101-040-9
US-09-754-853A-601
US-09-735-383A-5
US-09-735-383A-5
US-09-735-383A-5
US-09-735-383A-61
US-09-735-383A-61
US-09-735-383A-21
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US-10-165-884-1
US-10-006-191-40
US-10-006-191-40
 Total number of hits satisfying chosen parameters:
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US-10-006-191-46
US-10-006-191-46
 SUMMARIES
 Minimum Match 0%
Maximum Match 100%
Listing first 239 summaries
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Gapop 10.0 , Gapext 0.5
 210 segs, 3614 residues
 80
 Length
 rnpb.seq:*
 Minimum DB seq length: 8 Maximum DB seq length: 50
 Query
 April
 Post-processing:
 Title:
Perfect score:
Sequence:
 Scoring table:
 OM nucleic
 Database :
 Searched:
 Run on:
 Result
 Š.
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mcgarry191-19.rnpb

mcgarry191-19.rnpb

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TYPE: DNA ORGANISM: Glycine max
US-09-754-853A-601/c
 US-09-263-959-770
 US-09-735-363A-5
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 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SCHNIDT, Brian
APPLICANT: SCHNIDT, Brian
APPLICANT: SCHNIDT, Brian
APPLICANT: SCHNIDT, Brian
APPLICANT: CARNICHAEL, David
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS OF
TITLE OF INVENTION: USE
TITLE OF INVENTION: USE
TITLE OF INVENTION: USE
TITLE OF INVENTION: USER: US/10/101,040
CURRENT APPLICATION NUMBER: US/9/292,036
PRIOR APPLICATION NUMBER: US 09/292,036
PRIOR PILING DATE: 1999-04-14
PRIOR PILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: US 09/292,036
PRIOR APPLICATION NUMBER: US 09/187,478
 ATTLE OF INVENTION: OCNNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS OF TITLE OF INVENTION: USE: USE A CURRENT APPLICATION NUMBER: US/10/101,040
CURRENT FILING DATE: 2002-03-18
FRIOR PAPLICATION NUMBER: US/9/22,036
FRIOR PAPLICATION NUMBER: US 09/292,036
FRIOR PAPLICATION NUMBER: US 09/292,036
FRIOR PAPLICATION NUMBER: US 09/292,036
FRIOR PILING DATE: 1999-04-14
FRIOR FILING DATE: 1999-04-14
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 Gaps
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 Query Match
2.2%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 5.1;
Matches 24; Conservative 0; Mismatches 1; Indels
 Query Match 2.4%; Score 25; DB 1; Length 25; Best Local Similarity 100.0%; Pred. No. 3; Matches 25; Conservative 0; Mismatches 0; Indels
 ; OTHER INFORMATION: Antisense CTGF oligonucleotide US-10-101-040-10
) CTHER INFORMATION: Antisense CTGF oligonucleotide US-10-101-040-9
 1742 GIGAATITGCCTGTAACAAGCCAGA 1766
 1718 ATTAGACTGGACAGCTTGTGGCAAG 1742
 25 Arragacrosacaccrrerescaas 1
 5.10-101-040-10/c
Sequence 10, Application US/10101040
Publication No. US20020142353A1
 TYPE: DNA
ORGANISM: Artificial sequence
 FEATURE:
 RESULT 3
 B
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Squence 601, Application US/09754853A;

Publication No. USZ0030005491A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Hauge, Barnell, Laurence D.

APPLICANT: Parenell, Laurence D.

APPLICANT: Parenell, Laurence D.

APPLICANT: Wang, Ming Li

TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With

TITLE OF INVENTION: Soybean Cyst Nemarcode Resistance

TITLE OF INVENTION: Soybean Cyst Nemarcode Resistance

TITLE OF INVENTION: Soybean Cyst Nemarcode Resistance

CURRENT APPLICATION NUMBER: US/09/754,853A

CURRENT PILING DATE: 2000-01-07

PRIOR FILING DATE: 2000-01-07

NUMBER OF SEQ ID NOS: 1119

SEQ ID NO 601

LENGTH: 27
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 | Sequence
 FEATURE:
; OTHER INFORMATION: Clone ID: 240017_region_G3_11301_29_Forward_Primer
US-09-754-853A-601
 Gaps
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 Length 27;
 Query Match
2.2%; Score 23.4; DB 1; Length 27;
Best Local Similarity 96.0%; Pred. No. 5.2;
Matches 24; Conservative 0; Mismatches 1; Indels
 Indels
 Query Match 2.1%; Score 22.2; DB 1; Best Local Similarity 88.9%; Pred. No. 7.7; Matches 24; Conservative 0; Mismatches 3;
 ; OTHER INFORMATION: Synthetic Oligonucleotide US-09-735-363A-5
 1793 TGTGTGTGTGTGTGTGTGTATATAT 1819
 1795 TGTGTGTGTGTGTGTATAT 1819
 27 rerererererererererakakr 3
 Sequence 770, Application US/09263959; Patent No. US20220150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
 TYPE: DNA ORGANISM: Artificial Sequence
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Sequence 66, Application US/09735363A

| Sequence 66, Application US/09735363A
| Patent No. US20010041681A1
| GENERAL INFORMATION:
| APPLICANT: Filing. Maxio
| APPLICANT: Filing. Maxio
| APPLICANT: Filing. Maxio
| TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
| TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
| TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
| FILE REFERENCE: 02811-0181
| CURRENT FILING DATE: 2000-12-12
| PRIOR APPLICATION NUMBER: 60/170,325
| PRIOR APPLICATION NUMBER: 60/228,925
| PRIOR FILING DATE: 2000-08-29
| NUMBER OF SEQ ID NOS: 87
| SEQ ID NO 66
| SEQ ID NO 66
| LENGTH: 27
 Gaps
 Gaps
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 ..
0
 Treatment of Cancer
 2.1%; Score 21.8; DB 1; Length 27; illarity 92.0%; Pred. No. 8.8; Conservative 0; Mismatches 2; Indels
 Length 27;
 Indels
 .;
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 DB 1;
 Sequence 2, Application US/10168327
Sequence 2, Application US/10168327
Publication No. US20030176381A1
GENERAL INFORMATION:
APPLICANT: Fillion, Mario C.
FILE REFERENCE: 02811-0211 (42368-274915)
CURRENT APPLICATION NUMBER: US/10/168,327
CURRENT FILING DATE: 2002-10-07
FRIOR APPLICATION NUMBER: PCT/CA00/01562
PRIOR FILING DATE: 2000-12-28
 CTHER INFORMATION: Synthetic oligonucleotide US-10-168-327-2
 Score 21.8; D
Pred. No. 8.8;
 OTHER INFORMATION: Synthetic Oligonucleotide
 Query Match 2.1%; Score 21.8; Destroy Best Local Similarity 92.0%; Pred. No. 8.8; Bredches 23; Conservative 0; Mismatches
 1793 TGTGTGTGTGTGTGTGTATAT 1817
 GTGTATAT 1817
 1793 TGTGTGTGTGTGTGTGTGTATAT 1817
 26
 2 rererererererererereres
 rererererererererererer
 NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.1
SEQ ID NO
LENGTH: 27
 TYPE: DNA
ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence FEATURE:
 1793 TGTGTGTGTGTGTGTG
 Best Local Similarity
Matches 23; Conserv
 RESULT 9
US-09-735-363A-21
 US-09-735-363A-66
 US-09-735-363A-66
 TYPE: DNA
 Query Match
 FEATURE:
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 ਨੇ
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mcgarry.

APPLICANT: Rowen, Lee
APPLICANT: ROOP, Ben F.
TITLE ROOP, Ben F.
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth CITY: Seattle
STATE: Washing.
 ö
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 Sequence 1, Application US/09735363A

Patent No. US20010041681A1

GENERAL INFORMATION:
APPLICANT: Filion, Mario
APPLICANT: Filion, Mario
TILE OF INVENTIONS: Therapeutically Useful Synthetic Oligonucleotides
FILE REFERENCE: 02811-0181
CURRENT FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/170,325
PRIOR APPLICATION NUMBER: 60/170,325
PRIOR PLING DATE: 2000-08-29
PRIOR FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 87

SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 27
 Gaps
 Gaps
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 DB 1; Length 27;
 Length 27;
 Indels
 Indels
 COUNTRY: US
ZIF: 98104-7092
ZIF: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CCASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAWE: MCMASIERS, David D.
REGISTRATION NUMBER: 33,963
REFERENCY/DOCKET 33,963
REFERENCY/DOCKET (206) 622-4900
TELECOMMUNICATION INFORMATION:
TELEBRONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 770:
SEQUENCE CHARACTER/STICS:
INFORMATION FOR SEQ ID NO: 770:
SEQUENCE CHARACTER/STICS:
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
 Query Match
2.1%; Score 21.8; DB 1;
Best Local Similarity 92.0%; Pred. No. 8.8;
Matches 23; Conservative 0; Mismatches 2;
 FEATURE:
; OTHER INFORMATION: Synthetic Oligonuclectide
US-09-735-363A-1
 Query Match 2.1%; Score 22.2; D
Best Local Similarity 88.9%; Pred. No. 7.7;
Matches 24; Conservative 0; Mismatches
 1793 IGTGTGTGTGTGTGTGTGTATATAT 1819
 1 refererererererererererer 27
 TYPE: DNA
ORGANISM: Artificial Sequence
 linear
 ;
US-09-263-959-770
 -09-735-363A-1
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OTHER INFORMATION: Synthetic Oligonucleotide
 Query Match 2.0%; Score 21.4; D
Best Local Similarity 95.7%; Pred. No. 9.6;
Matches 22; Conservative 0; Mismatches
 GIGIGIGIAI 1815
 1793 TGTGTGTGTGTGTGTGTAT 1815
) OTHER INFORMATION: Synthetic Sequence US-09-776-479-1068
 RESULT 12
US-10-112-653-1012
Sequence 1012, Application US/10112653
Publication No. US20030050268A1
GENERAL INFORMATION:
 1 rerererererererererer 23
 rerererererererererer 23
 ORGANISM: Artificial Sequence
 TYPE: DNA ORGANISM: Artificial Sequence
 1793 TGTGTGTGTGT
 Best Local Similarity
Matches 22; Conserv
 US-10-112-653-1012
 US-10-017-995-1068
 Query Match
 TYPE: DNA
 RESULT 13
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 Sequence 22, Application US/09735363A

Sequence 22, Application US/09735363A

Patent No. US20010041681A1

GENERAL INFORMATION

APPLICANT: Fillon, Mario

APPLICANT: Fillon, Mario

TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides

FILE REFERENCE: 0281-0181

CURRENT APPLICATION NUMBER: US/09/735,363A

CURRENT APPLICATION NUMBER: 60/170,325

PRIOR PILING DATE: 1999-12-13

PRIOR FILING DATE: 2000-08-29

NUMBER OF SEQ ID NOS: 87

SOFTWARE PATENTIN VERSION 3.0

SEQ ID NO 22

LENGTH: 24
Sequence 21, Application US/09735363A
Fatent No. US20010041681A1
GENERAL INFORMATION:
APPLICANT: Filion, Mario
APPLICANT: Filion, Nigel
FILE NO INVENTION: The appeutically Useful Synthetic Oligonucleotides
FILE REFERENCE: 02811-0181
CURRENT APPLICATION NUMBER: US/09/735,363A
CURRENT APPLICATION NUMBER: 06/170,325
FRIOR PILING DATE: 1999-12-13
FRIOR PILING DATE: 1999-12-13
FRIOR FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 87
SOFTWARE PATENTIN VETSION 3.0
SEQ ID NO 21
LENGTH: 24
 Gaps
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 Query Match
2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity - 95.7%; Pred. No. 9.6;
Matches 22; Conservative 0; Mismatches 1; Indels
 Length 24;
 1; Indels
 Score 21.4; DB 1;
Pred. No. 9.6;
0; Mismatches 1;
 , OTHER INFORMATION: Synthetic Oligonucleotide US-09-735-363A-22
 ; OTHER INFORMATION: Synthetic Oligonuclectide US-09-735-363A-21
 1793 TGTGTGTGTGTGTGTGTAT 1815
 1793 TGTGTGTGTGTGTGTGTGTAT 1815
 Sequence 1068, Application US/09776479 Publication No. US20030087848A1 GENERAL INFORMATION:
 2 rerererererererererer
 1 rerererererererererer
 APPLICANT: Bratzler, Robert L. APPLICANT: Petersen, Deanna M.
 TYPE: DNA ORGANISM: Artificial Sequence
 TYPE: DNA ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 95.7%;
Matches 22; Conservative
 RESULT 11
US-09-776-479-1068
 RESULT 10
US-09-735-363A-22
 FEATURE:
 FEATURE:
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Gaps
 APPLICANT: Krieg, Arthur M.
APPLICANT: Krieg, Arthur M.
APPLICANT: Escy, Daniel J.
TITLE OF INVENTION: INMUNOSTIMULATORY NUCLEIC ACID FOR
TITLE OF INVENTION: INMUNOSTIMULATORY NUCLEIC ACID FOR
TITLE REPRENCE: COL0139/70060(AMS)
CURRENT APPLICATION NUMBER: US 60/210/112,653
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: US 60/279,642
PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 1040
SGCTYRARE: FastSEQ for Windows Version 3.0
LENGTH: 24
 ö
 Sequence 1068, Application US/10017995
Publication No. US20030055014A1
Publication No. US20030055014A1
APPLICANT: Bratzler, Robert i.
TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
FILE REPERENCE: C1037/7025 (HCL/Mat)
CURRENT APPLICATION NUMBER: US/10/017,995
CURRENT FILING DATE: 2001-12-18
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 1093
 Length 24;
 Length 24;
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Treatment of Asthma and Allergy FILE REFERENCE: C1037/013 (HCL/MAT) CURRENT APPLICATION NUMBER: US/09/776,479 CURRENT FILING DATE: 2001-02-02 PRIOR APPLICATION NUMBER: US 60/179,991 PRIOR FILING DATE: 2000-02-03 NUMBER OF SEQ ID NOS: 1093 SOFTWARE: PastSEQ for Windows Version 3.0 SEQ ID NO 1068 LENGTH: 24
 Indels
 2.0%; Score 21.4; DB 1;
ilarity 95.7%; Pred. No. 9.6;
Conservative 0; Mismatches 1;
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) OTHER INFORMATION: Synthetic Sequence US-09-776-479-907
 RESULT 16
US-10-112-653-876
, FEATURE:
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 Sequence 19, Application US/09735363A
Fatent No. US2010041681A1
Fatent No. US2010041681A1
GENERAL INFORMATION:
APPLICANT: Filion, Mario
APPLICANT: Filion, Mario
FILE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
FILE REFERENCE: 02811-0181
CURRENT FILING DATE: 2000-12-12
FRICR APPLICATION NUMBER: 60/170,325
FRICR APPLICATION NUMBER: 60/170,325
FRICR PLING DATE: 1999-12-13
FRICR FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 19
INCOMPLEE PARENTIN VERSION 3.0
SEQ ID NO 19
INCOMPLEE PARENTIN VERSION 3.0
SEQ ID NO 19
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 DB 1; Length 24;
 Query Match 2.0%; Score 21; DB 1; Length 21; Best Local Similarity 100.0%; Pred. No. 10; Matches 21; Conservative 0; Mismatches 0; Indels
 1; Indels
 Query Match
2.0%; Score 21.4; DI
Best Local Similarity 95.7%; Pred. No. 9.6;
Matches 22; Conservative 0; Mismatches
 ; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-19
 SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1068
LENGTH: 24
 1793 TGTGTGTGTGTGTGTGTGTAT 1815
) OTHER INFORMATION: Synthetic Sequence US-10-017-995-1068
 1793 TGTGTGTGTGTGTGTGT 1813
 1 rerererererererererer 23
 1 rererererererererer
 TYPE: DNA
ORGANISM: Artificial Sequence
 TYPE: DNA
ORGANISM: Artificial Sequence
 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
 RESULT 15
US-09-776-479-907
 RESULT 14
US-09-735-363A-19
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 APPLICANT: Krieg, Arthur M.
APPLICANT: Krieg, Daniel J.
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
FILE REPERENCE: CO1039/70060(AWS)
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: US 60/279,642
PRIOR APPLICATION NUMBER: US 60/279,642
PRIOR PILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 1040
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 876
LENGTH: 21
 US-10-017-995-907
US-10-017-995-907
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US-10-017-995-907
US-10-017-995-907
US-10-017-995-907
US-10-017-907
US-10-
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 Length 21;
 0; Indels
 Length 21;
 Length 21;
 Indels
 Query Match 2.0%; Score 21; DB 1;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 21; Conservative 0; Mismatches
 Query Match
2.0%; Score 21; DB 1;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 21; Conservative 0; Mismatches
Query Match 2.0%; Score 21; DB 1;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 21; Conservative 0; Mismatches (
 , OTHER INFORMATION: Synthetic Oligonucleotide US-10-112-653-876
 ; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-907
 1793 TGTGTGTGTGTGTGTGTGT 1813
 1793 TGTGTGTGTGTGTGTGT 1813
 1793 TGTGTGTGTGTGTGTGTGT 1813
 sequence 876, Application US/10112653
Publication No. US20030050268A1
GENERAL INFORMATION:
 1 TGTGTGTGTGTGTGTGTGT 21
 1 rererererererererer 21
 TYPE: DNA ORGANISM: Artificial Sequence
 TYPE: DNA
ORGANISM: Artificial Sequence
```

Gaps

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APPLICANT: Roach, Jeffrey Shawn
APPLICANT: Wolter, Andreas
TITLE OF INVENTION: MICROCALORIMETRIC DETECTION OF ANALYTES AND BINDING EVENTS
FILE REPERENCE: PROOF
CURRENT APPLICATION NUMBER: US/10/165,854
CURRENT FILING DATE: 2002-06-07
 US=10-085-906-33

Sequence 33, Application US/10085906

Publication No. US2003005437LA1

GENERAL INFORMATION:

APPLICANT: Ying, Vincent
APPLICANT: Wu, Paul

APPLICANT: Wu, Paul

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION UNMBER: US 01/26,215

PRIOR FILING DATE: 1999-03-25

PRIOR FILING DATE: 1999-03-24

PRIOR FILING DATE: 2000-03-24

PRIOR FILING DATE: 2000-03-24

NUMBER OF SEQ ID NOS: 545

SOFTWARE FEASTER FASTER OF WINDOWS VETSION 4.0

SEQ ID NO 33

LENGTH: 20
 FEATURE:

NAME/KEY: modified base

LOCATION: () OTHER INFORMATION: C at position 1 is substituted at the 5' position 0.74ER INFORMATION: with a fluorescein.
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Nucleic Acid Ligand
 Query Match
1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels
 Length 20;
 Indels
 1.9%; Score 20; DB 1;
ilarity 100.0%; Pred. No. 14;
Conservative 0; Mismatches
 1794 GTGTGTGTGTGTGTGTGT 1813
 1793 TGTGTGTGTGTGTGTGTG 1812
 Sequence 1, Application US/10165854 Publication No. US20030059807A1 GENERAL INFORMATION:
 Grerererererererer
 20 rererererererererere
 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
PRIOR FILING DATE: 1998-01-0
NUMBER OF SEQ ID NOS: 2
SOGTWARE: Patentin Ver. 2.0
SEQ ID NO 2
 ; TYPE: DNA; CORGANISM: Homo sapiens
US-10-085-906-33
 Query Match
Best Local Similarity
Matches 20; Conserval
 RESULT 21
US-10-165-854-1/c
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 Sequence 2, Application US/09845742B
Sequence 2, Application US/09845742B
Publication No. US20030215801A1
GENERAL INPORMATION:
APPLICANT: Picken, Molfgang
APPLICANT: Lathan-Timmons A, Hallie
APPLICANT: Lathan-Timmons A, Hallie
APPLICANT: Husar M, Gregory
TITLE OF INVENTION: CYCLOADDITION BIOCONUGATION METHOD
TITLE OF INVENTION: CYCLOADDITION BIOCONUGATION METHOD
FILE REPRENCE: PRO.03
CURRENT APPLICATION NUMBER: US/09/845,742B
 APPLICANT: Fleeks, woltsawy
APPLICANT: Wolter, Andraws
APPLICANT: Sebesta P. David
APPLICANT: Sebesta P. David
APPLICANT: Latham-limmons A, Hallie
APPLICANT: Latham-limmons A, Hallie
APPLICANT: Latham-limmons A, Hallie
APPLICANT: Latham-limmons A, Hallie
APPLICANT: Husar M, Gregory
ITILE OF INVENTION: WITHOD FOR IMMOBILIZING OLIGONUCLEOTIDES EMPLOYING THE
ITILE OF INVENTION: CYCLOADDITION BIOCONUGATION METHOD
ITILE OF INVENTION: CYCLOADDITON BIOCONUGATION METHOD
ITILE OF INVENTION: CYCLOADDITON BIOCONUGATION METHOD
ITILE OF INVENTION WINBER: 60/201,561
PRIOR PELING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: 60/265,020
PRIOR PILING DATE: 2001-01-03-0
PRIOR PILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO.1
LENGTH: 20
WANDER DATE: 1000-05-01
SEQ ID NO.1
 ;
0
 Gaps
 CTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Nucleic Acid Ligand
US-09-845-742B-1
 Query Match
1.9%; Score 20; DB 1, Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels
 CURRENT FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: 60/201,561
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/265,020
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: PCT/US98/00649
 1793 TGTGTGTGTGTGTGTGTG 1812
 Sequence 1, Application US/09845742B
Publication No. US20030215801A1
GENERAL INFORMATION:
APPLICANT: Pieken, Wolfgang
 1 rerererererererer 21
 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
CTHER INFORMATION: Synthetic Construct
US-10-219-238-1
 Query Match
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Sequence 2, Application US/10165854

Publication No. US2033059807A1

GENERAL INFORMATION

GENERAL INFORMATION

TILE OF INVENTION MICROCALORIMETRIC DETECTION OF ANALYTES AND BINDING EVENTS

TILLS OF INVENTION WINERS: US/10/165,854

CURRENT APPLICATION NUMBER: US/10/165,854

CURRENT PAPLICATION NUMBER: 60/296,685

PRIOR FILING DATE: 2002-06-07

NUMBER OF SEQ ID NOS: 4

SEQ ID NO 2

LEMOTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FRATURE:

CHIER INFORMATION: Synthetic Nucleic Acid Ligand

US-10-165-854-2
 ô
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 Gaps
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 | APPLICANT: Linnik, Matthew D. | APPLICANT: Linnik, Matthew D. | APPLICANT: Linnik, Matthew D. | APPLICANT: Linnik, Bonnie | APPLICANT: Hepburn, Bonnie | APPLICANT: Hepburn, Bonnie | ATTLE OF INVENTION: MEYTHEMATOSUS IN INDIVIDUALS HAVING; TITLE OF INVENTION: SIGNIFICANTLY IMPAIRED RENAL FUNCTION | TITLE OF INVENTION: SIGNIFICANTLY IMPAIRED RENAL FUNCTION | FILE REFERENCE: 222312007800 | CURRENT APPLICATION NUMBER: US 60/314,281 | PRIOR APPLICATION NUMBER: US 60/311,858 | PRIOR APPLICATION NUMBER: US 60/311,858 | PRIOR PILING DATE: 2001-08-13 | NUMBER OF SEQ ID NOS: 2 | NUMBER OF SEQ ID NOS: 2 | SEQ ID NO 1
 DB 1; Length 20;
14;
 Length 20;
 0; Indels
 OTHER INFORMATION: Synthetic Nucleic Acid Ligand US-10-165-854-1
 Query Match
1.9%; Score 20; DB 1;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches
 1.9%; Score 20; DB
100.0%; Pred. No. 14;
tive 0; Mismatches
 1793 TGTGTGTGTGTGTGTG 1812
PRIOR APPLICATION NUMBER: 60/296,685
PRIOR FILING DATE: 2001-06-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 1.
LENGTH: 20
 1793 TGTGTGTGTGTGTGTGTG 1812
 Sequence 1, Application US/10219238 Publication No. US20030114405A1 GENERAL INFORMATION:
 rerererererererere
 20 rererererererererere
 TYPE: DNA
ORGANISM: Artificial Sequence
 1.9%
Best Local Similarity 100.0
Matches . 20; Conservative
 -10-219-238-1
 FEATURE:
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US-10-06-191-39/c
US-10-06-191-39/c
Squence 39, Application US/10006191
Squence 39, Application US/10006191
Squence 39, Application No. US20030144223A1
GENERAL INFORMATION:
APPLICANT: William Gaarde
APPLICANT: William Gaarde
TITLE REFERENCE: TATALS 0274
TITLE REFERENCE: TAT-0.727
FILE REFERENCE: TAT-0.727
CURRENT APPLICATION NUMBER: US/10/006,191
CURRENT PILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 153
IENGTH: 20
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 Gaps
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0
 sequence 2, Application US/10219238
sequence 2, Application US/0219238
publication Wo. US20030114405A1
GENERAL INFORMATION:
APPLICANT: Linnik, Matthew D.
APPLICANT: Hepburn, Bonnie
TITLE OF INVENTION: BATHEMATOSUS IN INDIVIDUALS HAVING
TITLE OF INVENTION: SIGNIFICANTLY INDIVIDUALS PRINCE APPLICATION NUMBER: US/010/219,238
CURRENT FILING DATE: 2003-01-10
PRIOR PILING DATE: 2001-08-12
PRIOR APPLICATION NUMBER: US 60/311,858
PRIOR PILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 20
 1.9%; Score 20; DB 1; Length 20;
 Length 20;
Length 20;
 Indels
 0; Indels
 DB 1;
14;
 Query Match
1.9%; Score 20; DB 1;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches
 TYPE: DNA
ORGANIEM: Artificial Sequence
FEATURE:
FORTURE:
JOTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-39
Query Match
Best Local Similarity 100.0%; Pred. No. 14; Matches 20; Conservative 0; Mismatches
 , OTHER INFORMATION: Synthetic Construct
US-10-219-238-2
 1793 TGTGTGTGTGTGTGTGTG 1812
 1794 GIGIGIGIGIGIGIGIGI 1813
 1 Grerererererererer 20
 20 rererererererererer
 TYPE: DNA
ORGANISM: Artificial Sequence
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18-10-06-191-43/c

18-10-06-191-10

18-10-06-191-43/c

18-10-06-191-43
 US-10-006-191-44/c
US-10-006-191-44/c
US-10-006-191-44/c
Sequence 44, Application US/10006191
Publication No. US20030144223A1
Sequence 47, Mainten T. Watt
APPLICANT: William Gaarde
TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION TILE REFERENCE: RTS-0274
FILE REFERENCE: RTS-0274
CURRENT APPLICATION UNMER: US/10/006,191
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 153
TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
 Gaps
 Query Match 1.9%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 14; Matches 20; Conservative 0; Mismatches 0; Indels
 Query Match 1.9%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 14; Matches 20; Conservative 0; Mismatches 0; Indels
 Query Match 1.9%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 14;
) OTHER INFORMATION: Antisense Oligonucleotide US-10-006-191-42
 , OTHER INFORMATION: Antisense Oligonucleotide US-10-006-191-43
), OTHER INFORMATION: AntiBense Oligonucleotide US-10-006-191-44
 FILE REFERENCE: RTS-0274
CHRENT APPLICATION NUMBER: US/10/006,191
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 153
LENGTH: 20
 1832 AGTTATCTAAGTTAATTTAA 1851
 2098 GAACAATGGCCTTTATTAA 2117
 20 AGTTATCTAAGTTAATTTAA 1
 20 GAACAATGGCCTTTATTAA 1
 TYPE: DNA
ORGANISM: Artificial Sequence
 TYPE: DNA ORGANISM: Artificial Sequence
 TYPE: DNA ORGANISM: Artificial Sequence
 SEQ ID NO 43
LENGTH: 20
 SEQ ID NO 44
LENGTH: 20
 RESULT 30
 RESULT 29
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 US-10-006-191-40/c
US-10-006-191-40/c
US-10-006-191-40/c
Publication No. US20030144223A1
GENERAL INFORMATION:
APPLICANT: William Genarde
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH-FACTOR EXPRESSIG
FILE REPERENCE: RTS-0274
CURRENT APPLICATION NUMBER: US/10/006,191
CURRENT PILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 40
LENGTH: 20
 US-10-006-191-41/c

Sequence 41, Application US/10006191

Sequence 41, Application US/200144223A1

Sequence 41, Application No. US20030144223A1

GENERAL INFORMATION NO. US20030144223A1

GENERAL INFORMATION NO. SEQUENCE TO SET
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 y Match 1.9%; Score 20; DB 1; Length 20; Local Similarity 100.0%; Pred. No. 14; hes 20; Conservative 0; Mismatches 0; Indels
 0; Indels
 1.9%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 14; tive. 0; Mismatches 0; Indels
) OTHER INFORMATION: Antisense Oligonucleotide US-10-006-191-41
 Pred. No. 14;
 OTHER INFORMATION: Antisense Oligonucleotide
 0; Mismatches
 1724 CTGGACAGCTTGTGGCCAAGT 1743
 1827 TGTACAGITATCTAAGTTAA 1846
 1719 TTAGACTGGACAGCTTGTGG 1738
 RESULT 28
US-10-006-191-42/c
Sequence 42, Application US/10006191
Publication No. US20030144223A1
GENERAL INFORMATION:
 20 rradacredacacerrered 1
 20 credacaccricredcaacr 1
 20 rdracagrrarcraagrraa 1
 Best Local Similarity 100.0%; Matches 20; Conservative 0
 TYPE: DNA
ORGANISM: Artificial Sequence
 TYPE: DNA
ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 100.(
Matches 20; Conservative
 APPLICANT: William Gaarde APPLICANT: Andrew T. Watt
 US-10-006-191-40
 Query Match
 FEATURE:
 Matches
 RESULT 26
 RESULT 27
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Sequence 48, Application US/10006191
Publication No. US20030144223A1
GENERAL INFORMATION
APPLICANT: William GRATCH
APPLICANT: Milliam GRATCH
APPLICANT: MILLIAM GRATCH
APPLICANT: MILLIAM GRATCH
AND AND ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION TITLE OF INVENTION: ANTISENSE WOLDOOF, 191
CURRENT APPLICATION NUMBER: US/10/006,191
CURRENT FILLING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 153
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0
 Indels
 Length 20;
 Length 20;
 0; Indels
 Indels
 1.9%; Score 20; DB 1;
ilarity 100.0%; Pred. No. 14;
Conservative 0; Mismatches
 DB 1;
14;
 Ouery Match
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches (
 , OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-49
 , OTHER INFORMATION: Antisense Oligonucleotide US-10-006-191-48
 ; OTHER INFORMATION: Antisense Oligonucleotide US-10-006-191-47
 Query Match
1.9%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches
CURRENT APPLICATION NUMBER: US/10/006,191
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 47
LENGTH: 20
 2218 TGACCAAAAGTTACATGTTT 2237
 2213 GAGTGTGACCAAAAGTTACA 2232
 20 rgaccaaaagriacargrir 1
 20 gagrergaccaaaagrraca 1
 TYPE: DNA
ORGANISM: Artificial Sequence
 TYPE: DNA ORGANISM: Artificial Sequence
 TYPE: DNA ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity
Matches 20; Conserv
 US-10-006-191-49/C
 RESULT 34
US-10-006-191-48/c
 SEQ ID NO 48
LENGTH: 20
 FEATURE:
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 Sequence 47, Application US/10006191
Publication No. US20030144223A1
GENERAL INFORMATION:
APPLICANT: William Gaarde
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSIG
 Publication No. US20030144223A1

Publication No. US20030144223A1

GENERAL INFORMATION:

APPLICANT: William Gaarde

APPLICANT: William Garde

APPLICANT: WILLIAM GARDEW T. Watt

TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSIC

FILE REPRENCE: RIS-0274

CURRENT APPLICATION NUMBER: US/10/006,191

CURRENT FILING DATE: 2001-12-10

NUMBER OF SEQ ID NOS: 153

LENGTH: 20
 US-10-006-191-45/C
US-10-006-191-45/C
US-10-006-191-45/C
Publication No. US-20030144223A1
Publication No. US-20030144223A1
GENERAL INFORMATION:
APPLICANT: William Gaarde
APPLICANT: Andrew T. Watte
TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSIC
TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSIC
CURRENT APPLICATION NUMBER: US/10/006,191
CURRENT PILING DATE: 2001-12-10
MUMBER OF SEQ ID NOS: 153
SEQ ID NO 45
LENGTH: 20
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 DB 1; Length 20;
14;
 Query Match
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels
 0; Indels
 Indels
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0
 OTHER INFORMATION: Antisense Oligonucleotide
 Query Match 1.9%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 14; Matches 20; Conservative 0; Mismatches
 OTHER INFORMATION: Antisense Oligonucleotide
 0; Mismatches
 2208 GTTGAGAGTGTGACCAAAAG 2227
 2203 TATTIGITGAGAGIGIGACC 2222
 2198 CAGITIATITGTIGAGAGIG 2217
 Grreadagrercadocadade 1
 20 rarrdradadadadada 1
 20 cadrirarirgricadadre 1
 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
 TYPE: DNA ORGANISM: Artificial Sequence
 20; Conservative
 RESULT 33
US-10-006-191-47/c
 RESULT 32
US-10-006-191-46/c
 US-10-006-191-46
 US-10-006-191-45
 FEATURE:
 Matches
 RESULT 31
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Sequence 63, Application US/10006191
Publication Vo. US20030144223A1
GENERAL INFORMATION:
APPLICANT: William Gaarde
APPLICANT: Milliam Gaarde
APPLICANT: ANTIGENE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION FILE REPERENCE: RTS-0274
CURRENT APPLICATION NUMBER: US/10/006,191
CURRENT PILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 63
 Sequence 62 Application US/10006191
Publication No. US20030144223A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLS OF INVENTION: William Gaarde
APPLICANT: William Gaarde
APPLICANT: William Gaarde
APPLICANT: Wattew T. Watt
TILLS OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
FILE REPERENCE: RTS-0274
CURRENT FILING DATE: 2001-12-10
SUMBER OF SEQ ID NOS: 153
SEQ ID NO 62
LENGTH: 20
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 Length 20;
 DB 1; Length 20;
 Indels
 Indels
 Length 20,
 DB 1;
. 14;
 FEATURE: ; OTHER INFORMATION: Antisense Oligonucleotide US-10-006-191-63
 CTHER INFORMATION: Antisense Oligonucleotide US-10-006-191-62
 Query Match
1.9%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches
 TYPE: DNA
CRGANISM: Artificial Sequence
PEATURE:
CTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-61
 Query Match 1.9%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 14, Matches 20; Conservative 0; Mismatches
 Query Match
Best Local Similarity 100.0%; Pred. No. 14.
Matches 20; Conservative 0; Mismatches
CURRENT APPLICATION NUMBER: US/10/006,191
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 61
LENGTH: 20
 2206 TIGITGAGAGIGIGACCAAA 2225
 1834 TIATCTAAGTTAATTTAAAG 1853
 20 riarchagiraarrraaag 1
 TYPE: DNA ORGANISM: Artificial Sequence
 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
 US-10-006-191-63/c
 RESULT 39
US-10-006-191-62/c
 LENGTH: 20
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 g
 Sequence 60, Application US/10006191
Publication No. US20030144223A1
GENERAL INFORMATION:
APPLICANT: William Gaarde
APPLICANT: Watt
TILE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSIC CURRENT APPLICATION NUMBER: US/10/006,191
CURRENT APPLICATION NUMBER: US/10/006,191
CURRENT FILING DATE: 2001-12-10
SEQ ID NOS: 153
LENGTH: 20
 APPLICANT: William Gaarde
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSIG
FILE REFERENCE: RIS-0274
 GENERAL INFORMATION:
APPLICANT: William Gaarde
APPLICANT: William Gaarde
APPLICANT: William Gaarde
APPLICANT: Wadtew T. Watt
TITLE OF INVENTION: WATSENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSIC
FILE REPERBNCE: RTS-0274
CURRENT APPLICATION NUMBER: US/10/006,191
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 59
LENGTH: 20
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 Ouery Match 1.9%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 14; Matches 20; Conservative 0; Mismatches 0; Indels
 1.9%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 14; tive. 0; Mismatches 0; Indels
 ; OTHER INFORMATION: Antisense Oligonucleotide US-10-006-191-60
 ; OTHER INFORMATION: Antisense Oligonucleotide US-10-006-191-59
 1752 CIGTAACAAGCCAGAITITI 1771
 1723 ACTGGACAGCTTGTGGCAAG 1742
 Sequence 61, Application US/10006191 Publication No. US20030144223A1 GENERAL INFORMATION:
 2242 CTTTCTAGTTGAAAATAAAG 2261
 RESULT 36
US-10-006-191-59/c
Sequence 59, Application US/10006191
; Publication No. US20030144223A1
 20 creraccadeccadarrrrr 1
 20 Acresacascristescaas 1
 CTTTCTAGTTGAAATAAAG 1
 ORGANISM: Artificial Sequence FEATURE:
 TYPE: DNA
ORGANISM: Artificial Sequence
 Best Local Similarity 100.0
Matches 20; Conservative
 RESULT 37
US-10-006-191-60/c
 US-10-006-191-61/c
 20
 TYPE: DNA
 Query Match
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Sequence 94, Application US/10006191

Publication No. USZ0030144223A1

GENERAL INFORMATION:

APPLICANT: Milliam Gaarde

APPLICANT: Milliam Gaarde

APPLICANT: Milliam Gaarde

APPLICANT: MILLIAM GAARDERENCE: RTS-0274

TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION

FILE REPERENCE: RTS-0274

CURRENT PAPLICANTION NUMBER: US/10/006,191

CURRENT FILING DATE: 2001-12-10

NUMBER OF SEQ ID NOS: 153

SEQ ID NO 94

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 Length 20;
 Length 20;
 Indels
 Length 20;
 Indels
 Indels
 DB 1;
14;
 Query Match
1.9%; Score 20; DB 1;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches
 DB 1;
14;
 ; FEATURE:
, OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-94
) OTHER INFORMATION: Antisense Oligonucleotide US-10-006-191-93
 TYPE: DNA
CRGANIEM: Artificial Sequence
FEATURE:
COTER INFORMATION: Antisense Oligonucleotide
US-10-006-191-92
 Query Match
1.9%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches
 Query Match
1.9%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches
 1371 CCAGACACTGGTTTGAAGAA 1390
 1274 GIAGCACAAGTIATTIAAAT 1293
 1242 TCACATCTCATTTTCCGTA 1261
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 92
LENGTH: 20
 TYPE: DNA
ORGANISM: Artificial Sequence
 TYPE: DNA ORGANISM: Artificial Sequence
 US-10-006-191-94/c
 SEQ ID NO 93
LENGTH: 20
 RESULT 45
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 Sequence 65, Application US/10006191
Publication No. US2030144223A1.
GENERAL INFORMATION:
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GENERAL INFORMATION:
TITLE OF INVENTION:
AND ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSIC CURRENT APPLICATION NUMBER: US/10/006,191
CURRENT FILING DATE: 2001-12-10
SEQ ID NOS: 153
LENGTH: 20
 Sequence 64, Application US/10006191
Publication No. US20030144223A1
GENERAL INFORMATION:
APPLICANT: William Gaarde
APPLICANT: William Gaarde
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSIC FILE REFERENCE: RIS-0274
CURRENT APPLICATION NUMBER: US/10/006,191
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 64
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 Query Match
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels
 Query Match 1.9%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 14; Matches 20; Conservative 0; Mismatches 0; Indels
 ; OTHER INFORMATION: Antisense Oligonucleotide US-10-006-191-64
 OTHER INFORMATION: Antisense Oligonucleotide
 2243 TITCIAGITGAAATAAAGT 2262
 2219 GACCAAAGTTACATGTTTG 2238
 2212 AGAGTGTGACCAAAAGTTAC 2231
 rrrcracricaaaaraacr 1
 20 GACCAAAGTTACATGTTTG 1
 20 AGAGTGTGACCAAAAGTTAC 1
 ORGANISM: Artificial Sequence
 TYPE: DNA ORGANISM: Artificial Sequence
 RESULT 42
US-10-006-191-65/C
 US-10-006-191-64/c
 US-10-006-191-65
 TYPE: DNA
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RESULT 49
US-09-735-363A-20
i US-09-735-363A-20
i Sequence 20, Application US/09735363A
i Patent No. US20010041681A1
i GENERAL INFORMATION Mario
APPLICANT: Phillip, Nigel
TILE OF INVENTION: Therapeutically Useful Synthetic Oligonuclectides
TILE OF INVENTION: Therapeutically Useful Synthetic Oligonuclectides
TILE REFERENCE: 0201-0181
CURRENT APPLICATION NUMBER: US/09/735,363A
CURRENT APPLICATION NUMBER: 60/170,325
PRIOR PRILOR DATE: 1999-12-13
PRIOR FILING DATE: 1999-12-13
PRIOR FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 20
LENGTH: 21
 Gaps
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 Sequence 1, Application US/10385193
; Bequence 1, Application US/10385193
; Publication No. US20030229218A1
; GENERAL INFORMATION:
 APPLICANT: Nanda D. Sinha
; TITLE OF INVENTION: Synthoms for Oligonucleotide Synthesis
; TITLE OF INVENTION: Synthoms for Oligonucleotide Synthesis
; FILE REFRENCE: 2733.1001.001
; CURRENT APPLICATION NUMBER: US/10/385,193
; CURRENT FILING DATE: 2003-09-07
; PRIOR FILING: 2000-09-07
; NUMBER OF SEQ ID NOS: 2
; NUMBER OF SEQ ID NOS: 2
; SOFTHARE: FastSEQ for Windows Version 4.0
; SEQ ID NO :
 DB 1; Length 21;
14;
 Indels
 Length 20;
 Indels
 Query Match 1.9%; Score 20; DB 1;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches
 ; CTHER INFORMATION: Synthetic Oligonucleotide US-09-735-363A-20
 ; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; POTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-97
 Query Match 1.9%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 14, Matches 20; Conservative 0; Mismatches
 1794 GIGIGIGIGIGIGIGIGIGI 1813
 1713 TGTCGATTAGACTGGACAGC 1732
 1 Grerererererererer 20
 20 rercearradacredacade 1
 TYPE: DNA
ORGANISM: Artificial Sequence
 TYPE: DNA ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: synthetic US-10-385-193-1
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 97
LENGTH: 20
 JS-10-385-193-1/c
 FEATURE:
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 Sequence 96, Application US/10006191
Publication No. US20030144223A1
GENERAL INFORMATION:
APPLICANT: William Gaarde
APPLICANT: William Gaarde
APPLICANT: Milliam Gaarde
APPLICANT: Milliam Garde
APPLICANT: Milliam Garde
APPLICANT: NUMBER: US/10/006,191
FILE REPERENCE: RIS-0274
CURRENT APPLICANTON NUMBER: US/10/006,191
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 96
LENGTH: 20
 Sequence 97, Application US/10006191
Publication No. US20030144223A1
GENERAL INFORMATION:
PAPPLICANT: William Gaarde
APPLICANT: William Gaarde
APPLICANT: WINSWITON: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSIC FILE OF INVENTION: ANTISENSE WODULATION OF CURRENT APPLICATION NUMBER: US/10/006,191
CURRENT APPLICATION NUMBER: US/10/006,191
 S-10-006-191-95/c
Sequence 95, Application US/10006191
Sequence 95, Application US/10006191
Sublication No. USZ0030144223A1
GENERAL INFORMATION:
APPLICANT: William Gaarde
APPLICANT: William Gaarde
APPLICANT: William Gaarde
APPLICANT: William Gaarde
CURRENT SILING DATE: 20274
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 95
LENGTH: 20
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 1.9%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 14; cive 0; Mismatches 0; Indels
 DB 1; Length 20;
14;
 0; Indels
 ; FEATURE:
- OTHER INFORMATION: Antisense Oligonuclectide
US-10-006-191-95
 ; OTHER INFORMATION: Antisense Oligonucleotide US-10-006-191-96
 Query Match 1.9%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 14; Matches 20; Conservative 0; Mismatches
 1637 GTTGTTCCTTAAGTCAGAAC 1656
 1553 AAATTTTAGCGTGCTCACTG 1572
 20 CCAGACACTGGTTTGAAGAA 1
 20 AAATTTTAGCGTGCTCACTG
 TYPE: DNA ORGANISM: Artificial Sequence
 TYPE: DNA ORGANISM: Artificial Sequence
 Best Local Similarity 100. Matches 20; Conservative
 US-10-006-191-97/c
 US-10-006-191-96/c
 Query Match
 FEATURE:
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RESULT 53

US-10-357-488-5

US-10-357-488-5

US-10-357-488-5

Publication No. US20030194730a1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: No. US20030194730A1e1 FISSR-PCR primers and markers and markers for identifying genetic constitution and bree TITLE OF INVENTION: varities.
FILE REFERENCE: 782-indian
FILE REPERENCE: 782-indian
CURRENT APPLICATION NUMBER: US/10/357,488

CURRENT PILING DATE: 2003-02-04

PRIOR APPLICATION NUMBER: 260/MAS/2002

PRIOR APPLICATION NUMBER: 350/MAS/2002

NUMBER OF SEQ ID NOS: 37

SOFTWARE PATENTIN Version 3.1
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 Sequence 7, Application US/09557423
; Sequence 7, Application US/09557423
; Patent No. US2020094555A1
; GENERAL INFORMATION:
APPLICANT: Belocserkovskii, Boris
APPLICANT: Reddy, Gurucharan
; APPLICANT: Ascaling, David A.
; TITLE OF INVENTION: Locked Nucleic Acid Hybrids and Methods of Use
TILE REFERENCE: A-68112-1/RFT/RMS/BTC
CURRENT APPLICATION NUMBER: US/09/557, 423
; CURRENT FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: USSN 60/130,345
; NUMBER OF ERQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
 Gaps
 ; FEATURE:
; OTHER INFORMATION: A novel FISSR-PCR primer for genotyping eukaryotes
US-10-357-488-5
 Gaps
 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Z-DNA
 Query Match
1.8%; Score 19.4; DB 1; Length 23;
Best Local Similarity 95.2%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 1; Indels
 Length 23;
 DB 1;
 Query Match
1.9%; Score 19.8; E
Best Local Similarity 91.3%; Pred. No. 16;
Matches 21; Conservative 0; Mismatches
 1793 TGTGTGTGTGTGTGTGTAT 1815
 GTGT 1813
 23 rerererererarerererer 1
 3 raigrerererererererer 23
 TYPE: DNA ORGANISM: Artificial Sequence
 TYPE: DNA ORGANISM: Artificial Sequence
INFORMATION FOR SEQ 1D NO: 7;
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
LENGTH: nucleic acid
STRANDEDNESS: single
CS-09-263-959-774
 1793 TGTGTGTGTGTGTGTG
 US-09-557-423-7/c
 SEQ ID NO 7
LENGTH: 19
 SEQ ID NO 5
LENGTH: 23
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 Sequence 774, Application US/09263959

Ratent No. US20020150891A1

GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
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 Sequence 2, Application US/10385193
; Publication No. US2003022918A1
; GENERAL INFORMATION:
; APPLICANT: Nanda D. Sinha
; TITLE OF INVENTION: Synthons for Oligonucleotide Synthesis; TIER REFERENCE: 2733.1001-001
; CURRENT APPLICATION NUMBER: US/10/385,193
; CURRENT FILING DATE: 2003-03-07
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEC ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; LEMOTH. 21
 Query Match 1.9%; Score 20; DB 1; Length 21; Best Local Similarity 100.0%; Pred. No. 14; Matches 20; Conservative 0; Mismatches 0; Indels
 DB 1; Length 21;
14;
 0; Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 05-MAR-1999
 ADDRESSEE: Seed and Berry LLP
STREET: 6200 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
 Query Match 1.9%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 14; Matches 20; Conservative 0; Mismatches
 NAME: McMasters, David D.
REGISTATION NUNBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
 UMBER: US/09/263,959
05-MAR-1999
 1794 GTGTGTGTGTGTGTGT 1813
 1794 GTGTGTGTGTGTGTGTGT 1813
 1 Grerererererererer
 20 drerererererererer
 TYPE: DNA ORGANISM: Artificial Sequence
 ; FEATURE:
; OTHER INFORMATION: synthetic
US-10-385-193-2
 RESULT 52
US-09-263-959-774/c
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Sequence 155, Application US/1006191

Publication No. US2030144223A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: William Garde
APPLICANT: Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
FILE REFERENCE: RIS-02.01
CURRENT FILING DATE: 201-12-10
NUMBER OF SEQ ID NOS: 153
LENGTH: 20
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 Sequence 17, Application US/09735363A

| Sequence 17, Application US/09735363A
| Patent No. US20010041681A1
| GENERAL INFORMATION:
| APPLICANT: Filion, Mario
| APPLICANT: Filion, Mario
| APPLICANT: Filion, Mario
| APPLICANT: Filion, Mario
| TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
| TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
| TITLE TEPERENCE: 0281-0181
| CURRENT FILING DATE: 2000-12-12
| PRIOR PELICATION NUMBER: 60/170,325
| PRIOR PELICATION NUMBER: 60/170,325
| PRIOR PELICATION NUMBER: 60/228,925
| NUMBER OF SEQ ID NOS: 87
| SOFTWARE: Patentin Version 3.0
| SEQ ID NOS: 87
 ö
 Indels
 Indels
 Query Match 1.8%; Score 18.4; DB 1;
Best Local Similarity 95.0%; Pred. No. 23;
Matches 19; Conservative 0; Mismatches 1;
 Query Match
1.7%; Score 18; DB 1;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches
) OTHER INFORMATION: Synthetic Oligonucleotide US-09-735-363A-17
 , OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-153
 US-09-735-363A-18
; Sequence 18, Application US/09735363A
; Patent No. US20010041681A1
 2247 TAGTIGAAATAAAGTGTAT 2266
 1793 TGTGTGTGTGTGTGTG 1810
 20 ragricadadradagrarar 1
 TYPE: DNA ORGANISM: Artificial Sequence
 TYPE: DNA
ORGANISM: Artificial Sequence
 RESULT 57
US-10-006-191-153/c
 FEATURE:
 RESULT 59
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 Sequence 8, Application US/09557423

Sequence 8, Application US/09557423

Batent No. US2020094555A1

GENERAL INFORMATION:

APPLICANT: Beloteerkovskii, Boris

APPLICANT: Reddy, Gurucharan

APPLICANT: Zarling, David A.

TITLE OF INVENTION: Locked Nucleic Acid Hybrids and Methods of Use

FILE REFERENCE: A-68112-117F7/RWS/BTC

CURRENT APPLICATION NUMBER: US/09/557,423

CURRENT FILING DATE: 1999-04-21

PRIOR APPLICATION NUMBER: USN 60/130,345

PRIOR PILING DATE: 1999-04-21

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 8

LENGTH: 19
 Gaps
 Gapa
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 ;
0
 RESULT 56
US-09-669-373-3086/c
; Sequence 3086, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; TIER REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-05
; PRIOR FILING DATE: 2001-01-05
; PRIOR FILING DATE: 2001-01-05
; PRIOR FILING DATE: 2001-01-15
; PRIOR FILING DATE: 2001-01-15
; PRIOR FILING DATE: 2001-01-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 3086
; LENGTH: 19
 OTHER INFORMATION: Description of Artificial Sequence: Z-DNA
 1.8%; Score 19; DB 1; Length 19;
100.0%; Pred. No. 19;
ive 0; Mismatches 0; Indels
 Length 19;
 Indels
 Length 19;
 0; Indels
 Score 19; DB 1;
Pred. No. 19;
 1.8%; Scor.
100.0%; Pred. No. 1...
 Query Match 1.8%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 19; Matches 19; Conservative 0; Mismatches
 1793 TGTGTGTGTGTGTGT 1811
 1793 TGTGTGTGTGTGTGT 1811
 1 rerererererererer
 TYPE: DNA
ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 100.0
Matches 19; Conservative
 Query Match
Best Local Similarity 100.
Matches 19; Conservative
 ; ORGANISM: Glycine max US-09-969-373-3086
 RESULT 55
US-09-557-423-8
US-09-557-423-7
 US-09-557-423-8
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APPLICANT: Filion, Mario

1793 TGTGTGTGTGTGTGTGT 1811

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Indels
 Length 18;
 Indels
 OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Oligonucleotide
 ; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide
US-10-011-204-1
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0
 DB 1;
26;
 Query Match 1.7%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 26; Matches 18; Conservative 0; Mismatches
 0; Mismatches
 1.7%; Score 18;
100.0%; Pred. No.
 PRIOR FILING DATE: 1995-03-10
PRIOR APPLICATION NUMBER: GB 9404709.9
PRIOR FILING DATE: 1994-03-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2:1
SEQ ID NO
LENGTH: 18
 Sequence 26, Application US/10357488 Publication No. US20030194730A1 GENERAL INFORMATION:
 1794 GTGTGTGTGTGTGTGT 1811
 1793 TGTGTGTGTGTGTGTG 1810
 1 crererererererer 18
 18 rerererererererere
 TYPE: DNA
ORGANISM: Artificial Seguence
FEATURE:
 TYPE: DNA
ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 100.
Matches 18; Conservative
 RESULT 63
US-10-357-488-26
 US-10-011-204-2
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 APPLICANT: Boyce-Jeaven
APPLICANT: Solve, Jonathan
APPLICANT: Goelet, Philip
TILLE OF INVENTION: De No. US20020146704Alo or "Universal" Sequencing Array
FILE REPERENCE: 13019-2
CURRENT APPLICATION NUMBER: US/09/896,650A
CURRENT APPLICATION SOLVED
 ö
 APPLICANT: EXINS, Roger P
TITLE OF INVENTION: Binding assay using binding agents with tail groups
TITLE OF INVENTION: Binding assay using binding agents with tail groups
TITLE REPERENCE: 0380-P01180USO CURRENT APPLICATION NUMBER: US/10/011,204
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US/88/700,530
PRIOR PILING DATE: 1996-10-23
PRIOR APPLICATION NUMBER: PCT/GB95/00521
 Gaps
 Gaps
APPLICANT: Phillip, Nigel
TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
FILE REFERENCE: 02811-0181
CURRENT APPLICATION NUMBER: US/09/735,363A
CURRENT PILLIG DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/170,325
PRIOR APPLICATION NUMBER: 60/170,325
PRIOR APPLICATION NUMBER: 06/229,925
PRIOR PILLING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn version 3.0
SEQ ID NO 18
LENGTH: 18
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 Query Match 1.7%; Score 18; DB 1; Length 18; Best Local Similarity 100.0%; Pred. No. 26; Matches 18; Conservative 0; Mismatches 0; Indels
 Length 18;
 0; Indels
 Query Match
1.7%; Score 18; DB 1;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches
 , OTHER INFORMATION: Synthetic Oligonucleotide US-09-735-363A-18
 Sequence 28, Application US/09896650A Patent No. US20020146704A1 GENERAL INFORMATION:
 OTHER INFORMATION: Reagent Sequence
 1793 TGTGTGTGTGTGTGTG 1810
 Sequence 1, Application US/10011204 Publication No. US20020182617A1 GENERAL INFORMATION:
 1794 GIGIGIGIGIGIGIGI 1811
 rerererererererere
 1 Grererererererer
 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
 ORGANISM: Artificial Sequence
 US-09-896-650A-28
 -10-011-204-1/c
 US-09-896-650A-28
 TYPE: DNA
 RESULT 60
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APPLICANT: Centre For DNA Fingerprinting and Diagnostics
TITLE OF INVENTION: No. US20030194730A1e1 FISSR-PCR primers and markers and a method of TITLE OF INVENTION: Drimers and markers for identifying genetic constitution and breef TITLE OF INVENTION: varities.

FILE REFERENCE: 782-indian CURRENT APPLICATION NUMBER: US/10/357,488
PRIOR PRILCATION NUMBER: 2003-02-04
PRIOR PILICATION NUMBER: 260/MAS/2002
 VS-00-01.204-2

Sequence 2, Application US/10011204

Sequence 2, Application US/10011204

Publication No US20020182617A1

GENERAL INNORMATION:

APPLICANT: EKINS, Roger P

TILLE OF INVENTION: Binding assay using binding agents with tail groups

FILE REFREENCE: 0380-P0118001805/

CURRENT APPLICATION NUMBER: US/08/700,530

PRIOR APPLICATION NUMBER: US/08/700,530

PRIOR PILING DATE: 1996-10-23

PRIOR FILING DATE: 1995-01-11

PRIOR FILING DATE: 1995-03-10

PRIOR FILING DATE: 1994-03-11

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 2

LENGTH: 18
ó;
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Gaps
 Gaps
 .
 .
0
 DB 1; Length 18;
26;
```

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Sequence 705, Application US/09263959

Patent No. US20020150891A1

GENERAL INFORMATION:

APPLICANT: Rowen, Lee

APPLICANT: Second and Berry LLP

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP

CITY: Seattle

CITY: Seattle

CITY: Seattle

CONTRY: US
 DB 1; Length 17; 34;
 Indels
 COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDTION TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/263,959

FILING DATE: 05-MAR.1999

CLASSIFICATION:
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION WHERE: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
 Ouery Match 1.6%; Score 17; DB Best Local Similarity 100.0%; Pred. No. 34; Matches 17; Conservative 0; Mismatches
 ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 9200
TELEPHONE: (206) 622-4900
 ATTORNEY FACENT INFORMATION:
NAME: MCMASLETS, DAVID D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 92007
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 622-6930
INFORMATION FOR SEQ ID NO: 557:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
 1793 TGTGTGTGTGTGT 1809
 TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 LENGTH: 17 base pairs
 nucleic acid
 TOPOLOGY: linear
 STRANDEDNESS:
 US-09-263-959-557
 US-09-263-959-705
 a
 ઠે
 Sequence 557, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: KOOP, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
CARRESPONDENCE ADDRESS:
Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
 ö
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 Gaps
 TYPE: DNA
CRGANISM: Artificial Sequence
PEATURE:
CHEN INFORMATION: A novel FISSR-PCR primer for genotyping eukaryotes
US-10-357-488-26
 GENERAL INCREMINE SERVECT

APPLICANT: C. Frank Bennett

APPLICANT: Elizabeth J. Ackermann

APPLICANT: Exp. Cowest

TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION

FILE REPERENCE: 1894-0.53

CURRENT APPLICATION NUMBER: US/09/918,186A

CURRENT PILING DATE: 2001-07-30

PRIOR FILING DATE: 1999-04-05

PRIOR PLING DATE: 1999-04-05

PRIOR PLING DATE: 1998-09-29

NUMBER OF SEQ ID NOS: 250

EENGTH: 20

LENGTH: 20
 Indels
 Query Match
1.7%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels
 Query Match
1.7%; Score 17.4; DB 1;
Best Local Similarity 94.7%; Pred. No. 32;
Matches 18; Conservative 0; Mismatches 1;
 ; OTHER INFORMATION: Antisense Oligonucleotide US-09-918-186A-235
 Sequence 235, Application US/09918186A Patent No. US20020137708A1 GENERAL INFORMATION:
 1811 TGTATATATATATGT 1829
 1798 GTGTGTGTGTGTAT 1815
 TYPE: DNA ORGANISM: Artificial Sequence
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.1
SEQ ID NO 26
LENGTH: 20
 Washington
 COUNTRY: US
ZIP: 98104-7092
 STREET: 6300 COITY: Seattle
 JS-09-918-186A-235/c
 JS-09-263-959-557
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mcgarry191-19.rnpb

Page 18

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Sequence 68, Application US/10340192
Publication No. US20030170700A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sharg, Jin
APPLICANT: Bowen, Benjamin A
ITILE OF INVENTION: SECRETED AND CELL SURFACE POLYPEPTIDES AFFECTED BY CHOLESTEROL AND TITLE OF INVENTION: SECRETED AND CELL SURFACE POLYPEPTIDES AFFECTED BY CHOLESTEROL AND TITLE OF INVENTION: SECRETED AND SELLOWERS TELING DATE: 2003-01-08
NUMBER OF SEQ ID NOS: 88
SOFTWARE: Patentin Version 3.1
LENGTH: 17
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 US-09-69-373-2420

US-09-69-373-2420

Sequence 2420, Application US/09969373

Patent No. US20020133852A1

GENERAL INFORMATION:

APPLICANT: Effertz, Roger J.

APPLICANT: Effertz, Brian M.

TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REFERENCE: 38-10(52679)A

CURRENT APPLICATION NUMBER: US/09/969,373

CURRENT FILING DATE: 2001-01-05

PRIOR FILING DATE: 2001-01-05

PRIOR FILING DATE: 2001-01-13

SEQ ID NO 240

LEMOTH: 20

TWOMER OF SEQ ID NOS: 4593

LEMOTH: 20

TWOMER OF SEQ ID NOS: 4593
 Query Match 1.6%; Score 16.8; DB 1; Length 20; Best Local Similarity 90.0%; Pred. No. 39; Matches 18; Conservative 0; Mismatches 2; Indel8
 Query Match
1.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 17; Conservative 0; Mismatches 0; Indels
 Query Match
1.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 17; Conservative 0; Mismatches 0; Indels
 2141 GATCAGTTTTTCACCT 2157
 2141 GATCAGTTTTTCACCT 2157
 1 darcagririricacci 17
 1 GATCAGTTTTTTCACCT 17
SOFTWARE: Patentin version 3.1
 , ORGANISM: Homo sapiens
US-10-340-192-68
 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-339-782-333
 ; ORGANISM: Glycine max US-09-969-373-2420
 RESULT 69
US-10-340-192-68
 SEQ ID NO 333
 TYPE: DNA
 TYPE: DNA
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 Sequence 970, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANT: ROWEN, Ben F.
ITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SECUENCES: 1279
CORRESPONDENCE ADDRESS:
SECH and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
 Sequence 333, Application US/10339782
Publication No. US20030166026A1
GENERAL INFORMATION:
APPLICANT: Lynx Therapeutics, Inc.
APPLICANT: Goodman, Laurie J
APPLICANT: Bowen, Benjamin A
TITLE OF INVENTION: Identification of Specific Biomarkers for Breast Cancer Cells
FILE REFERENCE: 37-000110US
CURRENT APPLICANT: NOWHORER: US/10/339,782
CURRENT APPLICANT DO NOS: 495
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 Gaps
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 Query Match 1.6%; Score 17; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 34; Matches 17; Conservative 0; Mismatches 0; Indels
 Query Match
1.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 17; Conservative 0; Mismatches 0; Indels
 CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/263,959

FILING DATE: 0.05-MAR-1999

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: MCMBSTERS, 33,963

REGISTRATION NUMBER: 33,963

REGISTRATION NUMBER: 33,963

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFHONE: (206) 622-4900

TELEFAX: (206) 622-4900

INFORMATION FOR SEQ ID NO: 970:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs
 COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 1793 TGTGTGTGTGTGT 1809
 1793 TGTGTGTGTGTGTGT 1809
 1 rererererererer 17
 1 TGTGTGTGTGTGTGT 17
 ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-970
 RESULT 67
US-09-263-959-970
 RESULT 68
US-10-339-782-333
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Georgian of State of
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 Sequence 412, Application US/10085906

Sequence 412, Application US/10085906

Publication No. US20030054371A1

GENERAL INPORMATION:

APPLICANT: Wing, Vincent

APPLICANT: Wing, Vincent

APPLICANT: Gray, Gard,

TITLE OF INVENTION: POLYMORPIC ELEMENTS IN THE

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

FRIDE APPLICATION NUMBER: US 60/126,215

PRIOR FILING DATE: 2000-03-24

NUMBER: OF SEQ ID NOS: 545

SEQ ID NO 412

LENGTH: DATE

 Gaps
APPLICANT: Vicari, Alain P.
APPLICANT: Caux, Christophe
APPLICANT: LaFace, Drake
TILLE OF INVENTION: Chemokines as Adjuvants of Immune Response
TILLE OF INVENTION: Chemokines as Adjuvants of Immune Response
FILE REFERENCE: SF0896K US
CURRENT ELLING DATE: 2001-01-24
CURRENT ELLING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 21
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 OTHER INFORMATION: Description of Artificial Sequence: primer
 Query Match
1.6%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 2; Indels
 Length 21;
 Indels
 DB 1;
 Query Match
Best Local Similarity 90.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches
 1794 GTGTGTGTGTGTGTGT 1813
 1794 GIGIGIGIGIGIGIGIGI 1813
 21 Grererereacrereacrer 2
 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
 ; ORGANISM: Homo sapiens
US-10-085-906-412
 RESULT 75
US-09-263-959-983/c
 US-10-085-906-412
 US-09-768-917-10
 TYPE: DNA
 d
 ö
 Sequence 135, Application US/10006191
Sequence 135, Application US/2000144223A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: William Gaarde
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSIC
FILE REPERENCE: RTS-0274
CURRENT APPLICATION NUMBER: US/10/006,191
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 135
LENGTH: 20
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 Sequence 2422 Application US/09969373

Sequence 2422 Application US/09969373

Sequence 2422 Application US/09969373

Sequence 2422 Application US/09969373

SEQUENCENT INFORMATION:

APPLICANT: Hauge, Brian M.

TITLE OF INVENTION: Soybean SRR and Methods of Genotyping FILE REPERENCE: 38-10(52679)A;

CURRENT APPLICATION NUMBER: US/09/969,373

CURRENT FILING DATE: 2001-01-05

PRIOR APPLICATION NUMBER: US 09/754,853

PRIOR PILING DATE: 2001-01-05

PRIOR PILING DATE: 2001-01-05

PRIOR FILING DATE: 2001-01-13

PRIOR FILING DATE: 2001-01-13

NUMBER: OF SEQ ID NOS: 4593

SEQ ID NO 2422

LENGTH: 20
 Query Match
1.6%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 2; Indels
 DB 1; Length 20;
 2; Indels
 , OTHER INFORMATION: Antisense Oligonucleotide US-10-006-191-135
 Query Match 1.6%; Score 16.8; I
Best Local Similarity 90.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches
 1675 ATTCTGATTCGAATGACACT 1694
 1793 TGTGTGTGTGTGTGTG 1812
 Sequence 10, Application US/09768917
Patent No. US20020034494A1
GENERAL INFORMATION:
 1 rerereterriererere 20
 20 Arrergarrecagraacaer 1
 1 rereferetrierereres
 TYPE: DNA
ORGANISM: Artificial Sequence
 ; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-2422
 US-10-006-191-135/c
 US-09-768-917-10/c
 US-09-969-373-2422
 FEATURE:
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NUMBER OF SEQUENCES: 1279

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1 drerecererererer 18
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 Sequence 135, Application US/10085906

Sublication No. US20030084371A1

Sublication No. US20030084371A1

Sublication No. US20030084371A1

APPLICANT: Wing, Vincent

APPLICANT: Wing, Vincent

APPLICANT: Gray, Gary, Gar
 Gaps
 0; Gaps
 ö
 Query Match 1.6%; Score 16.4; DB 1; Length 18; Best Local Similarity 94.4%; Pred. No. 42; Matches 17; Conservative 0; Mismatches 1; Indels
 DB 1; Length 18;
 1; Indels
 ZIE: 98104-7092
ZIE: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: PROSENTED SYSTEM: PC-DOS/MS-DOS
SOFTING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FLING DATE: 05-MAR-1999
CLASSIFICATION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
 ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 983:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: mucleic acid
STRANDENNESS: single
 1.6%; Score 16.4; Di
94.4%; Pred. No. 42;
tive 0; Mismatches
 1793 TGTGTGTGTGTGTGTG 1810
 18 rerererargrerere 1
 17; Conservative
 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-906-135
 CITY: Seattle
STATE: Washington
 Query Match
Best Local Similarity
 ;
US-09-263-959-983
 US-10-085-906-135
 COUNTRY:
 Matches
 8
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1794 GTGTGTGTGTGTGT 1811

```
Sequence 26, Application US/10301844
Publication No. US20030100747A1
GENERAL INFORMATION:
APPLICANT: Ruddy, David A.
Nolff, Roger K.
TILLE OF INVENTION: POLYXORPHISMS IN THE REGION OF THE HUMAN
HEMOCHROMATOSIS GENE
 APPLICANT: Ruddy, David A.
MOLE, Roger K.
TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN
HEMOCHROMATOSIS GENE
 ò
 Query Match 1.6%; Score 16.4; DB 1; Length 20; Best Local Similarity 94.4%; Pred. No. 44; Matches 17; Conservative 0; Mismatches 1; Indels
 STATE: NY

COUNTRY: USA

ZUP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FactSEQ for Windows
SOFTWARE: FactSEQ for Windows
VETLING DATE: 20-No. US20030100747A1-2002
CLASSITICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMERE: US/10/301,844
FILING DATE: 20-No. US20030100747A1-2002
CLASSITICATION: AUMROWN->
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/852,495C
FILING DATE: 07-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: POSSBATE, Brian R
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0057-999
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION TO NOT 26:
SEQUENCE CASS OF 199-5556
TELECOMUNICATION:
SEQUENCE CHARACTERISTICS:
LINGORMATION CALL DENNIE
INFORMATION CALL DENNIE
SEQUENCE CHARACTERISTICS:
LINGORMANICATION:
TELECOMUNICATION:
TELECOMUNI
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
 CORRESPONDENCE ADDRESS:
ADDRESSEE: L155 Avenue of the Americas
CITY: New York
 ;
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-301-844-26
US-10-301-844-26; Sequence 26, Application US/10301844; Publication No. US20030100747A1; GENERAL INFORMATION:
 1813 TATATATATATGTA 1830
 2 TATATATATATATA 19
 NUMBER OF SEQUENCES: 26
 NUMBER OF SEQUENCES:
 US-10-301-844-26/c
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Sequence 971, Application US/09263959
Sequence 971, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Roop, Ben F.
ITILE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTINUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
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0
 Sequence 85, Application US/09888326; Bublication No. US2003026801A1; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wather, George
TITLE OF INVENTION: Methods for Enhancing Antibody-Induced; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced; TITLE OF INVENTION: Methods for Enhancing Cancer; TITLE OF INVENTION: Methods for Enhancing Cancer; FILE REFERENCE: C1039/7052 (AMS)
CURRENT PILING DATE: 2001-06-22
RIOR APPLICATION NUMBER: US 60/213,346
PRIOR PILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 848
SOFTWARE: FastsEQ for Windows Version 3.0
SEQ ID NO 85
LENGTH: 18
 DB 1; Length 18;
 Indels
 AUDRESSEE: Seed and Delly LE.
STREET: 6300 Columbia Center, 701 Fifth Avenue
STREET: 6300 Columbia Center, 701 Fifth Avenue
STREET: 8ashington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ORPEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: OS-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MACMASTERS, David D.
REGISTRATION NUMBER: 33,963
REGISTRATION NUMBER: 33,963
REGISTRATION NUMBER: 33,963
REGISTRATION NUMBER: 33,963
REGISTRATION INFORMATION:
TELEFHONE: (206) 622-4900
 ADDRESSEE: Seed and Berry LLP STREET: 6300 Columbia Center, 701 Fifth Avenue
 FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
NAME/KEY: misc_feature
 0; Mismatches
 Score 15.4;
Pred. No. 57
 1816 ATATATATATATGTACA 1832
 TELEFHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 971:
SEQUENCE CHARACTERISTICS:
 TYPE: DNA ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 94.1
Matches 16; Conservative
 LENGTH: 18 base pairs
 TYPE: nucleic acid
STRANDEDNESS: single
 ; TOPOLOGY: linear
US-09-263-959-971
 JS-09-888-326-85
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 Gaps
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 DB 1; Length 20;
 Length 16;
 0; Indels
 Indels
 SOFTWARE: FastSEQ LC.

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/301,844
FILING DATE: 20-No. US20030100747A1-2002
CLASSIFICATION NUMBER: US/08/852,495C
PRIOR APPLICATION NUMBER: US/08/852,495C
FILING DATE: 07-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Batan M
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0057-999
TELEPHONE: 650-493-5556
TELEPHONE: 650-493-5556
TELEPHONE: 650-493-5556
TELEPHONE: 650-493-5556
TELERAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
 COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IDM PC compatible
OPERATING SYSTEM: Windows Version 2.0b
 1.5%; Score 16; DB
100.0%; Pred. No. 46;
ive 0; Mismatches
 Query Match 1.6%; Score 16.4; I Best Local Similarity 94.4%; Pred. No. 44; Matches 17; Conservative 0; Mismatches
 ;
TOPOLOGY: linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-301-844-26
 Sequence 27, Application US/10092885 Publication No. US20030190618A1
 1813 TATATATATATATGTA 1830
 1794 GIGIGIGIGIGI 1809
 19 ratatatatatatata 2
 Query Match
Best Local Similarity 100.0
Matches 16; Conservative
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1793 TGTGTGTGTGTGT 1807
 1794 GIGIGIGIGIGIG 1808
 1 dreferererere 15
 Best Local Similarity 100.
Matches 15; Conservative
) ORGANISM: Homo sapiens
US-10-085-906-222
 US-10-085-906-258/c
 Query Match
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0
 US-09-735-363A-16

US-09-735-363A-16

Sequence 16, Application US/09735363A

Patent No. US20010041681A1

GENERAL INFORMATION:

APPLICANT: Filion, Mario

APPLICANT: Phillip, Nigel

TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides

FILE REFERENCE: 02811-0181

CURRENT APPLICATION NUMBER: US/09/735,363A

CURRENT PRILING DATE: 1999-127-13

PRIOR FILING DATE: 1999-127-13

PRIOR FILING DATE: 2000-12-12

PRIOR FILING DATE: 2000-08-29

NUMBER OF SEQ ID NOS: 87

SOFTWARE: PatentIn version 3.0

SEQ ID NO 16

LANGTH: 15
 Gaps
 Gaps
 ö
 ö
 Sequence 85, Application US/0988326;
Sequence 85, Application US/0988326;
Publication No. US20030026801A1
GENERAL INFORMATION:
APPLICANT: Weiner, George
TILE OF INVENTION: Methods for Enhancing Antibody-Induced;
TILE OF INVENTION: Methods for Enhancing Cancer;
TILE REFERENCE: C1039/7062 (Aws)
CURRENT APPLICATION NUMBER: US/09/888,326
CURRENT FILIAG DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 60/213,346
PRIOR PLING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 848
SOFTWARE: PRESEQ for Windows Version 3.0
LENGTH: 18
 DB 1; Length 18;
 Length 18;
 Indels
 1; Indels
 Score 15.4; DB 1;
Pred. No. 57;
0; Mismatches 1;
 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
5-09-735-363A-16
 FEATURE:
COTHER INFORMATION: Synthetic oligonucleotide
NAME/KEY: misc feature
LOCATION: (0)...(0)
LOCATION: (0)...(0)
COTHER INFORMATION: phosphorothioate backbone
US-09-888-326-85

; IOCATION: (0) ...(0)
; OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-85
 Query Match
1.5%; Score 15.4; E
Best Local Similarity 94.1%; Pred. No. 57;
Matches 16; Conservative 0; Mismatches
 1814 ATATATATATATGTA 1830
 1814 ATATATATATATGTA 1830
 1 ATATATATATATATA 17
 18 ATATATATATATA 2
 TYPE: DNA
ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 94.1%;
Matches 16; Conservative
 RESULT 82
US-09-888-326-85/c
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 US-10-05-906-231

US-10-05-906-231

Sequence 231, Application US/10085906

Publication No. US20030054371A1

GENERAL INFORMATION:
APPLICANT: Win, Paul

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

FILE REFERENCE: GNN-5343CP2

CURRENT APPLICATION NUMBER: US 60/126,215

PRIOR APPLICATION NUMBER: US 69/534,061

PRIOR PILING DATE: 1999-03-25

PRIOR FILING DATE: 1990-03-24

PRIOR FILING: DATE: 2000-03-24

NUMBER OF SEQ ID NOS: 545

SEQ ID NOS: 545

SEQ ID NO 231
 Gaps
 Gaps
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0
 1.4%; Score 15; DB 1; Length 16;
100.0%; Pred. No. 63;
 Length 16;
 Indels
 Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: OS-MAR-1999
FILING DATE: OS-MAR-1999
CLASSIFICATION NUMBER: US/09/263,959
FILING DATE: OS-MAR-1999
CLASSIFICATION NUMBER: 33,963
RECESTERNOR/DOCKET NUMBER: 33,963
RECESTERNOR/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4000
 100.0%; Pred. No.
 Query Match 1.4%; Score 15; DB Best Local Similarity 100.0%; Pred. No. 63; Matches 15; Conservative 0; Mismatches
 1813 TATATATATATAT 1827
 1813 TATATATATATAT 1827
 2 rarararararar 16
 15 rarararararar 1
 TYPE: DNA
ORGANISM: Homo sapiens
Washington
 Best Local Similarity
Matches 15; Conserv
 ;
US-09-263-959-540
 US-10-085-906-231
 COUNTRY:
 Query Match
 Best Loca
Matches
 LENGTH:
 RESULT 89
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 Sequence 540, Application US/09263959

Patent No. US20020150891A1

GENERAL INFORMATION:
APPLICANT: Hood, Lee APPLICANT: Roop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
 GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rower, Leroy E.
APPLICANT: Rower, Leroy E.
APPLICANT: Roop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
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 Gaps
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 ..
0
 DB 1; Length 16;
 0; Indels
 Length 15;
 0; Indels
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
 3: Seed and Berry LLP 6300 Columbia Center, 701 Fifth Avenue
 E: Seed and Berry LLP 6300 Columbia Center, 701 Fifth Avenue
 DB 1;
61;
 ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPAR: (206) 622-4900
TELEPAR: (206) 682-6031
INFORMATION FOR SEQ ID NO: 540:
SEQUENCE CHARACTERISTICS:
 1.4%; Score 15; DB 100.0%; Pred. No. 63; tive 0; Mismatches
 Mismatches
Query Match
1.4%; Score 15;
Best Local Similarity 100.0%; Pred. No.
Matches 15; Conservative 0; Mismatc
 COUNTRY: US
ZIP: 98104-7092
COMEUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 540, Application US/09263959
Patent No. US20020150891A1
 1813 TATATATATATAT 1827
 1813 TATATATATATAT 1827
 2 rarararararar 16
 Query Match
Best Local Similarity 100.0
Matches 15; Conservative
 15 TATATATATAT 1
 TYPE: nucleic acid
STRANDEDNESS: single
 STREET: 6300 Colun
CITY: Seattle
STATE: Washington
 linear
 CITY: Seattle
 US-09-263-959-540/c
 ;
TOPOLOGY:
US-09-263-959-540
 JS-09-263-959-540
 STREET:
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APPLICANT: LI, YUN
APPLICANT: HERMIDA, LEANDRO C.
APPLICANT: HERMIDA, LEANDRO C.
APPLICANT: HERMIDA, LEANDRO C.
APPLICANT: HOPPA, NANCY L.
APPLICANT: HOPPA, NANCY L.
TITLE OF INVENTION: METHOD FOR GENERATING FIVE PRIME BIASED TANDEM TAG
TITLE OF INVENTION: LIBRARIES OF CDNAS
FILE REFERENCE: 0109015/026
CURRENT APPLICATION NUMBER: US/10/092,885
CURRENT FILLING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 60
 Gaps
 ö
 Length 16;
 APPLICANT: Elizabeth Blackburn
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
TITLE OF INVENTION: THELAMEN TO TELOMERE LENGTH AND/OR
TITLE OF INVENTION: TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 57
CORRESPONDENCES: 57
CORRESPONDENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
CITY: Los Angeles
STREET: Suite 4700
CITY: Los Angeles
STREET: Suite 4700
CITY: Los Angeles
STREET: Suite 6700
CITY: Los Angeles
STREET: Suite 6700
CITY: Los Angeles
COMPTRY: U S.A.
ZIP: 90071-206
COMPTRY: U S.A.
ZIP: BMC COMPABLE PORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.49 Mb
MEDIUM TYPE: 3.5" Diskette, 1.99 Mb
MEDIUM TYPE: 3.5" Diskette, 1.99 Mb
MEDIUM TYPE: 3.5" Diskette, 1.99 Mb
MEDIUM TYPE: 3.5" Diskette, 3.4 Mb
MEDIUM TYPE: 3.5" Diskette, 1.99 Mb
MEDIUM TYPE: 3.5" DISKETS MB
MEDIUM TYPE: 3.5 MB
MEDIUM TYPE: 3.5 MB
MEDIUM TYPE: 3.5 MB
MEDIUM TYPE: 3.5 MB
M
 Indela
 0; Mismatches
 1.4%; Score 14.4;
nilarity 93.8%; Pred. No. 75
Conservative 0; Mismatche
 US-10-092-885-28; Application US/10092885; Sequence 28, Application US/10092881; Publication No. US20030190618A1; CENERAL INFORMATION: APPLICANT: SAMAL, BABRU
Jerry W. Shay
Woodring E. Wright
Elizabeth Blackburn
 1793 TGTGTGTGTGTGTG 1808
 TYPE: nucleic acid
STRANDEDNESS: single
 Query Match
Best Local Similarity
Matches 15; Conserva
 TOPOLOGY: linear
 US-08-463-404-57
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 RESULT 90

US-10-288-700-878

US-10-288-700-878

Sequence 878, Application US/10238700

Sequence 878, Application US/10238700

Sequence 878, Application US/10238700

Bublication No. US20030153521A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: McSwiggen, James

TITLE OF INVENTION:

APPLICANT: MCSwiggen, James

TITLE OF INVENTION:

CURRENT FILING DATE: 2002-09-18

PRIOR FILING DATE: 2002-09-18

PRIOR FILING DATE: 2002-09-29

PRIOR FILING DATE: 2001-09-10

NUMBER OF SEQ ID NOS: 4666

SOFTWARE: Patentin version 3.0

LENGTH: 17
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 Sequence 231, Application US/10085906
| Sequence 231, Application US/10085906
| Publication No. US20030054371A1
| GENERAL INFORMATION:
| APPLICANT: Ying, Vincent
| APPLICANT: Wu, Paul
| APPLICANT: Wu, Paul
| TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
| TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
| TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
| TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
| TITLE OF INVENTION: UNMBER: US/10/085,906
| CURRENT FILING DATE: 2002-02-27
| PRIOR FILING DATE: 1999-03-24
| PRIOR FILING DATE: 2000-03-24
| NUMBER OF SEQ ID NOS: 545
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 231
 Gaps
 ;
0
 Query Match
1.4%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 15; Conservative 0; Mismatches 0; Indels
 Query Match
1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 66.7%; Pred. No. 64;
Matches 10; Conservative 5; Mismatches 0; Indels
 Sequence 57, Application US/08463404, Publication No. US20020127634A1 GENERAL INFORMATION:
 1391 TGTTAAGACTTGACA 1405
 1813 TATATATATATAT 1827
 Michael D. West
 15 rarararararar
 ORGANISM: Homo sapiens
US-10-238-700-878
 TYPE: DNA
CORGANISM: Homo sapiens
US-10-085-906-231
 US-10-085-906-231/c
 JS-08-463-404-57
 APPLICANT:
 TYPE: RNA
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Gaps
 Gaps
 TILE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
FILE REFERENCE: BOUTOUR HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
CURRENT APPLICATION WINDER: US/10/066,756A
CURRENT FILING DATE: 2002-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
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 ; OTHER INFORMATION: Hypothetical Sequence for Exemplary Purposes US-09-321-005A-13
 Sequence 13, Application US/09321005A
Patent No. US20020162622A1
Patent No. US20020162622A1
Patent No. US20020162622A1
GENERAL INFORMATION:
APPLICANT: Gut, Ivo
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/321,005A
CURRENT PILLING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13
LENGTH: 17
 Length 17;
 Indels
 Indels
 -
 Query Match
1.4%; Score 14.4; DB 1;
Best Local Similarity 93.8%; Pred. No. 76;
Matches 15; Conservative 0; Mismatches 1;
 DB 1;
 Query Match
1.4%; Score 14.4; D
Best Local Similarity 93.8%; Pred. No. 75;
Matches 15; Conservative 0; Mismatches
 NUMBER OF SEQ ID NOS: 4804
SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 4088
; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-10-232-927A-80
 US-10-060-756A-4088

Sequence 4088, Application US/10060756A
; Publication No. US2003046717A1
; GENERAL INFORMATION:
 1891 ATATTTCAATGTTAGC 1906
 1793 TGTGTGTGTGTG 1808
 1 recercierererere
 16 ATATTTCAATGTCAGC 1
 TYPE: DNA
ORGANISM: Artificial
FEATURE:
 RESULT 94
US-09-321-005A-13/c
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 Gaps
 DB 1; Length 16;
 1; Indels
 Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
CONDITIONS RELATED TO
TEOLOMERE LENGTH AND/OR
TELOMERASE ACTIVITY
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/232,927A
FILING DATE: 29-Aug-2002
CLASSIFICATION: «Unknown»

PRIOR APPLICATION NUMBER: US/09/378,535
FILING DATE: 20-Aug-1999
APPLICATION NUMBER: 08/819,867
FILING DATE: «UNKNOWN»
 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FastSEQ for Windows 2.0
 Query Match
1.4%; Score 14.4; D
Best Local Similarity 93.8%; Pred. No. 75;
Matches 15; Conservative 0; Mismatches
 ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/232
TELECOMMUNICATION INFORMATION:
 Calvin B. Harley
Scott L. Weinrich
Catherine M. Strahl
Michael J. Moeachern
Jerry Shay
Woodring E. Wright
Blizabeth H. Blackburn
Nam Woo Kim
 NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
 TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 80: SEQUENCE CHARACTERISTICS:
 US-10-232-927A-80

Sequence 80, Application US/10232927A

Publication No. US20030190638A1

GENERAL INFORMATION:

APPLICANT: Michael D. West
 LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 1794 GIGIGIGIGIGIGI 1809
 1 Grricicisticistic 16
 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 28
 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-885-28
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US-09-735-363A-15

US-09-735-363A-15

Sequence 15, Application US/09735363A

PROTECT NO. US20010041681A1

GENERAL INFORMATION:

APPLICANT: Fillon, Mario

TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonuclectides

TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonuclectides

TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonuclectides

TILE REFERENCE: 02011-0181

CURRENT FILING DATE: 2000-12-12

PRIOR FILING DATE: 1999-12-13

PRIOR FILING DATE: 2000-08-29

NUMBER OF SEQ ID NOS: 87

SOFTWARE: Patentin version 3.0

LENGTH: 14
 GENERAL INCREMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Eric B. Swayze
APPLICANT: Eric B. Swayzet
APPLICANT: Lex M. COWSETT
TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
FILE REFERENCE: ISPH-0585
CURRENT APPLICATION NUMBER: US/09/918,186A
CURRENT PILING DATE: 2001-07-30
PRIOR FILING DATE: 2001-07-30
PRIOR PRICK APPLICATION NUMBER: 09/26,694
PRIOR FILING DATE: 1999-04-05
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 250
SEQ ID NO 235
LENGTH: 20
 ; OTHER INFORMATION: Description of Artificial Sequence: Capture US-10-297-068-1015
 Length 20;
 Length 18;
 Indels
 1; Indels
 Query Match
Best Local Similarity 84.2%; Pred. No. 84;
Matches 16; Conservative 0; Mismatches 3;
 DB 1;
 OTHER INFORMATION: Antisense Oligonucleotide
 Query Match 1.4%; Score 14.4; I Best Local Similarity 93.8%; Pred. No. 77; Matches 15; Conservative 0; Mismatches
 RESULT 98
US-09-918-186A-235
; Sequence 235, Application US/09918186A
; Patent No. US20020137708A1
; GENERAL INFORMATION:
 1814 ATATATATATATATACA 1832
 1 ACATATATATATAAACA 19
 1470 GGGTACCAGCAGAAAG 1485
 ORGANISM: Artificial Sequence
 TYPE: DNA
ORGANISM: Artificial Sequence
 2 degraccadecadaded 17
 US-09-918-186A-235
SEQ ID NO 1015
LENGTH: 18
 FEATURE:
 à
 g
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 Gaps
 Gaps
 Sequence 4089, Application UG/10060756A
; Publication No. US2003046717A1
; GENERAL INFORMATION:
 APPLICANT: DANG, Jian
 APPLICANT: Zhang, Jian
 APPLICANT: Zhang, Jian
 APPLICANT: APPLICANTON HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
 FILE REPRENCE: PED177

CURRENT APPLICATION NUMBER: US/10/0667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR DATE: 2001-01-30
PRIOR DATE: 2001-01-30
PRIOR DATE: 2001-0
 Sequence 1015, Application US/10297068
; Publication No. US20030228585A1
; Publication No. US20030228585A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: RAGIYA, Taeko
APPLICANT: RAGIYA, Taeko
APPLICANT: MORIYA, Shogo
APPLICANT: MORIYA, Shogo
APPLICANT: MORIYA, Morio
; APPLICANT: NISHIDA, Michio
; TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES
FILE REFERENCE: 13140P1174
; CURRENT APPLICATION NUMBER: US/10/297,068
; CURRENT FILING DATE: 2000-164798
; PRIOR FILING DATE: 2000-06-01
; WUMBER OF SEQ ID NOS: 1298
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 Query Match
1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 76;
Matches 15; Conservative 0; Mismatches 1; Indels
 DB 1; Length 17;
 1; Indels
 1.4%; Score 14.4; D
93.8%; Pred. No. 76;
tive 0; Mismatches
 2162 GCATTTGTTTCTACTT 2177
 2162 GCATTIGITICTACTT 2177
 1 GCATTTGTTTCTAGTT 16
 Query Match
Best Local Similarity 93.8
Matches 15; Conservative
 ORGANISM: Homo sapiens
US-10-060-756A-4089
 US-10-060-756A-4088
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Gaps

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Sequence 811. Application US/09263959

Sequence 811. Application US/09263959

PREMERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: KOOP, Ben F.
ITILE OF INVENTION:
DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STREET: Mashington
COUNTRY: US
CONDUTER: ISH PC Compatible
CONDUTER: ISH PC Compatible
COMPUTER: ISH PC Compatible
COMPUTER: ISH PC Compatible
COMPUTER: US FORM:
MEDIUM TYPE: TOOS/MS-DOS
SOFTWARE: PREADLATION DATA:
COMPUTER: US PC COMPATA:
FILING DATE:
CURRENT APPLICATION NUMBER: US/09/263,959
FILING DATE:
CREATION NUMBER: US/09/263,959
DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI 1279
 Gaps
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 DB 1; Length 14;
82;
 Indels
 NUMBER OF SEX-CARESS:
ADDRESSES:
ADDRESSES:
ADDRESSES:
Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seatlle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER: IBM PC COMPATIBLE
SOUTHWARE: PATENTIN DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-WAR-1999
CLASSIFCATION NUMBER: 33,963
REGISTRATION NUMBER: 33,963
REGISTRATION NUMBER: 920010.426C2
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 658:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
 920010.426C2
 1.3%; Score 14;
100.0%; Pred. No.
tive 0; Mismatcl
 ATTORNEY AGENT INFORMATION:
NAME: MCMatters, David D.
REGISTATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920
IELECOMMUNICATION INFORMATION:
 1793 TGTGTGTGTGTG 1806
 1 rerererererere 14
 0.0ery Match
Best Local Similarity 100.0
Matches 14; Conservative
 NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
 TITLE OF INVENTION:
 CLASSIFICATION:
 US-09-263-959-658
 US-09-263-959-811
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 Sugargence 479, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Howen, Lee
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANT: ROWEN, Ben F.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
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 Gaps
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 DB 1; Length 14;
82;
 0; Indels
 Length 14;
 0; Indels
 COMPUTER READABLE PORM:

COMPUTER READABLE PORM:

MEDIUM TYPE: Floppdible
COMPUTER: IBM PC compatible
COMPUTER: IB
 7
 0B
82;
 ; OTHER INFORMATION: Synthetic Oligonuclectide US-09-735-363A-15
 Mismatches
 Query Match 1.3%; Score 14; DB Best Local Similarity 100.0%; Pred. No. 82; Matches 14; Conservative 0; Mismatches
 Score 14;
Pred. No.
 Sequence 658, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
 Query Match
Best Local Similarity 100.0%; P
Matches 14; Conservative 0;
 1794 GTGTGTGTGTGT 1807
 1793 TGTGTGTGTGTG 1806
 TYPE: DNA ORGANISM: Artificial Seguence
 1 rerererererere
 14 Grererererer 1
 CITY: Seattle
STATE: Washington
COUNTRY: US
 -09-263-959-479/c
 ;
US-09-263-959-479
 RESULT 101
US-09-263-959-658
 FEATURE:
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 Q
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APPLICANT: SUNAMACHI, Hicoki
APPLICANT: TAKAHASHI, Michiaki
APPLICANT: TAKAHASHI, Michiaki
APPLICANT: TAKAHASHI, Michiaki
APPLICANT: YAMANISHI, Koichi
TITLE OF INVENTION: Wethod for Quality Control of an Attenuated Varicella Live Vaccine
TITLE REPERENCE: 0216-04549
CURRENT APPLICATION NUMBER: US/09/913,514
CURRENT FILING DATE: 2001-12-07
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3.1
FENGTH: 14
TYPE
 Sequence 27, Application US/09913514
; Sequence 27, Application US/09913514
; Publication No. US20030082210A1
; GENERAL INFORMATION:
 APPLICANT: SUNAMACHI, Hiroki
 APPLICANT: SUNAMACHI, Hiroki
 APPLICANT: TAKARASHI, Michiaki
 PRICR APPLICATION NUMBER: US/09/913,514
 CURRENT PAPLICATION NUMBER: PZ 2000-62734
 PRICR PILING DATE: 2000-01-31
 NUMBER OF SEQ ID NOS: 42
 SEOTHARE: PatentIn version 3.1
 ö
 Gaps
 APPLICANT: Ruddy, David A.
APPLICANT: Ruddy, David A.
Wolff, Roger K.
TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN
HEMOCHROMATOSIS GENE
 .
0
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 Length 14;
 Length 14;
 0; Indels
 Mismatches
 US-10-301-844-19; Sequence 19, Application US/10301844; Publication No. US20030100747A1; GENERAL INFORMATION:
 1.3%; SCO.
100.0%; Pre
 1.3.,
100.0%; Pr
 1813 TATATATATATA 1826
 1813 TATATATATATA 1826
 1 rararararara 14
 14 rararararara 1
 Query Match 1.3%
Best Local Similarity 100.0
Matches 14; Conservative
 Query Match
Best Local Similarity 100.
Matches 14; Conservative
 TYPE: DNA
, ORGANISM: Varicella virus
US-09-913-514-27
 TYPE: DNA ORGANISM: Varicella virus
 US-09-913-514-27
 SEQ ID NO 27
LENGTH: 14
 ઠે
 ò
 Sequence 811, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANT: ROWEN, Ban P.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
 ö
 ö
 1.3%; Score 14; DB 1; Length 14;
 Query Match 1.3%; Score 14; DB 1; Length 14; Best Local Similarity 100.0%; Pred. No. 82; Matches 14; Conservative 0; Mismatches 0; Indels
 CIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDOPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATORING NAS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
NAME: MCMASters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 811:
SEQUENCE CHARACTERISTICS:
 Sequence 27, Application US/09913514 Publication No. US20030082210A1
 Query Match
Best Local Similarity 100.0%; F
Matches 14; Conservative 0;
 1814 ATATATATATAT 1827
 TELEPAN: (206) 622-521
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 81
SEQUENCE CHARACTERISTICS:
TOWATH: 14 base pairs
 1814 ATATATATATAT 1827
 1 ATATATATATAT 14
 TYPE: nucleic acid
STRANDEDNESS: single
 ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPLOGY: linear
US-09-263-959-811
 CITY: Seattle
STATE: Washington
COUNTRY: US
 TOPOLOGY: linear
 09-263-959-811/c
 US-09-263-959-811
 US-09-913-514-27
 RESULT 104
```

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Sequence 384, Application US/09827998

Sequence 384, Application US/09827998

Batent No. US20022102252A1

GENERAL INFORMATION:
APPLICANT: Gu, Yizhong
APPLICANT: Shannon, Mark
TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
FILE REFERENCE: MDhMORF-8
 US-10-085-906-428, Application US/10085906

Sequence 258, Application No. US20030054371A1

GENERAL INFORMATION:

APPLICANT: Wu, Paul

APPLICANT: Wu, Paul

APPLICANT: Gray, Gary

TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS

CURRENT APPLICATION NUMBER: US/10/085,906

CURRENT FILING DATE: 1209-03-27

PRIOR FILING DATE: 1209-03-24

PRIOR FILING DATE: 2000-03-24

PRIOR FILING DATE: 2000-03-24

PRIOR FILING DATE: 2000-03-24

NUMBER OF SEQ ID NOS: 545

SOFTWARE: FREEERY FALSED FOR WINDOW VERSION 4.0
 Gaps
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0
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 DB 1; Length 15; 83;
 Query Match
1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 14; Conservative 0; Mismatches 0; Indels
 Indels
 ö
 NAME: Poissant, Brian M
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0057-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
 Query Match 1.3%; Score 14; DB Best Local Similarity 100.0%; Pred. No. 83; Matches 14; Conservative 0; Mismatches
APPLICATION NUMBER: US/08/852,495C
 SEQUENCE DESCRIPTION: SEQ ID NO: 19:
 TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ 1D NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
 ATTORNEY/AGENT INFORMATION
 TYPE: nucleic acid
STRANDEDNESS: single
 1814 ATATATATATAT 1827
 1813 TATATATATATA 1826
 1 ATATATATATAT 14
 14 TATATATATATA 1
 TOPOLOGY: linear
 TYPE: DNA
CRGANISM: Homo sapiens
US-10-085-906-258
 FILING DATE:
 RESULT 109
US-09-827-998-384
 US-10-085-906-258
 US-10-301-844-19
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 Gaps
 Sequence 19., Application US/10301844
Publication No. US20030100747A1
GENERAL INFORMATION: David A.
APPLICANT: Ruddy, David A.
Wolff, Roger K.
TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN
HEMOCHROMATOSIS GENE
 ö
 Query Match
1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 14; Conservative 0; Mismatches 0; Indels
 COUNTRY: USA
ZIP: 10036-2011
COMPUTER READBLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPALIble
COMPUTER: WINGOWE
SOPTWARE: FASTEED for Windows Version 2.0b
 COMPUTER: IBM PC compatible
COMPATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/301.844
FILING DATE: 20-No. US20030100747A1-2002
CLASSIFICATION: <univolent Classification DATA:
 CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/10/301,844
FILLING DATE: 20-No. US20030100747A1-2002
CLASSIFICATION: «UNKNOWN»
 APPLICATION NUMBER: US/08/852,495C
PILING DATE: OT-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M
REGISTRATION NUMBER: 28,462
REPERENCE/DOCKET NUMBER: 8907-0057-999
TELECOMMUNICATION INFORMATION:
 NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
 SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-301-844-19
 COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 TELEPHONE: 650-493-4935
 TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
 TYPE: nucleic acid
STRANDEDNESS: single
 1813 TATATATATATA 1826
 PRIOR APPLICATION DATA
 NUMBER OF SEQUENCES: 26
 US-10-301-844-19/c
 RESULT 107
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Sequence 387, Application US/09827998

Sequence 387, Application US/09827998

Patent No. US20020102252A1

GENERAL INFORMATION:
APPLICANT: Gu, Yizhong
APPLICANT: Shannon, Mark
TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED FROTEIN E
FILE REFERENCE: MDHMORE-8
CURRENT PAPLICATION NUMBER: US/09/827,998
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PELING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 1881
SEQ ID NO 387

LENGTH: 17
 APPLICANT: G4, Yizhong
APPLICANT: G4, Yizhong
APPLICANT: Shamnon, Mark
TITLE OF INVENTION.

TITLE OF INVENTION NUMBER: US/09/827,998
CURRENT PILICATION NUMBER: US/09/827,998
CURRENT FILING DAFE: 2001-04-06
PRIOR PPPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-05-7
PRIOR PILING DATE: 2000-05-7
PRIOR PRIOR FILING DATE: 2000-05-7
PRIOR PILING DATE: 2000-05-7
PRIOR FILING DATE: 2000-05-7
PRIOR FILING DATE: 2000-05-7
PRIOR FILING DATE: 2000-05-7
PRIOR FILING DATE: 2000-05-7
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 DB 1; Length 17;
 DB 1; Length 17;
 Indels
 Indels
 Indels
 Score 13.8; DB 1;
Pred..No. 91;
 Query Match 1.3%; Score 13.8; D. Best Local Similarity 88.2%; Pred. No. 91; Matches 15; Conservative 0; Mismatches
 Query Match
1.3%; Score 13.8; D:
Best Local Similarity 88.2%; Pred..No. 91;
Matches 15; Conservative 0; Mismatches
 1.3%; Score 13.8; I
88.2%; Fred. No. 91;
tive 0; Mismatches
 Sequence 388, Application US/09827998
Patent No. US20020102252A1
GENERAL INFORMATION:
 1793 TGTGTGTGTGTGT 1809
 1794 GTGTGTGTGTGTGTG 1810
 rererrereaererer 17
 1 GrererricheAcrere 17
 Query Match
Best Local Similarity 88.4
Best Local Similarity 88.4
 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-388
 TYPE: DNA
CORGANISM: Homo sapiens
US-09-827-998-387
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-386
 US-09-827-998-388
 RESULT 112
US-09-827-998-387
 SEO ID NO 388
 LENGTH:
 ò
 g
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 g
 Sequence 385, Application US/09827998

Sequence 385, Application US/09827998

Patent No. US2002010252A1

SERNERAL INFORMATION:
APPLICANT: Gu, Yizhong
APPLICANT: Gu, Vizhong
APPLICANT: Ghannon, Mark
ITILE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
FILE REFERENCE: MDMORR-8

CURRENT APPLICATION NUMBER: US/09/827,998

CURRENT FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-09-27

NUMBER OF SEQ ID NOS: 1881

SEQ ID NO 385

LENGTH: 17
 Sequence 386, Application US/09827998

Faceur C 386, Application US/09827998

Faceur D USZO020102252A1

GENERAL INFORMATION:
APPLICANT: GW. Yizhong

APPLICANT: GW. Yizhong

APPLICANT: Shannon, Mark

TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN FREGNANCY-ASSOCIATED PROTEIN E

FILE REPERENCE: MDHANER: US/09/827,998

CURRENT APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-27

FRICH APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

NUMBER: OF SEQ ID NOS: 1881

SEQ ID NO 386
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 Gaps
 Gaps
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 Query Match
1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 2; Indels
 DB 1; Length 17;
 Indels
 Query Match 1.3%; Score 13.8; I Best Local Similarity 88.2%; Pred. No. 91; Matches 15; Conservative 0; Mismatches
 CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 1881
SOFTWARE: Acomica Sequence Listing Engine; SQ ID NO 384
LENGTH: 17
 CURRENT APPLICATION NUMBER: US/09/827,998
 1793 TGTGTGTGTGTGTGT 1809
 1794 GIGIGIGIGIGIGIG 1810
 rerererriereagiei 17
 1 crercriricreacre 17
 TYPE: DNA
CRGANISM: Homo sapiens
US-09-827-998-385
 TYPE: DNA
CRGANISM: Homo sapiens
US-09-827-998-384
 US-09-827-998-386
 RESULT 110
US-09-827-998-385
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Sequence 837, Application US/09263959
; Sequence 837, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
 APPLICANT: Hood, Leroy E.
 APPLICANT: Roop, Ben F.
 TILE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
 TILE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
 TILE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
 TILE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
 STREET: Seed and Berry LLP
 STREET: Seed and Berry LLP
 STREET: Seattle
 STREET: Seattle
 STREET: Seattle
 STREET: PABLIE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER READABLE FORM:
 MEDIUM TYPE: TROPS COMPATING SYSTEM: PC-DOS/MS-DOS
 OPERATING SYSTEM: PC-DOS/MS-DOS
 OPERATING SYSTEM: PC-DOS/MS-DOS
 OPERATING SYSTEM: PC-DOS/MS-DOS
 MEDIUM TYPE: TROPS COMPATING SYSTEM: PC-DOS/MS-DOS
 OPERATING SYSTEM: PC-DOS/MS-DOS
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 Gaps
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 DB 1; Length 17;
 Length 17;
 Indels
 Indels
 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959 FILING DATE: 05-MAR-1999
 1.3%; Score 13.8; DB 1;
88.2%; Pred. No. 91;
tive 0; Mismatches 2;
 Mismatches
 1.3%; Score 13.8;
88.2%; Pred. No. 91
 920010.426C2
 Sequence 132, Application US/09843676
Patent No. US20020164786A1
GENERAL INFORMATION:
 ATTORNEY AGENT INFORMATION:
NAME: MCMasters, David D
REGISTATION UNDRER: 33,963
REFRENCE/DOCKET NUMBER: 92001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 837:
SEQUENCE CHARACTERISTICS:
 1799 TGTGTGTGTGTGTAT 1815
 APPLICANT: Cech, Thomas R.
Lingner, Joachim
 Chapman, Karen B
 ;
0
 1814 ATATATATATATGTA 1830
 1 Argrardrarardra 17
 17 rerargrererarerar 1
 Conservative
 17 base pairs
 nucleic acid
IDNESS: single
TYPE: nucleic acid
STRANDEDNESS: sing
 Query Match
Best Local Similarity
Matches 15; Conserva
 Query Match
Best Local Similarity
Matches 15; Conserv
 linear
 CLASSIFICATION:
 STRANDEDNESS:
 JS-09-263-959-837/c
 US-09-263-959-837
 US-09-843-676-132
 ;
TOPOLOGY:
US-09-263-959-546
 LENGIH:
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 Sequence 546, Application US/09263959

Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Lee
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANT: ROSD, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Beiry LLP
 FACENCE OF ON. USZUZOLU WAZ PARTENIA OF USZUZOLU WAZ PARTENIA OF USZUZOLU WAZ PARTENIA ON. USZUZOLU WAZ PAPLICANT: GU, YIZhONG APPLICANT: GU, YIZHONG TITLE OF INVENTION: NOVEL ISCFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E FILE OF INVENTION: NOVEER: US/09/827,998
CURRENY APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/236,359
 ö
 ö
 DB 1; Length 17;
 Indels
 COUNTRY: US
ZIP: 98104-7092
CONFUTER READABLE FORM:
MEDIUM TYPE: FLOPDY disk
CONFUTER: IBM PC compatible
OCNENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR.1999
CCASSIFICATION:
 E: Seed and Berry LLP 6300 Columbia Center, 701 Fifth Avenue
 ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEFHONE: (206) 622-4900
TELEFAX: (206) 622-4900
INFORMATION FOR SEQ ID NO: 546:
SEQUENCE CHARACTERISTICS:
 Query Match 1.3%; Score 13.8; I
Best Local Similarity 88.2%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches
 Sequence 389, Application US/09827998
Patent No. US20020102252A1
 1799 TGTGTGTGTGTGTAT 1815
 1798 GTGTGTGTGTGTGTA 1814
 1 TGTTTGTGAGTGTGTAT 17
 Grerrrereadrerera 17
 TYPE: DNA
CORGANISM: Homo sapiens
US-09-827-998-389
 Washington
: US
 STREET: 6300 Co
CITY: Seattle
STATE: Washingt
 JS-09-263-959-546
 RESULT 114
US-09-827-998-389
 RESULT 115
```

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Gaps
 ö
 1.3%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 91;
 COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IN PC Compatible

COMPUTER: IN PC Compatible

CORPUTER: IN PC COMPASS.

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/766,253

FILING DATE: 19-3n-2001

CLASSIFICATION NUMBER: 08/846,017

APPLICATION NUMBER: 08/846,017

APPLICATION NUMBER: 08/846,017

FILING DATE: 1997-04-25

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-07-1996

ATTORNEY PAGENT INFORMATION:

NAME: APPL:

REGISTRATION NUMBER: 35,429

REGISTRATION NUMBER: 35,429

REGISTRATION NUMBER: 35,429

REGISTRATION NUMBER: 35,429
 GENERAL IN CONTINUED TO CECH, Thomas R.
APPLICANT: Linguer, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Morin, Gregg B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Callin
APPLICANT: Harley, William H.
APPLICANT: Harley, William H.
APPLICANT: Barley, William H.
APPLICANT: Barley, Silvin
APPLICANT: Wo. US20030009019Alel Telomerase
NUMBER OF SEQUENCES: 223
CORRESPONDENCES ADDRESS:
ADDRESSE: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111-3834
COMPUTER: FRIDABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: SPANABLE FORM:
MEDIUM TYPE: Poppy disk
COMPUTER: Perentin Release #1.0, Version #1.30
 Indels
 0; Mismatches
 United States of America
 , SEQUENCE DESCRIPTION: SEQ ID NO: 132: US-09-766-253-132
 SUCTABLY APPLICATION DATA:
APPLICATION NUMBER: US/09/438,486
FILING DATE: 12-NOV-1999
 Sequence 132, Application US/09438486 Publication No. US20030009019A1 GENERAL INFORMATION:
 1865 TTTTTTTTTTTT 1881
 LENGTH: 17 base pairs
 TYPE: nucleic acid
STRANDEDNESS: single
 TELEFAX: (415) 576-0.
INFORMATION FOR SEQ ID NO: 132
 SEQUENCE CHARACTERISTICS
STATE: California
 (415)
 linear
 Query Match
Best Local Similarity 88.2
Matches 15; Conservative
 FILING DATE: 12-NOV-
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
 TELEPHONE:
 RESULT 119
US-09-438-486-132
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 d
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0
 Gaps
 ö
 Score 13.8; DB 1; Length 17; Pred. No. 91; 0; Mismatches 2; Indels
 Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TILE OF INVENTION: NO. US20020164786Alel Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
 STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORMY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
 LLP
 ADDRESSEE: Townsend and Townsend and Crew STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
 NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 5.6
PRIOR APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 10-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 01-OCT-1966
ATTORNEY/AGENT INFORMATION:
 TOPOLOGY: linear seq ID NO: 132: US-09-843-676-132
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
 1865 TTTTATTTTTTT 1881
 LENGTH: 17 base pairs
 TELEFAX: (415) 576-03
INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
 TYPE: nucleic acid
STRANDEDNESS: single
 Query Match 1.3%;
Best Local Similarity 88.2%;
Matches 15; Conservative
 CITY: San Francisco
 US-09-766-253-132
```

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) FEATURE:
; OTHER INFORMATION: designed seguence for nucleic acid purification
US-10-208-357-23
 1.3%; Score 13.8; DB 1; Length 17;
88.2%; Pred. No. 91;
tive 0; Mismatches 2; Indels
 Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. US20030032075Alel Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
 STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDION TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
 APPLICANT: Wagner, Richard
TITLE OF INVENTION: Peptide Acceptor Ligation Methods
FILE REPERENCE: 50036/031002
CURRENT FILING DATE: 2002-07-30
CURRENT FILING DATE: 2002-07-30
PRIOR RELING DATE: 2000-07-19
PRIOR RILING DATE: 2000-07-19
PRIOR PILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 17
 ADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/053,758
TILING DATE: 18-0an-2002
CLASSIFICATION: 36
PRIOR APPLICATION: 36
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 36-429
 RESULT 124

US-10-053-758-132

Sequence 132, Application US/10053758

Publication No. US20030032075A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

NAKAMUTA, TOTU

CHAMAN, KAREN B.
 1865 TITITATITITATIT 1881
 TYPE: DNA
ORGANISM: Artificial Sequence
 15; Conservative
 Lohse, Peter
 Query Match
Best Local Similarity
Matches 15; Conserva
 APPLICANT:
 ठे
 В
 Sequence 2098, Application US/09848754A
Publication No. US20030073207A1
Publication No. US20030073207A1
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
TITLE OF INVENTION: Lavels Of Epidermal Growth Factor Receptors
FILE REPERENCE: MBHB00-958-I (400/018)
CURRENT APPLICATION UNDER: US/09/848,754A
CURRENT PILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 9645
SOOTWARE: ParentIn version 3.0
SEQ ID NO 2098
LENGTH: 17
 Gaps
 0; Gaps
 Query Match 1.3%; Score 13.8; DB 1; Length 17; Best Local Similarity 88.2%; Pred. No. 91; Matches 15; Conservative 0; Mismatches 2; Indels
 DB 1; Length 17;
 2; Indels
 015389-002931US
 Score 13.8; D
Pred. No. 91;
0; Mismatches
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION DATA:
APPLICATION 536
PRIOR APPLICATION STA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INCORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,499
REFERENCE, DOCKET NUMBER: 36,499
REFERENCE, DOCKET NUMBER: 36,499
 US-10-208-357-23/c

; Sequence 23, Application US/10208357
; Publication No. US20020182687A1
; GENERAL INFORMATION:
 REFERENCE/DOCKET NUMBER: 01538
TELECOMPUNICATION INDORMATION:
TELEPHONE: (415) 576-0200
TELETAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 1789 ATATTGTGTGTGTGT 1805
 1865 TTTTTATTTTTTT 1881
 Query Match
Best Local Similarity 88.2%;
Matches 15; Conservative (
 17 Arrirgrardrerer 1
 ORGANISM: Homo sapiens
US-09-848-754A-2098
 APPLICANT: Kurz, Markus
 linear
 RESULT 120
US-09-848-754A-2098/c
 US-09-438-486-132
 TYPE: RNA
 RESULT 121
```

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, SEQUENCE DESCRIPTION: SEQ ID NO: 132: US-10-054-295-132
 1865 TTTTTTTTTTTTT 1881
 1865 TITITATITITIT 1881
 1 ttattatatatati 17
 ORGANISM: Artificial Sequence
 0.0ery Match
Best Local Similarity 88.28
Matches 15; Conservative
 Query Match
Best Local Similarity 88.21
Matches 15, Conservative
TOPOLOGY: linear
 NAME/KEY: misc feature LOCATION: (1)..(19)
 US-10-060-756A-4087
 RESULT 124
US-10-117-267-5
 DNA
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0
 Gaps
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 APPLICANT: Cech, Thomas R.

APPLICANT: Cech, Thomas R.

Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: NO. US20030044953Alel Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
 DB 1; Length 17;
 2; Indels
 COMPUTER REALBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
 ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
 NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
 REFERENCE/DOCKET NUMBER: 015389-002930US
 PRICR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
 1.3%; Score 13.8; Di
Best Local Similarity 88.2%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches
 COUNTRY: United States of America ZIP: 94111
 ; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 132:
US-10-053-758-132
 Sequence 132, Application US/10054295
Publication No. US20030044953A1
GENERAL INFORMATION:
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 132:
 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
 1865 TITITATTITIT 1881
 LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 LENGTH: 17 base pairs
 TYPE: nucleic acid
STRANDEDNESS: single
 1 Trititritritritit 17
 SEQUENCE CHARACTERISTICS:
 JS-10-054-295-132
 RESULT 123
```

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Sequence 5. Application US/10117267

| Sequence 5. Application US/10117267
| Publication No. US2003004569811
| GRNERAL INFORMATION:
| GRNERAL INFORMATION:
| APPLICANT: Mancharan, Muthiah
| TITLE OF INVENTION: Compounds, Processes And Intermediates For Synthesis Of Mixed Backl
| TITLE OF INVENTION: Oligomeric Compounds
| TITLE OLIGOMERI
 ö
 Gaps
 0; Gaps
 APPLICANT: Zhang, Jian
TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
FILE REFERENCE: PB0177
CURRENT APPLICATION NUMBER: US/10/060,756A
CURRENT PILING DATE: 2002-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
 ö
 1.3%; Score 13.8; DB 1; Length 17;
88.2%; Pred. No. 91;
ive 0; Mismatches 2; Indels
DB 1; Length 17;
 OTHER INFORMATION: 2'-methoxyethoxy (MOE); phosphorothioate; OTHER INFORMATION: internucleoside linkage US-10-117-267-5
 2; Indels
1.3%; Score 13.8; Di
88.2%; Pred. No. 91;
iive 0; Mismatches
 OTHER INFORMATION: Synthetic Construct
 Sequence 4087, Application US/10060756A Publication No. US20030046717A1 GENERAL INFORMATION:
```

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RESULT 128
US-09-263-959-971/c
 US-10-054-611-132
 TYPE: RNA
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 Gaps
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 Sequence 121.7. Application 418/10054611

Sequence 121.7. Application 418/10054611

GENERAL INFORMATION

Information No. US20030059787A1

GENERAL INFORMATION

Information Georgia

Makamura, Toru

Chapman, Karen B.

Morin, Greeg B.

Harley, Galvin

IIILE OF INVENTION: No. US20030059787A1e1 Telomerase

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

MADDRESSEE: Twomsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco
 Query Match 1.3%; Score 13.8; DB 1; Length 17; Best Local Similarity 88.2%; Pred. No. 91; Matches 15; Conservative 0; Mismatches 2; Indels
 2; Indels
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CPRATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NDER: US/10/054,611
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
 NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REPERENCE JOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: CURNOWN-
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
NUMBER OF SEQ ID NOS: 4804
SEQ ID NO 4087
 STATE: California
COUNTRY: United States of America
ZIP: 94111
 2160 AAGCATTTGTTTCTACT 2176
 ATTORNEY/AGENT INFORMATION:
 LENGTH: 17 base pairs
TYPE: nucleic acid
 TRLEFAX: (415) 576-03
INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
 1 Ardcarrrdrrrdragr 17
 COMPUTER READABLE FORM:
 ; ORGANISM: Homo sapiens
US-10-060-756A-4087
 US-10-054-611-132
 TYPE: DNA
 RESULT 126
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Sequence 1628, Application US/10156306
Publication No. US20030119017A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSaviggen, James
TITLE OF INVENTION: Levels of IKK-Gamma and PKR
TITLE OF IKK-GAMMA and IK
 Sequence 971, Application US/09263959
Patent No. US2020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSER: Seed and Berry LLP
 Gaps
 Gaps
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0
 DB 1; Length 17;
 1.3%; Score 13.8; DB 1; Length 17;
88.2%; Pred. No. 91;
tive 0; Mismatches 2; Indels
 2; Indels
 COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
 E: Seed and Berry LLP 6300 Columbia Center, 701 Fifth Avenue
 1.3%; Score 13.8; D
88.2%; Pred. No. 91;
iive 0; Mismatches
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 132:
 ATTORNEY/AGENT INFORMATION:
NAME: MCMARETS, David D.
REGISSPRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
 US/09/263,959
 1865 TTTTTTTTTTTTTT 1881
 1476 CAGCAGAAAGGTTAGTA 1492
 1 Trititritriti
 17 crecadadadriagia 1
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/009 FILING DATE: 05-MAR-1999
 Ouery Match
Best Local Similarity 88.2%
Matches 15, Conservative
 Query Match
Best Local Similarity 88.23
Matches 15; Conservative
) ORGANISM: Homo sapiens
US-10-156-306-1628
 CITY: Seattle
STATE: Washington
COUNTRY: US
 CLASSIFICATION:
 RESULT 127
US-10-156-306-1628/c
```

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US-09-543/C
US-09-543/C
US-09-543/C
Sequence 543, Application US/09263959
Sequence 543, Application:
TITLORY NOW THAT HOOK, Lee No. Le
 ..
0
 Indels
 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
 AUDERCO.

STREET: 633 West FILL: U.C. STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-206
COMPUTE READABLE FORM:
MEDIUM TYPE: 35 " Diskette, 1.44 Mb
MEDIUM TYPE: 35 " Diskette, 1.44 Mb
MEDIUM TYPE: 35 " Diskette, 1.44 Mb
MEDIUM TYPE: BROADELDE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: OS-JUN-1995
COMPUTER: NOT PERFECT 5.1
CURRENT APPLICATION NUMBER: US/08/463,404
FILING DATE: May 13, 1995
APPLICATION NUMBER: 08/060,952
FILING DATE: May 13, 1993
APPLICATION NUMBER: 08/089,766
FILING DATE: May 13, 1993
APPLICATION NUMBER: 08/038,766
FILING DATE: May 13, 1993
ATTORNEY/AGENT INPORMATION:
NAME: WATDURG, RICHARG J.
REPERRONE/DOCKET NUMBER: 202/045
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEFRAX: ... 213) 955-0440
 Query Match
1.3%; Score 13.4;
Best Local Similarity 93.3%; Pred. No. 95
Matches 14; Conservative 0; Mismatche
 1792 TIGIGIGIGIGIG 1806
 1 redrerererere 15
 TELEFAX: (213) 955-0440
TELEX: 67.3510
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: single
 E: Lyon & Lyon
633 West Fifth
Suite 4700
CORRESPONDENCE ADDRESS:
 ;
US-08-463-404-51
 à
 g
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OR QUANTIFICATION OF NUCLE
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OR QUANTIFICATION OF NUCLE
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF QUANTIFICATION OF METHODS AND CURRENT PAPLICATION NUMBER: US /10/187, 251A
CURRENT FILING DATE: 1997-10-09
PRIOR PAPLICATION NUMBER: US 08/912,885
PRIOR PAPLICATION NUMBER: US 08/912,885
PRIOR PAPLICATION NUMBER: US 08/912,503
PRIOR PAPLICATION NUMBER: US 08/912,503
PRIOR PALING DATE: 1997-07-14
PRIOR PAPLICATION NUMBER: US 08/912,951
PRIOR PAPLING DATE: 1997-01-16
PRIOR PAPLING DATE: 1997-01-16
PRIOR APPLICATION NUMBER: US 08/784,787
PRIOR PAPLING DATE: 1997-01-16
SPRIOR DATE: 1997-01-16
SPRIOR DATE: 1997-01-16
SPRIOR DATE: 1
 ö
 Score 13.6; DB 1; Length 15;
Pred. No. 94;
 Score 13.8; DB 1; Length 18; Pred. No. 92;
 Sequence 51, Application US/08463404
Publication No. US20020127634A1
GENERAL INFORMATION:
APPLICANT: Wichael D. West
APPLICANT: Woodsting E. Wright
APPLICANT: Woodsting E. Wright
APPLICANT: Woodsting E. Wright
APPLICANT: Blackburn
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
TITLES OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR
TITLE OF INVENTION: TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 57
 Query Match 1.3%; Score 13.6; D
Best Local Similarity 92.9%; Pred. No. 94;
Matches 13; Conservative 1; Mismatches
 0; Mismatches
 TYPE: DNA
ORGANISM: Artificial sequence
FPEATURE:
OTHER INFORMATION: Synthetic primer
US-10-187-251A-2
 Sequence 2, Application US/10187251A Publication No. US20030108897A1 GENERAL INFORMATION:
 TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INPORMATION FOR SEQ ID NO: 971:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-971
 1811 TGTATATATATAT 1827
 TELECOMMUNICATION INFORMATION:
 1863 CCTTTTTATTTTG 1876
 Query Match
Best Local Similarity 88.2%;
Matches 15; Conservative
 RESULT 129
US-10-187-251A-2/c
```

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Sequence 877 Application US/09263959

Patent No. US20020150891A1

Patent No. US20020150891A1

APPLICANT: Rowen, Lee

APPLICANT: Rowen, Le
 FEATURE:
LOCATION: (167867)...(167881)
OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber =
 ö
 Gaps
 .
0
 APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE CASTERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/287,919
CURRENT APPLICATION NUMBER: US/2002-11-05
NUMBER OF SEQ ID NOS: 2706
SEQ ID NO SEZ.
LENGTH: 15
 Indels
 COUNTRY: Seaffale
STREET: 6300 Columbia Center, 701 Fifth Avenue
STREET: 6300 Columbia Center, 701 Fifth Avenue
STATE: Mashington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
 TYPE: DNA
ORGANISM: Methanococcus jannaschii complete genome.
 Mismatches
 Query Match
Best Local Similarity 93.3%; Pred. No. 95
Matches 14; Conservative 0; Mismatch
 US-10-287-919-582/c
; Sequence SS. Application US/10287919
; Sequence SS. Application US/10287919
; GENERAL INFORMATION:
 FILING DATE: V-CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCMASTERS, DAVIG D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 92001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 877:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
 1813 TATATATATATAT 1827
 15 rarararrararar 1
 15 ratararararar 1
 TYPE: nucleic acid
STRANDEDNESS: single
 linear
 RESULT 133
US-09-263-959-877/c
 US-09-263-959-877
 ð
 g
 Sequence 545, Application US/09263959

Patent No. US20020150891A1

GENERAL INFORMATION:
APPLICANT: Howen, Lee
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANT: ACO, ISTORAGE
APPLICANT: ACO, ISTO
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 ;
0
 Gaps
 Gaps
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 DB 1; Length 15;
 DB 1; Length 15;
 Indels
 1; Indels
 CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Propy disk
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
 1.3%; Sco...
93.3%; Pred. No. >-,
 FILING DALL.
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCMRSTERS, David D.
REGISTRATION NUMBER: 33 953
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF CAS-4900
 1.3%; Score 13.4; Di
Best Local Similarity 93.3%; Pred. No. 99;
Matches 14; Conservative 0; Mismatches
 920010.426C2
US/09/263,959
 FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCMASTERE, 33,963
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 92001
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 622-4900
TELEFAX: (206) 622-4900
TELEFAX: (206) 632-631
INFORMATION FOR SEQ ID NO: 543:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
 1813 TATATATATATAT 1827
APPLICATION NUMBER: US/09
FILING DATE: 05-MAR-1999
 TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
 LENGTH: 15 Das.
TYPE: nucleic acid
STRANDEDNESS: single
 Query Match
Best Local Similarity 93.33
Matches 14; Conservative
 TOPOLOGY: linear
 RESULT 132
US-09-263-959-545/c
 US-09-263-959-545
 US-09-263-959-543
```

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Ouery Match 1.3%; Score 13.4; DB 1; Length 15; Best Local Similarity 93.3%; Pred. No. 99; Matches 14; Conservative 0; Mismatches 1; Indels
 Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS RELATED TO TEOLOMERE LENGTH AND/OR
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/378,535
FILING DATE: 20-aug-1999
APPLICATION NUMBER: 08/819,867
FILING DATE: clucknown-
ATTORNAY AGENT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 24/232
TELECOMMUNICATION INFORMATION:
 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible
OPERATING SYSTEM, IBM P.C. DOS 5.0
SOFTWARE: FRASESD for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/232,927A
FILLING DATE: 29-Aug-2002
CLASSIFICATION: <UNKNOWN>
 TELOMERASE ACTIVITY
 TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 79:
 CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
Sequence 79, Application US/10232927A
Publication No. US20030190638A1
GENERAL INFORMATION:
APPLICANT: Michael D. West
Scott L. Wehnrich
Cathorine M. Strahl
Michael J. Mceachern
 Jerry Shay
Woodring E. Wright
Blizabeth H. Blackburn
Nam Woo Kim
 Sequence 208, Application US/10271602B; Publication No. US20040002073A1; AppLICANT.
 TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
 TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
 TYPE: nucleic acid
STRANDEDNESS: single
 1792 TIGIGIGIGIGIG 1806
 storage
 1 recreréréreres 15
 NUMBER OF SEQUENCES: 80
 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
 RESULT 138
US-10-271-602B-208
 US-10-232-927A-79
 g
) LOCATION: (1596075)...(1596090)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 3341
US-10-287-919-2620
 LOCATION: (167867)...(167881)
OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber =
 ò
 ö
 Gaps
 0; Gaps
 ó
 ö
 Sequence 583, Application US/10287919
Publication No. US2030085830A1
GENERAL INFORMATION:
APPLICANT: Feldman, Richard J.; Global Determinants, Inc.;
TITLE OF INVENTION: Methanococcus jannaschii complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/287,919
CURRENT FILING DATE: 2002-11-05
NUMBER OF SEQ ID NOS: 2706
SOFTWARE: Proprietary
LENGTH: 15
 DB 1, Length 15;
 Sequence 2620, Application US/10287919
Publication No. US030085830A1
GENERAL INFORMATION: Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Methanococcus jamnaschii complete genome.
FILE REPERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/287,919
CURRENT FILING DATE: 2002-11-05
NUMBER OF SEQ ID NOS: 2706
SSOTHARE: Proprietary
LENGTH: 15
 Query Match 1.3%; Score 13.4; DB 1; Length 15; Best Local Similarity 93.3%; Pred. No. 99; Matches 14; Conservative 0; Mismatches 1; Indels
 1.3%; Score 13.4; DB 1; Length 15; 93.3%; Pred. No. 99;
 1; Indels
 1; Indels
 TYPE: DNA ORGANISM: Methanococcus jannaschii complete genome.
 ORGANISM: Methanococcus jannaschii complete genome.
 Query Match
1.3%; Score 13.4; Di
Best Local Similarity 93.3%; Pred. No. 99;
Matches 14; Conservative 0; Mismatches
 0; Mismatches
 1866 TITIATITITITI 1880
 1866 TITIATITITI 1880
 1879 TITAAIGCITIGATA 1893
 15 TTTTATTTCGTTTT 1
 15 rirrarrircerrir 1
 15 rrradicerrradia 1
 14; Conservative
 Best Local Similarity
 RESULT 136
US-10-287-919-2620/c
 US-10-287-919-583/c
 US-10-287-919-583
 US-10-287-919-582
 RESULT 137
US-10-232-927A-79
 Query Match
 TYPE: DNA
 RESULT 135
 Matches
 9
 à
 g
 ò
```

0; Gaps

```
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: NOOP, BEN F.
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDERSS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
 DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
 Gaps
 Gaps
 .
0
 Indels
 1; Indels
 STREET: 0000
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
 Score 13.4; DB 1;
Pred. No. 1e+02;
 Mismatches
 Mismatches
 Sequence 544, Application US/09263959
Patent No. US20020150891A1
 US-09-263-959-541/c
; Sequence 541, Application US/09263959
; Patent No. US20020150891A1
 FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INPORATION:
NAME: MCMASTETS, DAVID D.
REGISTRATION NUMBER: 33,963
REPERSUCE/DOCKET NUMBER: 9200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
 Query Match
Best Local Similarity 93.3%; Pri
Matches 14; Conservative 0;
 1813 TATATATATATAT 1827
 1813 TATATATATATAT 1827
 GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
TITLE OF INVENTION: DIAGNOS
NUMBER OF SEQUENCES: 1279
 16 rararararararar 2
 1 rararacararar 15
 TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
 Query Match 1.3
Best Local Similarity 93.3
Matches 14, Conservative
 TYPE: nucleic acid
STRANDEDNESS: single
STRANDEDNESS: single;
TOPOLOGY: linear
US-09-263-959-541
 linear
 ;
US-09-263-959-541
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 d
 Sequence 541, Application US/09263959
Patent No. US20020150831A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
 APPLICANT: MICHAEL SEUI

TITLE OF INVENTION: MULTIPLEXED ANALYSIS OF POLYMORPHIC LOCI
TITLE OF INVENTION: MULTIPLEXED ANALYSIS OF POLYMORPHIC LOCI
TITLE OF INVENTION: BY CONCURRENT INTERROGATION AND ENZYME-MEDIATED DETECTION
FILE REFERENCE: EMAP-US
CURRENT APPLICATION NUMBER: 06/329, 427
PRIOR PELING DATE: 2001-10-14
PRIOR PILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 60/329, 428
PRIOR PLING DATE: 2001-10-14
PRIOR PLING DATE: 2001-10-14
PRIOR PLING DATE: 2001-10-14
PRIOR PLING DATE: 2001-10-14
PRIOR PELING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 60/329, 619
PRIOR PILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 60/329, 619
PRIOR PILING DATE: 2001-10-15
PRIOR PILING DATE: 2001-10-15
PRIOR PLING D
 0
 FEATURE:
CTHER INFORMATION: Probe sequence derived from human genomic sequence
US-10-271-602B-208
 Gaps
 Query Match
Best Local Similarity 93.3%; Pred. No. 99;
Matches 14; Conservative 0; Mismatches 1; Indels
 COUNTRY. US.

ZIP: 98104-7092

COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
 E: Seed and Berry LLP 6300 Columbia Center, 701 Fifth Avenue
 ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 92010.426C2
TELECOMMUNICATION INFORMATION:
 1580 TGTAGCCCCAGTGAC 1594
 TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 541
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
 TYPE: DNA
ORGANISM: Artificial Sequence
 Washington
 ADDRESSEE:
```

```
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
 Gaps
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 1.3%; Score 13.4; DB 1; Length 16; 93.3%; Pred. No. 1e+02; tive 0; Mismatches 1; Indels
 Length 13;
 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PCOMPUTER: PCOMPUT
 1.2%; Score 13; DB 1; L
100.0%; Pred. No. 1.1e+02;
iive 0; Mismatches 0;
 AUGASIELALION:
ATTORNEY/AGENT INFORMATION:
NAME: MCMASLEES, David D.
REGISTRATION VUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
FELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAR: (206) 682-633
INFORMATION FOR SEQ ID NO: 508:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
 US-09-263-959-548
; Sequence 548, Application US/09263959; Patent No. US202020150891A1
; GENERAL, INFORMATION:
APPLICANT: Hood, Leroy E.
 US-05-263-959-508
US-06-263-959-508
Sequence 508, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION
 1813 TATATATATATAT 1827
 1793 TGTGTGTGTGT 1805
 16 rarararacararar 2
 1 rererererer 13
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 16 base pairs TYPE: nucleic acid STRANDEDNESS; single
 Best Local Similarity 100. Matches 13; Conservative
 14; Conservative
 nucleic acid
EDNESS: single
 Washington
 Query Match
Best Local Similarity
Matches 14; Conserva
 linear
 CITY: Seattle
STATE: Washingt
COUNTRY: US
 STRANDEDNESS:
 TYPE: nucleic
STRANDEDNESS:
;
TOPOLOGY: lin
US-09-263-959-544
 US-09-263-959-508
 Query Match
 RESULT 144
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 g
 à
 DB 1; Length 16;
 Indels
 COUNTRY: US
ZIP: 98104-708
ZIP: 98104-708
ZIP: 98104-708
ZIP: 98104-708
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION NUMBER: 33,963
REGISTRATION NUMBER: 33,963
REPRERENCE/DOCKET NUMBER: 92010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAM: (206) 622-4900
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
 Mismatches
 ATTORNEY/AGENT INFORMATION:
NAME: WGMASCES, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 92010.426C2
TELECOMMUNICATION: INFORMATION:
 Score 13.4;
Pred. No. 1e
 Query Match
Best Local Similarity 93.3%; Pr
Matches 14; Conservative 0;
 1813 TATATATATATAT 1827
 1 TATATGTATATAT 15
 TYPE: nucleic acid
STRANDEDNESS: single
 STATE: Washington COUNTRY: US
 linear
 RESULT 142
US-09-263-959-544/c
 US-09-263-959-544
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g

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US-09-263-959-704

US-09-263-959-704

Sequence 704, Application US/09263959

Patent No. US20020150891A1

PAPPLICANT: Hood, Leroy E.

APPLICANT: Koop, Ben F.

TITLE OF INVEXTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:
 ö
 Gaps
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 Query Match 1.2%; Score 13; DB 1; Length 13; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 13; Conservative 0; Mismatches 0; Indels
 Length 13;
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Ploppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATE: US/09/263,959
FILING DATE: 05-MAR-1999
 STREET: Seed and Berry Lip
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
ZUPRY: US
 1.2%; Score 13; DB 1; Ld
100.0%; Pred. No. 1.1e+02;
 ATTORNEY AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRAINON NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 62-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
TYPE: mucleic acid
STRANDENNESS: single
 Query Match
1.2%; Score 13; DB 1
Best Local Similarity 100.0%; Pred. No. 1.14
Matches 13; Conservative 0; Mismatches
 920010.426C2
REFERENCE/DOCKET NUMBER: 92001
TELECOMMUNICATION INPORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-631
INFORMATION FOR SEQ ID NO: 548:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 1794 GTGTGTGTGTGTG 1806
 1813 TATATATATAT 1825
 1 Grerererere 13
 13 ratarararar
 ; TOPOLOGY: linear
US-09-263-959-548
 linear
 US-09-263-959-704
 RESULT 147
US-09-263-959-723
APPLICANT: Rowen, Lee
APPLICANT: Xoop, Ben F.
TILE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
 Sequence 548, Application US/09263959
Fatent No. US20020150991A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rowen, Lee
APPLICANT: Seed and Berry LLP
STREET: G300 Columbia Center, 701 Fifth Avenue
GTTY: Seatle
STRATE: Washington
 Query Match 1.2%; Score 13; DB 1; Length 13; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 13; Conservative 0; Mismatches 0; Indels
 CURRENT READMELE FORM:
COMPUTER READMELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TOPPY FLODS/MS-DOS
SOFTWARE: PETALIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
 CIR. 38104-7092
CIP. 38104-7092
COMPUTER READMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
COMPUTER: IBW PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIPICATION:
 FILING DALE.

CLASSIFICATION:
ATTONEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REGISTRATION NUMBER: 920010.426C2
RELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INPORMATION FOR SEQ ID NO: 548:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
 ATTORNEY/AGENT INFORMATION:
NAME: MCMasters, David D.
REGISTRATION NUMBER: 33,963
 1814 ATATATATATA 1826
 1 ATATATATATA 13
 ADDREST: 6300
STREET: 6300
CITY: Seattle
 RESULT 145
US-09-263-959-548/c
 US-09-263-959-548
 COUNTRY:
```

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0; Gaps
 US-08-892-503-1

// Sequence 1, Application US/08892503

// Publication No. US20020042048A1

// GENERAL INFORMATION:

// APPLICANT: Dramanac, Radoje

// TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION

// TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION

// TITLE OF INVENTION: OR QUANTIFICATION OF NUCLEIC ACID SPECIES

// TITLE OF INVENTION: US QUANTIFICATION OF NUCLEIC ACID SPECIES

// TITLE OF INVENTION: USPREAMENCE: 1959-013-999

// CURRENT FILLING DATE: 1997-07-14

// NUMBER OF SEQ ID NOS: 13

// SEQ ID NO 1

// LENGTH: 15
 ö
 Sequence 2, Application US/08892503
Fublication No. US2020042048A1
GENERAL INFORMATION:
APPLICANT: Dramac, Radoje
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TITLE OF INVENTION: OR QUANTIFICATION OF NUCLEIC ACID SPECIES
TILE REFERENCE: 9598-0013-999
CURRENT APPLICATION NUMBER: US/08/892,503
CURRENT PILING DATE: 1997-07-14
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 15
 FEATURE:
OTHER INFORMATION: Artificially synthesized oligonucleotide
NAME/KEY: misc_feature
LOCATION: (1) ... (15)
OTHER INFORMATION: n = A,T,C or G
US-08-892-503-1
 1.2%; Score 13; DB 1; Length 13; 100.0%; Pred. No. 1.1e+02; tive 0; Mismatches 0; Indels
 Query Match 1.2%; Score 13; DB 1; Length 15; Best Local Similarity 92.9%; Pred. No. 1.1e+02; Matches 13; Conservative 0; Mismatches 1; Indels
 ATTORNEY/AGENT INPORMATION:

NAME: MCMSSters, David D.

REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INPORMATION:
FELEPAK: (206) 682-6900
FELEPAK: (206) 682-6031
INFORMATION FOR SEQ ID NO: 723:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
FORDALCSY: linear
US-09-263-959-723
 ORGANISM: Artificial Sequence
 1863 CCTTTTTATTTTG 1876
 1814 ATATATATATA 1826
 1 ccirririniriris 14
 Best Local Similarity 100.0
Matches 13; Conservative
 13 ATATATATATA 1
 CLASSIFICATION:
 RESULT 150
US-08-892-503-2/c
 Query Match
 TYPE: DNA
 ઠે
 a
 δ
Sequence 723, Application US/09263959

Patent No. US20020150891A1

GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Roop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
 US-09-263-959-723/C
SEQUENCE 723, Application US/09263959
SEQUENCE 723, Application US/09263959
SEQUENCE 723, Application US/09263959
SECONDATION:
APPLICANT: Hood, Lerry B.
APPLICANT: Koop, Ben F.
TITE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
 Query Match 1.2%; Score 13; DB 1; Length 13; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 13; Conservative 0; Mismatches 0; Indels
 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: US-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WASAGENT INFORMATION:
REGISTRATION NUMBER: 33,963
REGISTRATION NUMBER: 33,963
REGISTRATION NUMBER: 33,963
REGISTRATION NUMBER: 37,063
REGISTRATION NUMBER: 37,063
REGISTRATION NUMBER: 37,063
REGISTRATION NUMBER: 37,063
REFERENCE/DOCKET NUMBER: 37,063
REGISTRATION NUMBER: 37,063
REGISTRATION NUMBER: 37,063
REGISTRATION NUMBER: 37,063
REGISTRATION NO: 723: SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
TYPE: NUCLAIC acid
RERANDEDNESS: single
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
 ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
 ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
 ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 1813 TATATATATAT 1825
 1 TATATATATAT 13
 Washington
 Washington
 linear
 98104-7092
 COUNTRY: US
 TOPOLOGY:
US-09-263-959-723
 COUNTRY:
```

mcgarry191-19.rnpb

```
Sequence 121, Application US/10056414
Publication No. US20030003463A1
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
Draper, Kenneth G.
MCSWiggen, Vames
TITLE OF INVENTION: BISEASES OR CONDITIONS
) OTHER INFORMATION: synthetic 805:814 junction US-09-896-095-245
 1863 CCTTTTTATTTTG 1876
 TYPE: DNA ORGANISM: Artificial Sequence
 1846 ATTTANAGITGIT 1858
 15 CCTTTTTNTTTTG 2
 ORGANISM: Artificial
 RESULT 154
US-10-056-414-121/c
 US-09-896-095-245/c
 TYPE: DNA
 Matches
 ò
 g
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 Gaps
 0; Gaps
 OTHER INFORMATION: Exemplary oligonucleotide primer used in sequence OTHER INFORMATION: assembly process
 .
0
 NAME/KEY: misc_feature

LOCATION: (8)...(8)

OTHER INFORMATION: n=a, t, c, g or

OTHER INFORMATION: 1-(2-deoxy-D-ribfuranosyl)-3-nitropyrrole
US-09-918-995-38044
 ACOUNT 19-95

ACOUNT 19-95

ACOUNT 19-95

BUDDICATION OF US20030073623A1

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION NOVEL NUCLEIC ACID SEQUENCES

TITLE OF INVENTION NOVEL NUCLEIC ACID SEQUENCES

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTHARE: FEAST SEQ for Windows Version 3.0

SEQ ID NO 38045
 US-09-918-995-38044
US-09-918-995-38044

Sequence 38044, Application US/09918995

Publication No. US20030073623A1

GENERAL INFORMATION:

APPLICANT: Hyeeq, Inc.

TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

FILLE REPERSENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT PILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOCITAND 38044

LENGTH: 15
 PEATURE:
OTHER INFORMATION: Artificially synthesized oligonucleotide
NAME/KEY: misc feature
LOCATION: (1)...(15)
OTHER INFORMATION: n = A,T,C or G
US-08-892-503-2
 Query Match 1.2%; Score 13; DB 1; Length 15; Best Local Similarity 92.9%; Pred. No. 1.1e+02; Matches 13; Conservative 0; Mismatches 1; Indels
 Query Match 1.2%; Score 13; DB 1; Length 15; Best Local Similarity 92.9%; Pred. No. 1.1e+02; Matches 13; Conservative 0; Mismatches 1; Indels
TYPE: DNA ORGANISM: Artificial Sequence
 1863 CCTTTTTATTTTG 1876
 1863 CCTTTTTATTTTG 1876
 ORGANISM: Artificial Seguence
 1 CCTTTTTTTTTTG 14
 15 CCTTTTTNTTTTG 2
 TYPE: DNA
 FEATURE:
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 0; Gaps
OTHER INFORMATION: Exemplary oligonucleotide primer used in sequence OTHER INFORMATION: assembly process
 Sequence 245,C

Sequence 245,Application US/0996095

Publication No. US2003021986A1

Sequence 245,Application No. US2003021986A1

Septication No. US2003021986A1

APPLICANT: LADNER, Charles C.

APPLICANT: GUTERNAN, Sonia K.

APPLICANT: ROBERTS, Bruce L.

APPLICANT: RARKLAND, William

APPLICANT: REX. Archur C.

APPLICANT: LEY, Archur C.

APPLICANT: LEY, Archur C.

APPLICANT: LEY, Archur C.

APPLICANT: LEY, Archur C.

APPLICANT: RENT, Rachel B.

TITLE OF INVENTION DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS

FILE REFERENCE: LADNER-7L

CURRENT FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: 08/415,922

PRIOR PELING DATE: 1993-01-26

PRIOR PILING DATE: 1993-01-26

PRIOR FILING DATE: 1991-03-01

PRIOR FILING DATE: 1991-03-01

PRIOR FILING DATE: 1991-03-01

PRIOR FILING DATE: 1991-03-01

PRIOR FILING DATE: 1991-12-18

NUMBER OF SED ID NOS: 274

SOFTHARE: PACENTIN VERSION 3.2

SEQ ID NO 245

LENGTH: 15
 FEATURE:
NAME/KEY: misc_feature
COCATION: (8)...(8)
OTHER INFORMATION: n=a, t, c, g or
OTHER. INFORMATION: 1-(2-deoxy-D-ribfuranosyl)-3-nitropyrrole
US-09-918-995-38045
 Query Match 1.2%; Score 13; DB 1; Length 15; Best Local Similarity 92.9%; Pred. No. 1.1e+02; Matches 13; Conservative 0; Mismatches 1; Indels
 Ouery Match 1.2%; Score 13; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 13; Conservative 0; Mismatches 0; Indels
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Query Match
1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels
 Sequence 310, Application US/10056414
; Publication No. US2003003469A1
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; Draper, Kenneth G.
MCSWiggen, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; BELATED TO LEVELS OF
; NF-KB
 COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,414
FILING DATE: 23-Jan-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/291,932A
FILING DATE: August 15, 1994
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/087,132
FILING DATE: December 7, 1992
 COUNTRY: 0.000
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
Storage
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible OPERATION SYSTEM: IBM P.C. DOS 5.0 SOFFWARE: WORD PERfect 5.1 CURRENT APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 23,327
REFERENCE/DOCKET NUMBER: 208/157
TELECOMMUNICATION:
TELEPHONE: (213) 489-1600
 TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 194: US-10-056-414-194
 CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
 TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
 TELEX: 67-3510
INFORMATION FOR SEQ ID NO. 194:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 NUMBER OF SEQUENCES: 830
 2152 TCACCTGGAAGCA 2164
 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
 15 rcaccrocaacca 3
 RESULT 156
US-10-056-414-310/c
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 Gaps
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0
 Query Match
1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.18+02;
Matches 13; Conservative 0; Mismatches 0; Indels
 APPLICANT: Stinchcomb, Dan T.
Draper, Kenneth G.
McSwiggen, James
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
RELATED TO LEVELS OF
 COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,414
FILING DATE: 23-Jan-2002
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/245,466
FILING DATE: August 15, 1994
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
ATTORNEY ARRET INFORMATION:
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/157
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATI
 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
RELATED TO LEVELS OF NF-KB
 SEQUENCE DESCRIPTION: SEQ ID NO: 121:
 CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
613 Mest Fifth Street
 ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
 Sequence 194, Application US/10056414; Publication No. US20030003469A1; GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO: 121: SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 storage
 NUMBER OF SEQUENCES: 830
CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES: 830
 2152 TCACCTGGAAGCA 2164
 CITY: Los Angeles
STATE: California
 TOPOLOGY: linear
 15 rcaccreeaagca 3
 US-10-056-414-194/c
 US-10-056-414-121
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Sequence 57, Application US/10191997
Sequence 67, Application US/10191997
Sequence 67, Application US/10191997
Sequence 67, Application No. US20030207834A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DAIE, Roderic M. K.
APPLICANT: THOMPSON, Terry
TITLE OF INVENTION: Oligonuclectide-Containing Pharmacological Compositions And Their
FILE REPERENCE: 54800-5613
CURRENT APPLICATION NUMBER: US/10/191,997
CURRENT FILING DATE: 2002-07-10
PRIOR FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 132
SOFTWARE: Patentin version 3.1
SEQ ID NO 67
LENGTH: 16
 ö
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 0; Gaps
 Gaps
 Lukhtanov, Eugeny A.
Gamper, Howard B.
Meyer Jr., Rich B.
TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
Groove Binder Conjugates
 ö
 CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LIP
STREET: Tow Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PATCHIA. Release #1.0, Version #1.30
 Query Match 1.2%; Score 13; DB 1; Length 16; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 13; Conservative 0; Mismatches 0; Indels
 1; Indels
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/415,370
FILING DATE: 03-APPL
APPLICATION NUMBER: US 09/141,764
 0; Mismatches
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/739,928
 OTHER INFORMATION: CD40L oligonucleotide
 FILING DATE: 11-May-2001
CLASSIFICATION: <Unknown>
 Sequence 2, Application US/09739928 Patent No. US20020052482A1 GENERAL INFORMATION:
 APPLICANT: Kutyavin, Igor V.
 1863 CCTTTTTATTTTG 1876
 ORGANISM: Artificial sequence
 1688 TGACACTGTTCAG 1700
 1 ccrrrrrrrrrrr 14
 Matches 13; Conservative
 4 reacacrerrand 16
 NUMBER OF SEQUENCES:
 -10-191-997-67
 US-10-191-997-67
 -09-739-928-2
 YPE: DNA
 FEATURE:
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 0; Gaps
 1.2%; Score 13; DB 1; Length 15; 92.9%; Pred. No. 1.1e+02;
 Query Match
1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels
 APPLICATION NUMBER: US/08/291,932A
FILING DATE: August 15, 1994
APPLICATION NUMBER: 08/25,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warbburg, Richard J.
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 208/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
 ; LOCATION: (8) -

A OTHER INFORMATION: n = A or T or G or C or M

US-10-187-251A-1
 APPLICATION NUMBER: US/10/056,414
 TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 310: US-10-056-414-310
 FILING DATE: 23-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
 OTHER INFORMATION: Synthetic primer
 Sequence 1, Application US/10187251A Publication No. US20030108897A1 GENERAL INFORMATION:
 TELEY, (213) 955-0440
TELEY, 67-3510
INFORMATION FOR SEQ ID NO: 310:
SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
STRANDEDNESS: single
 ORGANISM: Artificial sequence
 2152 TCACCTGGAAGCA 2164
 15 TCACCTGGAAGCA 3
 NAME/KEY: misc feature
 Query Match
Best Local Similarity
 RESULT 157
US-10-187-251A-1
 TYPE: DNA
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TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF USE FILE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF USE FILE REFREENCE: AM102.P.LUS
CURRENT FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: US 60/189,190
PRIOR APPLICATION NUMBER: US 60/189,190
PRIOR APPLICATION NUMBER: US 60/250,334
PRIOR FILING DATE: 2000-11-30
 GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
 ö
 Gaps
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 Score 12.8; DB 1; Length 16;
Pred. No. 1.2e+02;
0; Mismatches 2; Indels
 STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle STATE: Washington COUNTRY: US 21P: 98:04-7092 COUNTRY: US COUNTRY: US COUNTRY: SEATH FORM: WEDIUM TYPE: FIDEPY disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PSPLICATION DATA: CURRENT APPLICATION DATA: US/09/263,959
 E: Seed and Berry LLP 6300 Columbia Center, 701 Fifth Avenue
 APPLICANT: Fernandez, Joseph
APPLICANT: Archdeacon, Dorcthy
APPLICANT: Archdeacon, John
APPLICANT: Chakhmakhcheau, Okeana
APPLICANT: Choob, Mikhail
APPLICANT: Choob, Mikhail
 Sequence 950, Application US/09263959 Patent No. US20020150891A1
 Sequence 9, Application US/09805296D Patent No. US20020155989A1
 CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCMASCERS, David D.
REFERRATION NUMBER: 33,963
REFERRENCE/DOCKET NUMBER: 92001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6930
INFORMATION FOR SEQ ID NO: 950:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
 1866 TITITITITITITI 1881
 GENERAL INFORMATION:
APPLICANT: Active Motif
APPLICANT: Efimov, Vladimir
APPLICANT: Fernandez, Joseph
APPLICANT: Archdeacon, Dorothy
APPLICANT: Archdeacon, John
 Query Match
Best Local Similarity 87.5%;
Matches 14; Conservative (
 05-MAR-1999
 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
 FILING DATE:
 US-09-263-959-950
 -09-805-296D-9
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 Gaps
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 OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Oligonucleotide US-09-152-059-70
 ö
 Query Match
1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
 Query Match
1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
 NAME: RECEST, WILLIAM B.
REGISTRATION NUMBER: 37,369
REFERENCE/DOCKET NUMBER: 17682A-003510US
TELECOMMUNICATION INFORMATION:
TELEPRAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 Sequence 70, Application US/09152059

Sequence 70, Application US/09152059

Setent No. US20200668708A1

GREERAL INFORMATION:
APPLICANT: WENGEL, JESPER
APPLICANT: WENGEL, JESPER
APPLICANT: WENGEL, JESPER
APPLICANT: WENGEL, JESPER
CURRENT FILING DATE: 1994.05/059

CURRENT APPLICATION NUMBER: 06/058,541

PRIOR FILING DATE: 1997-09-11

PRIOR FILING DATE: 1997-09-12

PRIOR APPLICATION NUMBER: 60/068,293

PRIOR APPLICATION NUMBER: 60/068,293

PRIOR PILING DATE: 1998-01-16

PRIOR FILING DATE: 1998-01-16

PRIOR FILING DATE: 1998-01-05

PRIOR FILING DATE: 1998-01-05

PRIOR FILING DATE: 1998-01-05

PRIOR FILING DATE: 1998-01-03

PRIOR FILING DATE: 1998-01-03

PRIOR FILING DATE: 1998-01-03

PRIOR FILING DATE: 1998-01-05

PRIOR FILING DATE: 1998-01-28

NUMBER OF SEQ ID NOS: 146

SOFTWARE: PALCATION NUMBER: 60/094,355

PRIOR FILING DATE: 1998-01-28

NUMBER OF SEQ ID NOS: 146

SEQ ID NO 70

LENGTH: 16
 APPLICATION NUMBER: US 09/507,345 FILING DATE: 18-FEB-2000 ATTORNEY/AGENT INFORMATION:
 TOPOLOGY: linear

MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-739-928-2
FILING DATE: 27-AUG-1998
 1865 TITITITITITI 1880
 TYPE: DNA ORGANISM: Artificial Sequence
 1865 TITITATITI
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;
US-09-843-676-131
 (415) 576-0200
 Sequence 131, Application US/09766253 Publication No. US20020187471A1 GENERAL INFORMATION:
 1865 TITITATITATIT 1880
 ATTORNEY/AGENT INFORMATION
 1880
 STRANDEDNESS: single
 INFORMATION FOR SEQ ID NO: 13.
SEQUENCE CHARACTERISTICS
 CITY: San Francisco
STATE: California
 16 Tririririririri
 16 frifiritiriti
 (415)
 Best Local Similarity
Matches 147 Conserv
 1865 TTTTTATT
 US-09-766-253-131/c
 US-09-766-253-131
 Query Match
 RESULT 165
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 Gaps
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 APPLICANT: Loceth, Thomas R.

Inigner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: No. U$20020164786A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
STREET: Two Embarcadero Center, 8th Floor
 Length 16;
 Indels
 COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
 NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
 Query Match
1.2%; Score 12.8; DB 1;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2;
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION S36
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
PILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
 TYPE: DNA
CRANISM: Artificial Sequence
CRANISM: Artificial Sequence
FEATURE:
CTHER INFORMATION: Synthetic Construct
NAME/KEY: misc_feature
CHER INFORMATION: Synthetic Construct
US-09-805-296D-9
 Sequence 131, Application US/09843676 Patent No. US20020164786A1 GENERAL INFORMATION:
 ATTORNEY/AGENT INFORMATION:
 FGTTTT 1880
 CITY: San Francisco
 INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS
 NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 16
 1865 TITTTATIT
 US-09-843-676-131/c
 RESULT 163
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 Gaps
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 APPLICANT: Cech, Thomas R.
APPLICANT: Cech, Thomas R.
Inigner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020187471Alel Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
 Length 16;
 Length 16;
 Indels
 Indels
 CONTROL SYSTEM PC Compatible
COMPUTER: IBM PC Compatible
OPERATIOG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION: <UNKNOWN>
 ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
 NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION INFORMATION:
 ch 1.2%; Score 12.8; DB 1; Similarity 87.5%; Pred. No. 1.2e+02; 14; Conservative 0; Mismatches 2;
Query Match 1.2%; Score 12.8; DB 1; Best Local Similarity 87.5%; Pred. No. 1.2e+02; Matches 14; Conservative 0; Mismatches 2;
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
 COUNTRY: United States of America 22P: 9411. COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
 TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 131:
```

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Gaps
 TYPE: DNA; CRGANISM: Artificial Sequence; FRATURE: FEATURE: OTHER INFORMATION: designed sequence for nucleic acid purification US-10-208-357-22
 ö
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 05-ARY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 05-ARY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 05-ARY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 05-ARY-1997
APPLICATION NUMBER: US 08/844,419
 Query Match
1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
 Andrews, William H.
TITLE OF INVENTION: No. US20030032075Alel Telomerase NUMBER OF SEQUENCES: 225
APPLICANT: ALL APPLICANT: APPLICANT: APPLICANT: APPLICANT: Wagner, Richard TITLE OP INVENTION: Peptide Acceptor Ligation Methods FILE OF INVENTION: Peptide Acceptor Ligation Methods FILE REFERENCE: 50036/031002
CURRENT FILING DATE: 2002-07-30
CURRENT FILING DATE: 2002-07-30
FRIOR APPLICATION NUMBER: 60/145,834
FRIOR APPLICATION NUMBER: 60/145,834
FRIOR APPLICATION NUMBER: 60/145,834
FRIOR PILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 16
 CORRESPONDENCE ADDRESS:
ADDRESSER: Fownsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
 STATE: California
COUNTRY: United States of America
 Sequence 131, Application US/10053758
Publication No. USZO030032075A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachlim
Nakamura, Toru
Chapman, Karen B.
 1865 TITITATITITI 1880
 -10-053-758-131/c
 à
 g
 APPLICANT: Cech, Thomas R.
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
APPLICANT: Andrews, William H.
CORRESPONDENCES: 223
CORRESPONDENCE ADDRESS:
 COMPUTER READABLE FORM:

MEDIUM TYPE Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Batentin Release #1.0, Version #1.30

SOFTWARE: Batentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

GURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/438,486

FILING DATE: 12-NOV.1997

CLASSIFICATION NUMBER: US 08/851,843

FILING DATE: 25-APR-1997

CLASSIFICATION DATA:

APPLICATION NUMBER: US 08/846,017

FILING DATE: 18-APR-1997

CLASSIFICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

CLASSIFICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

CLASSIFICATION NUMBER: US 08/844,419

FILING DATE: 10-APR-1996

CLASSIFICATION NUMBER: US 08/724,643

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

CLASSIFICATION: 536

ANDAR: APPLICATION: ASA

ANDAR: APPLICATION:

NUMBER: US 08/724,643

ANDAR: APPLICATION:

NUMBER: US 08/724,643

ANDAR: APPLICATION:

NUMBER: US 08/724,643
 SEE: Townsend and Townsend and Crew LLP: Two Embarcadero Center, 8th Floor San Francisco
 NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REPERENCE/DOCKET NUMBER: 015389-002931US
TELECOMMUNICATION INFORMATION:
 CITY: San Francisco
STATE: California
COUNTRY: United States of America
Application US/09438486
5. US2003009019A1
 Randolph T.
 TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 131:
SEQUENCE CHARACTERISTICS:
 TYPE: nucleic acid
STRANDEDNESS: single
 linear
 US-09-438-486-131
 ADDRESSEE:
STREET: T
```

ATTORNEY/AGENT INFORMATION

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Gaps

Ouery Match
1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels

. 1865 TTJ

US-10-208-357-22/c ; Sequence 22, Application US/10208357 ; Publication No. US20020182687A1

RESULT 166

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Gaps
 Gaps
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 MATINE OF INVENTION: NO. US20030059787A1E1 TELOMERASE
ANGTEWS, William H.
TITLE OF INVENTION: NO. US20030059787A1E1 TELOMERASE:
CORRESPONDENCES 225
CORRESPONDENCE ADDRESS:
ADDRESSE: TWO EMbarcadero Center, 8th Floor
CITY: San Francisco
SIATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BAPPER PC DOMPATIBLE
COMPUTER: DECENTION PC DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
ARBURCATION: 536
CLASSIFICATION: 536
 Query Match 1.2%; Score 12.8; DB 1; Length 16; Best Local Similarity 87.5%; Pred. No. 1.2e+02; Matches 14; Conservative 0; Mismatches 2; Indels
 Score 12.8; DB 1; Length 16;
Pred. No. 1.2e+02;
0; Mismatches 2; Indels
 NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/POCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: CURNOWN:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 01-0CT-1996
 SEQUENCE DESCRIPTION: SEQ ID NO: 131:
US-10-054-611-131
 TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 131: US-10-054-295-131
 Sequence 131, Application US/10054611 publication No. US20030059787A1 GENERAL INFORMATION:
 FILING DATE: 01-OCT-1993 ATTORNEY/AGENT INFORMATION:
 APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
 1865 TTTTTTTTTTTT 1880
 INFORMATION FOR SEQ ID NO: 131
 Query Match 1.2*;
Best Local Similarity 87.5*;
Matches 14; Conservative
 RESULT 169
US-10-054-611-131/c
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 Gaps
 1.2%; Score 12.8; DB 1; Length 16; 87.5%; Pred. No. 1.2e+02; tive 0; Mismatches 2; Indels
 Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TILE OF INVENTION: No. US20030044953Alel Telomerase
NUMBER OF SEQUENCES: 225
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
 NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
 REGISTRATION NUMBER: 36,429
REFERENCE TOWNER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-0an-2002
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: 08/854,050
APPLICATION NUMBER: 08/894,050
FILING DATE: 25-APP-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1966
ATTORNEY/AGENT INFORMATION:
 STATE: California
COUNTRY: United States of America
ZIP: 94111
 TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 131: US-10-053-758-131
 Sequence 131, Application US/10054295
Publication No. US20030044953A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Randolph T
 TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 131:
 1865 TTTTATTTTTT 1880
 INFORMATION FOR SEQ ID NO: 131:
 SEQUENCE CHARACTERISTICS
 14; Conservative
 Best Local Similarity
Matches 14; Conserva
 JS-10-054-295-131/c
 Query Match
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2935
 . LOCATION: (1424659)...(1424675)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = US-10-287-919-2293
 ö
 Gaps
 Gaps
 Gaps
 .
0
 ö
 ô
 Query Match 1.2%; Score 12.8; DB 1; Length 16; Best Local Similarity 87.5%; Pred. No. 1.2e+02; Matches 14; Conservative 0; Mismatches 2; Indels
 APPLICANT: Feldman, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Methanococcus jannaschii complete genome.
FILE REFRENCE: Jim Zeger Law Offices - 703-684-8333
CURRENT PERLICATION VIMBER: US/10/287,919
CURRENT FILING DATE: 2002-11-05
NUMBER OF SEQ ID NOS: 2706
SOFTWARE: Proprietary
SEQ ID NO 2293
LENGTH: 16
 Length 16;
 Length 16;
 yeaquence 21, Application US/10227001

publication No. US20030113765A1

GENERAL INFORMATION:

APPLICANT: Dempcy, Robert O.

APPLICANT: Aponia, Irina Aleksandrovna
APPLICANT: Aponia, Irina Aleksandrovna
APPLICANT: Booch Biosciences, Inc.

APPLICANT: Booch Biosciences, Inc.

TILE OF INVENTION: Hybridization-Triggered Fluorescent
TILE OF INVENTION: Hybridization-Triggered Fluorescent
TILE OF INVENTION: Detection of Nucleic Acids
FILE REFERENCE: 17682A-004210US

CURRENT APPLICATION NUMBER: US 09/428,236

PRIOR FILING DATE: 1999-10-26

NUMBER OF SEQ ID NOS: 24

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 21

LENGTH: DATE

LENGTH: DATE

LENGTH: APPLICATION NUMBER: PARENCE APPLICATION NUMBER OF SEQ ID NOS: 24

SEQ ID NO 21

LENGTH: LENGTH: APPLICATION NUMBER OF SEQ ID NOS: 24

LENGTH: LENGTH: LENGTH: APPLICATION NUMBER OF SEQ ID NOS: 24

LENGTH: LENGTH: LENGTH: APPLICATION NUMBER OF SEQ ID NO 21

LENGTH: LENGTH: APPLICATION NUMBER OF SEQ ID NO 21
 Indels
 Indels
) OTHER INFORMATION: R2 (ODN) of fluorophore-MGB-ODN) OTHER INFORMATION: conjugate US-10-227-001-21
 TYPE: DNA
ORGANISM: Methanococcus jannaschii complete genome.
Query Match
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2;
 Query Match
1.2%; Score 12.8; DB 1;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2;
 Sequence 2293, Application US/10287919
Publication No. US20030085830A1
GENERAL INFORMATION:
 1865 TTTTATTTTGTTTT 1880
 1869 TATTITIGITITIAAT 1884
 1869 TATTTTTTTTTAT 1884
 TYPE: DNA ORGANISM: Artificial Sequence
 1 TATTTTGCTTTTTAAT 16
 1 rarrracrrrraar 16
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 GENERAL INCHARATION

GENERAL INCHARATION

APPLICANT: Etimov, Vladimir

APPLICANT: Etimov, Vladimir

APPLICANT: Etimov, Vladimir

APPLICANT: Etimov, Vladimir

APPLICANT: Archdeacon, Dorothy

APPLICANT: Archdeacon, John

APPLICANT: Archdeacon, John

APPLICANT: Chackmaskcheau, Oksana

APPLICANT: Chackmaskcheau, Oksana

APPLICANT: Chackmaskcheau, Oksana

APPLICANT: Hondorp, Kyle

TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF US

FILE REPRENCE: AM102.P.1.1US

CURRENT APPLICATION NUMBER: US 60/189,190

PRIOR APPLICATION NUMBER: US 60/189,190

PRIOR APPLICATION NUMBER: US 60/250,334

PRIOR FILING DATE: 2000-03-14

PRIOR FILING DATE: 2001-03-13

PRIOR FILING DATE: 2001-03-13

NUMBER OF SEQ ID NOS: 36

SSOFTWARE: PALENTING DATE: 2010-03-13

NUMBER OF SEQ ID NOS: 36

LEMENT PRIOR PLILING DATE: 2010-03-13

NUMBER OF SEQ ID NOS: 36

LEMENT PRIOR PLILING DATE: 2010-03-13

NUMBER OF SEQ ID NOS: 36

LEMENT PRIOR PLILING DATE: 2010-03-13

NUMBER OF SEQ ID NOS: 36

LEMENT PLILING DATE: 2010-03-13

NUMBER OF SEQ ID NOS: 36

LEMENT PLILING DATE: 2010-03-13

NUMBER OF SEQ ID NOS: 36

LEMENT PLILING DATE: 2010-03-13

LEMENT PLILING DATE: 2010-03-13

NUMBER OF SEQ ID NOS: 36

LEMENT PLILING DATE: 2010-03-13
 1675
 FEATURE:
; LOCATION: (644443)...(644458)
; LOCATION: (644443)...(644458)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = US-10-287-919-1350
 ô
 Gaps
 ö
 Sequence 1350, Application US/10287919;
Publication No. US20030085830A1;
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.;
TITLE OF INVENTION: Methanococcus jannaschii complete genome.;
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333;
CURRENT APPLICATION NUMBER: US/10/287,919;
CURRENT FILING DATE: 2002-11-05;
NUMBER OF SEQ ID NOS: 2706;
SOFTWARE: Proprietary
SEQ ID NO 1350
 Ouery Match 1.2%; Score 12.8; DB 1; Length 16; Best Local Similarity 87.5%; Pred. No. 1.2e+02; Matches 14; Conservative 0; Mismatches 2; Indels
 TYPE: DNA ORGANISM: Methanococcus jannaschii complete genome
 FEATURE:
OTHER INFORMATION: Synthetic Construct
 NAME/KEY: misc_feature

// OTHER INFORMATION: Synthetic Construct

US-10-072-975-9
 Sequence 9, Application US/10072975
Publication No. US20030059789A1
GENERAL INFORMATION:
 1865 TITITATITITI 1880
 1865 TTTTTTTTTTT 1880
 TYPE: DNA ORGANISM: Artificial Sequence
 US-10-287-919-1350
 -10-072-975-9
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 Gaps
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; ; OTHER INFORMATION: oligonucleotide
US-10-208⁵650-70
 ò
 Query Match 1.2%; Score 12.8; DB 1; Length 16; Best Local Similarity 87.5%; Pred. No. 1.2e+02; Matches 14; Conservative 0; Mismatches 2; Indels
 Indels
 Ouery Match 1.2%; Score 12.8; DB 1; Best Local Similarity 87.5%; Pred. No. 1.2e+02; Matches 14; Conservative 0; Mismatches 2;
 US-10-208-500-70

Sequence 70, Application US/10208650

Publication No. US20030144231A1

GENERAL INFORMATION:
APPLICANT: WENGEL, JESPER
APPLICANT: WENGEL, JESPER
APPLICANT: WENGEL, JESPER
TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
FILE REFERENCE: 49165-C2 (71994)
CURRENT APPLICATION NUMBER: US/10/008,029
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: 06/058,541
PRIOR APPLICATION NUMBER: 60/058,541
PRIOR APPLICATION NUMBER: 60/058,541
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1998-09-14
PRIOR FILING DATE: 1998-09-14
PRIOR FILING DATE: 1998-03-03
PRIOR FILING DATE: 1998-03-03
PRIOR FILING DATE: 1998-03-03
PRIOR FILING DATE: 1998-03-03
PRIOR FILING DATE: 1998-04-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
SEQ ID NO 70
LENGTH: 16
 ; NAME/KEY: misc_feature
; OTHER INFORMATION: Synthetic Construct
US-10-051-436-9
 RESULT 177
US-10-203-780-9
Sequence 9, Application US/10203780
Publication No. US20030165914A1
GENERAL INFORMATION:
 1865 TITITATITITI 1880
 1865 TITITATITITIT 1880
 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
 1 rrrrrrrrrrrrrr 16
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 16
 TYPE: DNA ORGANISM: Artificial Sequence
 FEATURE:
 B
 ઠે
 ò
 g
 APPLICANT: Active Motif
APPLICANT: Efimov, Vladimir
APPLICANT: Efimov, Vladimir
APPLICANT: Fernandez, Joseph
APPLICANT: Archdeacon, John
APPLICANT: Archdeacon, John
APPLICANT: Archdeacon, John
APPLICANT: Chakhmakhcheu, Oksana
APPLICANT: Chakhmakhcheu, Oksana
APPLICANT: Chakhmakhcheu, Oksana
APPLICANT: Chakhmakhcheu, Oksana
APPLICANT: Choob, Mikhail
APPLICANT: Hondorp, Kyle
ITILE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF US
FILE REPERENCE: AMIO2.P.1US
CURRENT APPLICATION NUMBER: US/10/051,436
CURRENT PILING DATE: 2002-01-18
PRIOR FILING DATE: 2000-03-14
PRIOR APPLICATION NUMBER: US 60/250,334
PRIOR FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 18
 ;
0
 Gaps
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: oligonucleotide
 ô
 Query Match
1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
 Sequence 70, Application US/10008029
FUBLICATION NO. US20030134808A1
GRARRAL INFORMATION SERVER
APPLICANT: WENGEL, JESPER
APPLICANT: WENGEL, JESPER
APPLICANT: WIELSEN, FOUL
TITLE OF INVENTION: OLIGONUCLECTIDE ANALOGUES
FILE OF INVENTION: OLIGONUCLECTIDE ANALOGUES
FRIOR APPLICATION NUMBER: 09/152,059
FRIOR FILING DATE: 1998-09-11
FRIOR FILING DATE: 1998-01-16
FRIOR FILING DATE: 1998-01-16
FRIOR FILING DATE: 1998-01-16
FRIOR FILING DATE: 1998-01-05
 Sequence 9, Application US/10051436 Publication No. US20030138045A1 GENERAL INFORMATION:
 1865 TITITATITITIT 1880
 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
 1 TTTTTTTTTTTTT 16
 1 TTTTTTTTTTTT 16
 US-10-008-029-70
 -10-051
```

```
APPLICANT Fernandez, Joseph
APPLICANT Fernandez, Joseph
APPLICANT Archdeacon, Dorothy
APPLICANT Archdeacon, Dorothy
APPLICANT Archdeacon, John
APPLICANT Choob, Mikhail
TITLE OF INVENTION: OLICONUCLEOTIDE ANALOGUES AND METHODS OF USE FOR MODULATING GENE
TITLE OF INVENTION: EXPESSION
TITLE OF INVENTION: EXPESSION
FILE REPRENCE: AM102.P.1.1.103
CURRENT FILING DATE: 2003-02-07
FILE REPRENCE: AM102.P.1.1.1.03
CURRENT FILING DATE: 2002-02-09
FRIOR FILING DATE: 2002-03-13
FRIOR FILING DATE: 2001-03-13
FRIOR APPLICATION NUMBER: US 60/189,190
FRIOR FILING DATE: 2000-03-14
 ö
 Gaps
 ô
 Length 16;
 GENERAL INCOMPATION:

GENERAL INCOMPATION:

APPLICANT: Modering E. West

APPLICANT: Woodring E. Weight

APPLICANT: Woodring E. Weight

APPLICANT: Woodring E. Weight

TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS

TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR

TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR

TITLE OF INVENTION: RELATED TO TELOMERASE ACTIVITY

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: G13 West Fifth Street

STREET: G13 West Fifth Street

STREET: LOS Angeles

STREET: LOS Angeles

STREET: LOS Angeles

STREET: Suite 4700

CITY: LOS Angeles

STREET: Suite A700

CITY: LOS ANGELES

COMPUTER: READABLE FORM:
MEDIUM TYPE: Storage

COMPUTER: Storage

COMPUTER: Storage

COMPUTER: STREET: Suite A700

SOFTWARRE: WOACH PERFECT 5.1

CURRENT APPLICATION NUMBER: USO 5.0

SOFTWARRE: MOACH PERFECT 5.1

CURRENT APPLICATION NUMBER: USO 5.0
 Indels
 Query Match
1.2%; Score 12.8; DB 1;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2;
 LASSIFICATION DATE: US/08/463,404
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/06
 ; NAME/KEY: misc_feature
; OTHER INFORMATION: Synthetic Construct
US-10-360-275-9
 FEATURE: OTHER INFORMATION: Synthetic Construct
 Sequence 56, Application US/08463404 Publication No. US20020127634A1 GENERAL INFORMATION:
 1865 TTTTTTTTTTT 1880
 TYPE: DNA
ORGANISM: Artificial Sequence
 g
 ò
APPLICANT: CUZIN, MARC
APPLICANT: PELTIE, PHILIPPE
APPLICANT: PONTECAVE, MARC
APPLICANT: PONTECAVE, MARC
APPLICANT: PONTECAVE, MARC
APPLICANT: DECOUT, JEAN-LUC
APPLICANT: DUEYMES, CECILE
TITLE OF INVENTION: ANALYSIS OF BIOLOGICAL TARGETS USING A BIOCHIP COMPRISING A FLUOR
TITLE OF INVENTION: ANALYSIS OF BIOLOGICAL TARGETS USING A BIOCHIP COMPRISING A FLUOR
TITLE OF INVENTION: ANARKER
FILLS REFERENCE: 226286U50XPCT
CURRENT APPLICATION NUMBER: PC7/FR01/00516
PRIOR APPLICATION NUMBER: PC7/FR01/00516
PRIOR FILING DATE: 2001-02-22
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN VERSION 3.1
LENGTH: 16
TYPE: DNA
ORGANISM: ARTIFICIAL SEQUENCE
 ö
 ö
 Sequence 71, Application US/10309775A
Publication No. US20040006032A1
Publication No. US20040006032A1
APPLICANT: LOPEZ, Ricardo A.
TITLE OF INVENTION: IMMUNOSTIMULATORY CLIGONUCLEOTIDES AND USES THEREOF
FILE REFERENCE: 2501/0327
CURRENT APPLICATION NUMBER: US/10/309,775A
CURRENT FILING DATE: 2002-12-04
PRIOR PAPLICATION NUMBER: CA 2,388,049
PRIOR PAPLICATION NUMBER: CA 2,388,049
PRIOR FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 74
SEQ ID NO 71
SEQ ID NO 71
LENGTH: 16
 Gaps
 Gaps
 NAME/KEY: modified_base

) LOCATION: (1)..(1)

) CTHER INFORMATION: t is modified with a covalent linkage to flavin

US-10-203-880-9
 Query Match
1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
 Query Match
1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
 ; Sequence 9, Application US/10360275; Publication No. US20040014644A1; GENERAL INFORMATION:
 FEATURE:
OTHER INFORMATION: SYNTHETIC DNA
FEATURE:
 1865 TITITITITITI 1880
 1866 TITIATITITITI 1881
 TYPE: DNA
GRGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR primer
US-10-309-775A-71
 1 TITICALTITICATITI 16
 RESULT 178
US-10-309-775A-71
 RESULT 179
US-10-360-275-9
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Sequence 530, Application US/09263959;
Sequence 530, Application US/09263959;
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Kowen, Lee
APPLICANT: Kowen, Lee
APPLICANT: Kowen, Lee
APPLICANT: Koop, Ben F.
TITLE OP INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND WETHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDER EADLESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
STREET: 6300 Columbia Center, 701 Fifth Avenue
COUNTRY: Manington
COUNTRY: Backload FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CONFUTER: PatentIn Release #1.0, Version #1.25
COMPUTER: DatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/263,959
FILING DATE: OS-MAR-1999
CLASSITICATION: ATTORNEY APPLICATION
ATTORNEY APPLICATION:
 RESULT 183
US-09-532
US-09-532-532
Sequence 532, Application US/09263959
Patent No. US20020150891A1
Patent No. US20020150891A1
PAPLICANT: Nood, Leroy E.
PAPLICANT: Roop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
ADDRESSEE: Seed and Berry LLP
ADDRESSEE: Seed and Berry LLP
 ö
 Length 14;
 1; Indels
 Query Match
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1;
 ATTORNEY/AGENT INPORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INPORMATION:
TELEPHONE: (206) 622-4900
 TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 530:
SEQUENCE CHARACTERISTICS:
 1814 ATATATATATAT 1827
1814 ATATATATATAT 1827
 1 ATATATATGTATAT 14
 14 ATATACATATAT 1
 LENGTH: 14 base pairs
 STREET: 6300 Columb
CITY: Seattle
STATE: Washington
COUNTRY: US
 linear
 ZIP: 98104-7092
 STRANDEDNESS:
 ;
US-09-263-959-530
 ઠે
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 g
 APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANTON: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
COMPRESSEE: Geed and Berry LLP
STREET: Galo Columbia Center, 701 Fifth Avenue
COUNTRY: Washington
COUNTRY: Washington
COUNTRY: RAADABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
COMPUTER: DATA:
APPLICATION NUMBER: US/09/263,959
FILLING DATE: 09-MAR.1999
CLASSIFICATION: ANDREWED THE COMPUTER: OF-MAR.1999
FILLING DATE: OF-MAR.1999
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 1.2%; Score 12.4; DB 1; Length 14; 92.9%; Pred. No. 1.3e+02; tive 0; Mismatches 1; Indels
 1.2%; Score 12.4; DB 1; Length 14; 92.9%; Pred. No. 1.3e+02; tive 0; Mismatches 1; Indels
 ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEFAM: (206) 622-4900
INFORMATION FOR SEQ ID NO: 530:
SEQUENCE CHARACTERISTICS:
FILING DATE: May 13, 1992
APPLICATION NUMBER: 08/038,766
FILING DATE: MATCH 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: WATCHUEY, RICHARY 0.
RECISTRATION NUMBER: 202/045
REFERENCE/DOCKET NUMBER: 202/045
TELEPHONE: (213) 489-1600
TELEPAK: (713) 489-1600
TELEPAK: (713) 955-0440
INFORMATION POR SEQ ID NO: 56: SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: NUCleic acid
STRANDEDNESS: Single
 US-09-263-959-530
; Sequence 530, Application US/09263959
? Patent No. US20020150891A1
; GENERAL INFORMATION:
 1793 TGTGTGTGTGTG 1806
 LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 Best Local Similarity 92.9
Matches 13; Conservative
 Best Local Similarity 92.5
Matches 13; Conservative
 linear
 linear
 US-09-263-959-530
 ;
TOPOLOGY:
US-08-463-404-56
 Query Match
 Query Match
```

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US-09-263-599-562

US-09-263-599-562

US-09-263-599-562

Sequence 562, Application US/09263959

Fatent No. US20020150891A1

GENERAL INFORMATION:

APPLICANT: Rowen, Lee

APPLICANT: Scop, Benn F.

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry Lib

STREET: Seat le

CITY: Seat le

CONFUTEN: Washington

COMPUTEN: Babable FORM:

MEDIUM TYPE: Floppy disk

COMPUTEN: IBM PC Compatible

COMPUTEN: IBM PC Compatible

COMPUTEN: IBM PC Compatible

COMPUTEN: IBM PC Compatible

COMPUTEN: BEADABLE FORM:

COMPUTEN: IBM PC Compatible

COMPUTEN: SYSTEM: PC-DOS/MS-DOS

COMPUTEN: PC-DOS/MS-DOS

COMPUTEN: PC-DOS/MS-DOS

COMPUTEN: PC-DOS/MS-DOS
 Sequence 562, Application US/09263959
Sequence 562, Application US/09263959
Sequence 562, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Rowen, Leroy E.
APPLICANT: Kowen, Lee
APPLICANT
 ö
 ö
 Gaps
 Gaps
 ;
0
 ..
0
 Query Match
1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels
 E. Seed and Berry LLP
6300 Columbia Center, 701 Fifth Avenue
 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
 ATTORNEY/AGENT INFORMATION:
NAME: MCMASTERS, David D.
REGISCHATION NUMBER: 33,963
REFERENCE/COCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPAN: (206) 622-4900
TELEPAN: (206) 682-6031
INFORMATION FOR SEQ ID NO: 562:
SEQUENCE CHARACTERISTICS:
 1814 ATATATATATAT 1827
 Best Local Similarity 92.9
Matches 13; Conservative
 TYPE: nucleic acid
STRANDEDNESS: single
 US-09-263-959-562/c
 US-09-263-959-562
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 Sequence 532, Application US/09263959

Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Lee
APPLICANT: Roop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry Lip
 ö
 Score 12.4; DB 1; Length 14; Pred. No. 1.3e+02;
 ADDRESSEE: Seed and Berry LLP
STREET: 6100 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OCMPUTER: IBM PC compatible
COMPUTER: DEALIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION: WIMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
 CURRATION STSIEM:

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

PLING DATE: 05-MAR-1999

CLASSIFICATION:

ATORNEY/AGENT INFORMATION:

NAME: MCMaters, David D.

REGISTRATION:

TELECOMMUNICATION:

TELECOMMUNICATION:

TELEPHONE: (206) 682-690

TELEPHONE: (206) 682-601

TELEPHONE: (206) 682-601

INFORMATION FOR SEQ ID NO: 532:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

TOPOLOGY: linear
 ATTORNEY AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 532:
SEQUENCE CHRACTERISTICS:
 Query Match
1.2%; Score 12.4; D
Best Local Similarity 92.9%; Pred. No. 1.3e
Matches 13; Conservative 0; Mismatches
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 1814 ATATATATATAT 1827
 1 ArArArcharar 14
 LENGTH: 14 base pairs
 RESULT 184
US-09-263-959-532/c
 ;
US-09-263-959-532
```

```
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
 APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
TILLS OF INVENTION: Ben F.
TILLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
 Gaps
 ö
 1; Indels
 ADDRESSES:
STREET: Seatle
STREET: Seatle
STREET: Washington
CITY: Seatle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDTUM TYEE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FLING DATE: O5-MRR-1999
CLASSIFICATION:
ATTORNATION NUMBER: 33,963
REGISTRATION NUMBER: 33,963
REGISTRATION NUMBER: 33,963
REGISTRATION NUMBER: 33,963
REGISTRATION NUMBER: 33,963
RELEPRANCE/DOCKET NUMBER: 33,963
RELEPRANCE CAPARTERISTICS:
TELEPROMUNICATION INFORMATION:
TELEBROWN FOR SCO ID NO: 592:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYRANDENDESS: SINGLE
STRANDENDESS: SINGLE
TOTAL TABLE ACT THE ACT T
 E: Seed and Berry LLP (6300 Columbia Center, 701 Fifth Avenue
 Score 12.4; DB 1;
Pred. No. 1.3e+02;
0; Mismatches 1;
 1.2%; Scor.
92.3%; Pred. No. ...
 Sequence 726, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
 Sequence 592, Application US/09263959
Patent No. US20020150891A1
 Query Match 1.2%; Scr
Best Local Similarity 92.9%; Prr
Matches 13; Conservative 0;
 1814 ATATATATATATAT 1827
 1814 ATATATATATAT 1827
 1 ATATATATGTATAT 14
 14 ATATACATATATA 1
 Query Match
Best Local Similarity 92.9
Matches 13; Conservative
 linear
 STRANDEDNESS:
;
TOPOLOGY: li
US-09-263-959-592
 RESULT 188
US-09-263-959-592/C
 TOPOLOGY:
US-09-263-959-592
 ð
 셤
 ò
 Sequence 592, Application US/09263959
; Sequence 592, Application US/09263959
; Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STREET: 6300 Columbia Center, 701 Fifth Avenue
COUWRRY: US
STATE: Washington
COUWRRY: US
STATE: Rabballe FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
STRING DATE: US-MAR-1999
STRING DATE: US-MAR-1999
 ö
 Query Match 1.2%; Score 12.4; DB 1; Length 14; Best Local Similarity 92.9%; Pred. No. 1.3e+02; Matches 13; Conservative 0; Mismatches 1; Indels
 ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
NAME: MCMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCETON INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAM: (206) 682-691
INFORMATION FOR SEQ ID NO: 592:
SEQUENCE CHARACTERISTICS:
 ATTORNEY/AGENT INFORMATION:
NAME: McMatters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPANE: (206) 622-4900
TELEPAN: (206) 682-6031
INFORMATION FOR SEQ ID NO: 562:
SEQUENCE CHARACTERISTICS:
 1814 ATATATATATAT 1827
 LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 Washington
 linear
Seattle
 ;
US-09-263-959-562
 JS-09-263-959-592
```

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Gegrance 730, Application US/09263959;
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESSE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
 Gaps
 Gaps
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 1.2%; Score 12.4; DB 1; Length 14; 92.9%; Pred, No. 1.3e+02; tive 0; Mismatches 1; Indels
 Query Match
1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels
 CITY: Seattle
CONTRY: Washington
COUNTRY: Use Seattle
CONTRY: Use Seattle
COMPUTER. Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION NUMBER: Use Seattle
REFERENCE-POCKET NUMBER: 92010.426C2
TELECOMMUNICATION NUMBER: 92010.426C2
TELECOMMUNICATION NUMBER: 92010.426C2
TELECOMMUNICATION NUMBER: 92010.426C2
TELECOMMUNICATION NUMBER: 92010.426C2
 US-09-263-959-730/c
; Sequence 730, Application US/09263959
; Tatent No. US20020150891A1
; GENERAL INFORMATION:
 1814 ATATATATATAT 1827
 TELEFAX: (206) 682-6031
INPORMATION FOR SEQ. ID NO: 73
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
 1813 TATATATATATA 1826
 INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CERRACIESTISTICS.
LEWGTH: 14 base parrs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TOPOLOGY: linear
 1 TATATATATATA 14
 (206) 682-6031
 14 ATÁTÁTÁCÁTÁTÁT 1
 Query Match
Best Local Similarity 92.9
Matches 13; Conservative
 ,
TOPOLOGY:
US-09-263-959-726
 , TOPOLOGY:
US-09-263-959-730
 US-09-263-959-730
 TELEFAX:
 RESULT 192
 Sequence 726, Application US/09263959
Patent No. US20020156891A1
GENERAL INFORMATION:
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
STREET: 6300 Columbia Center, 701 Fifth Avenue
 ö
 1.2%; Score 12.4; DB 1; Length 14; 92.9%; Pred. No. 1.3e+02; tive 0; Mismatches 1; Indels
 COUNTRY: UG.

ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPARE: Datentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-WAR-1999
 COMPUTER READBLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
 ATTORNEY/AGENT INFORMATION:
NAME: MCMSterer, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELEPORMUNICATION INFORMATION:
TELEPAX: (206) 682-6910
TELEPAX: (206) 682-6911
INFORMATION FOR SEQ ID NO: 726:
SEGUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: uncleic acid
STRANDEDNESS: single
 NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
**REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
 1814 ATATATATATAT 1827
 ATTORNEY/AGENT INFORMATION:
 1 ATATGTATATA 14
 Query Match
Best Local Similarity 92,9%
Matches 13; Conservative
 Washington
 Washington
 STREET: 6300 C
 CATION:
 US-09-263-959-726/c
 ;
TOPOLOGY:
US-09-263-959-726
 STATE: WE COUNTRY:
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REBULT 194

OGENERAL INFORMATION

Sequence 752, Application US/09263959

Sequence 752, Application US/09263959

Sequence 752, Application US/09263959

Sequence 752, Application US/09263959

SEXERAL INFORMATION

APPLICANT: Rood, Leroy E.

APPLICANT: Rood Columbia Center, 701 Fifth Avenue

CITY: Seattle

CITY: Seattle

STREET: 600 Columbia Center, 701 Fifth Avenue

CITY: Roadlington

CONTRY: Washington

CONTRY: Washington

STREET: 500 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STREET: 600 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STREET: 600 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STREET: 600 Columbia Center, 701 Fifth Avenue

CONTRY: Washington

STREET: 800 Columbia Center, 701 Fifth Avenue

CONTRY: Washington

STREET: 800 Columbia Center, 701 Fifth Avenue

CONTRY: Washington

STREET: 800 Columbia Center, 702 Fifth Avenue

CONTRY: Washington

STREET: 800 Columbia Center, 702 Fifth Avenue

CONTRY: Washington

CONTRY: Washington

STREET: 800 Columbia Center, 701 Fifth Avenue

CONTRY: Washington

STREET: 800 Columbia Center, 702 Fifth Avenue

CONTRY: Washington

CONTRY: Washington

STREET: 800 Columbia

CONTRY: Washington

STREET: 800 Columbia

CONTRY: Washington

CONTRY: Washington

CONTRY: Washington

CONTRY: Washington

STREET: 800 Columbia

CONTRY: Washington

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 1.2%; Score 12.4; DB 1; Length 14; 92.9%; Pred. No. 1.38+02; tive 0; Mismatches 1; Indels
 Indels
 Score 12.4; DB 1;
Pred. No. 1.3e+02;
0; Mismatches 1;
 REFERENCE/DOCKET NUMBER: 9200
TELECOMMINICATION INFORMATION:
TELEPAX: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 752:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 Query Match 1.2%; Scc
Best Local Similarity 92.9%; Pro
Matches 13; Conservative 0;
 1814 ATATATATATAT 1827
 (206) 622-4900
 1814 ATATATATATAT 1827
 TELEPHONE: (206) 622-499
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 1 ATATATACATATAT 14
 Best Local Similarity 92.9
Matches 13; Conservative
 TYPE: nucleic acid
STRANDEDNESS: single
 linear
 US-09-263-959-752
 US-09-263-959-752
 TOPOLOGY:
 Query Match
 RESULT 195
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 g
 Sequence 752, Application US/09263959

Patent NO. US20020150891A1

GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Koop, Ben F.
TITLE OF INVENTION:
DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Scattle
STATE: Washington
 APPLICANT: ROOF, LES
APPLICANT: ROOP, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
 ö
 Gaps
 Query Match 1.2%; Score 12.4; DB 1; Length 14; Best Local Similarity 92.9%; Pred. No. 1.3e+02; Matches 13; Conservative 0; Mismatches 1; Indels
 STAIL:
COUNTRY: US
ZIP: 98104-7092
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATEN: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
TT-NG DATE: 05-MAR-1999
 ADDRESSEE: Geed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
STREET: 6300 Columbia Center, 701 Fifth Avenue
STREET: 6300 Columbia Center, 701 Fifth Avenue
STATE: 4000 Columbia Center, 701 Fifth Avenue
COUNTRY: US
ZIP: 98104-7092
COMPUTER: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLESSIFICATION:
 ATTORNEY/AGENT INFORMATION:
NAME: MCMSELER, DAVIG D.
REGISTRATION NUMBER: 33,963
TELECONVANICATION INFORMATION:
TELEPHONE: (206) 622-6031
INFORMATION FOR SEQ ID NO: 730:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
 1813 TATATATATATA 1826
 TTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
Hood, Leroy E.
 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
 ;
US-09-263-959-730
 JS-09-263-959-752
```

```
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
 ö
 0
 Query Match 1.2%; Score 12.4; DB 1; Length 14; Best Local Similarity 92.9%; Pred. No. 1.3e+02; Matches 13; Conservative 0; Mismatches 1; Indels
 1.2%; Score 12.4; DB 1; Length 14; 92.9%; Pred. No. 1.3e+02; tive 0; Mismatches 1; Indels
 CONTRACTOR TO THE TEACH TO THE TEACH TO THE TEACH TO THE TEACH THE
 STREET: Seed and Berry LLP STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle STATE: Washington COUNTRY: US
 ATTORNEY FACENT INFORMATION:
NAME: MCMARLENER: David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION NUMPER: 920010.426C2
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 822:
SEQUENCE CHARATERISTICS:
LENGTH: 14 base pairs
TENGTH: 17000001: 110001
FILING DATE: 05-MAR-1999

CLASSIFICATION:
NAME: NCMSELES, David D.
REGIGERATION NUMBER: 33,963
REFIRENCE/DOCKET NUMBER: 920010.426C2
TELEPHONE: (206) 622-4900
TELEPRAK: (206) 622-691
INFORMATION FOR SEQ ID NO: 764:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANEDNESS: single
 Sequence 822, Application US/09263959; Patent No. US20020150891A1; GENERAL INFORMATION:
 1814 ATATATATATAT 1827
 1814 ATATATATATAT 1827
 1.2%
Best Local Similarity 92.9%
Matches 13; Conservative
 14 ATATATTTATATAT 1
 ;
US-09-263-959-822
 US-09-263-959-764
 US-09-263-959-822
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 RESULT 196

US-09-263-559-764/c

US-09-263-559-764/c

Sequence 764, Application US/09263959

Sequence 764, Application US/09263959

Sequence 764, Application US/09263959

Sequence 764, Application US/09263959

APPLICANT: Rowen, Lee

APPLICANT: Rowen, Lee

APPLICANT: Koop, Ben F.

ITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI

NUMBER OF SEQUENCES: 1279

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP

STREE: Seattle

CITY: Seattle

STATE: Mashington
 Sequence 764, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: ROWEN, Ben F.
TITLE OF INVENTION:
DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
COMMESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
 Gaps
 .
0
 Query Match 1.2%; Score 12.4; DB 1; Length 14; Best Local Similarity 92.9%; Pred. No. 1.3e+02; Matches 13; Conservative 0; Mismatches 1; Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Parentin Release #1.0, Version #1.25
CURRNT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
 ATTORNEY/AGENT INFORMATION:
NAME: McMatters, David D.
REGISTRATION NUMBER: 33.963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 62-4900
TELEFAX: (206) 62-6031
INFORMATION FOR SEQ ID No: 764:
SEQUENCE CHARACTERISTICS:
 1814 ATATATATATAT 1827
 1 ATATATAAATATAT 14
 LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 Seattle
Washington
 linear
 FILING DATE: 0 CLASSIFICATION:
 ;
TOPOLOGY:
US-09-263-959-764
 US-09-263-959-764
 COUNTRY:
 CITY: STATE:
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Sequence 543, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Roop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
 Length 14;
 Indels
 ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
STATE: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
 1.2%; Score 12.4; DB 1;
92.9%; Pred. No. 1.3e+02;
tive 0; Mismatches 1;
 CITY: Los Angeles
STATE: California
COUWIRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/232,927A
FILING DATE: 29-Aug-2002
CLASSIFICATION NUMBER: US/09/378,535
PRIOR APPLICATION NUMBER: US/09/378,535
PILING DATE: 20-Aug-1999
APPLICATION NUMBER: 08/819,867
FILING DATE: -UNFROMM-1999
APPLICATION NUMBER: 08/819,867
FILING DATE: -UNFROMM-1999
APPLICATION NUMBER: 03/491
REGISTRATION NUMBER: 34,561
REGISTRATION NUMBER: 34,561
REGISTRATION NUMBER: 34,561
REGISTRATION NUMBER: 34,561
 TOPOLOGY: linear ; SEQUENCE DESCRIPTION: SEQ ID NO: 78: US-10-232-927A-78
 SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
 TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
 INFORMATION FOR SEQ 1D NO: 78:
SEQUENCE CHRAACTERISTICS:
LENGTH: 14 base pairs
 1793 TGTGTGTGTGTG 1806
 ADDRESSEE: Lyon &
STREET: 633 West F
Suite 4700
 1 recercicione 14
CORRESPONDENCE ADDRESS
 Query Match
Best Local Similarity 92.9%
Matches 13; Conservative
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 g
 APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
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 Gaps
 ;
0
 Query Match 1.2%; Score 12.4; DB 1; Length 14; Best Local Similarity 92.9%; Pred. No. 1.3e+02; Matches 13; Conservative 0; Mismatches 1; Indels
 STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle STATE: Washington COUNTRY: US
ZIP: 98104-7092
ZIP: 98104-7092
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/263,959 FILING DATE: 05-MAR-1999 CLASSIFICATION:
 E: Seed and Berry LLP 6300 Columbia Center, 701 Fifth Avenue
 TITLE OF INVENTION: THERARY AND DIAGNOSIS OF CONDITIONS RELATED TO TEOLOMERE LENGTH AND/OR TELOMERASE ACTIVITY
 ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION UNDBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
 Woodring E. Wright
Elizabeth H. Blackburn
Nam Woo Kim
 Sequence 78, Application US/10232927A
Publication No. US20030190638A1
GENERAL INFORMATION:
APPLICANT: Michael D. West
Calvin B. Harley
Scott L. Weinrich
Catherine M. Strahl
Michael J. Mceachern
Jerry Shay
 Sequence 822, Application US/09263959
Patent No. US20020150891A1
 TELECORNICE (206) 622 - TELEPHONE (206) 682-6031
INFORMATION FOR SEQ ID NO: 82
SEQUENCE CHARACTERISTICS:
 1814 ATATATATATAT 1827
 NUMBER OF SEQUENCES: 80
 1 ATATATGTATAT 14
 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
 US-09-263-959-822
 -10-232-927A-78
```

```
APPLICANT: Draper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jave
APPLICANT: Morisasey, Dave
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REPERENCE: MBH300-845-H (400/029)
CURRENT APPLICATION NUMBER: US 00/982,712
PRIOR APPLICATION NUMBER: US 07/982,712
PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR FILING DATE: 2000-03-20
PRIOR FILING DATE: 1200-06-09
PRIOR FILING DATE: US 09/636,385
PRIOR FILING DATE: 2000-08-09
 ö
 1.2%; Score 12.4; DB 1; Length 15; 92.9%; Pred. No. 1.38+02; tive 0; Mismatches 1; Indels
 ATTORNEY AGENT INFORMATION:
NAME: MCMASters, David D.
REGISTRATION NUMBER: 33,963
REPERENCE/DOCKET NUMBER: 920010.426C2
TELEFONNICATION INFORMATION:
TELEFAX: (206) 622-6931
INFORMATION FOR SEQ ID NO: 877:
SEQUENCE CHARACTERISTICS:
ILENGTH: 15 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
 Sequence 6011, Application US/09877478
Publication No. US20030068301A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
 1814 ATATATATATAT 1827
 1 ATATATAAATATAT 14
1 ATATATGTATAT 14
 Local Similarity 92.9
 linear
 US-09-877-478-6011/c
 US-09-263-959-877
 Query Match
 Best Loca
Matches
 ઠે
 Sequence 545, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hood, Lery E.
APPLICANT: Rowen, Lee

 ö
 0; Gaps
 Query Match 1.2%; Score 12.4; DB 1; Length 15; Best Local Similarity 92.9%; Fred. No. 1.3e+02; Matches 13; Conservative 0; Mismatches 1; Indels
 Query Match 1.2%; Score 12.4; DB 1; Length 15; Best Local Similarity 92.9%; Pred. No. 1.3e+02; Matches 13; Conservative 0; Mismatches 1; Indels
 STATE: WHENLIND....
CONTURY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PRE-BER-DOS
SOFTWARE: PATENTIN PATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MARBERES, DAVIG D.
REGISTRATION NUMBER: 33,963
REGISTRATION NUMBER: 33,963
REGISTRATION NUMBER: 33,963
REJERNOZ/POCKET UNMBER: 33,963
RELEFANCE/CONTURNER: 33,963
TELEFANCE (206) 622-4900
 920010.426C2
 TILING DALE:

ATTORNEY/AGENT INFORMATION:

MAME: MCMRAGERS, DAVID D.

REGISTRATION UNDRER: 33,963

REFERENCE/DOCKET NUMBER: 92001

TELEFONNICATION INFORMATION:

TELEFOND INFORMATION:

TELEFOND (206) 682-6031

INFORMATION FOR EGO ID NO: 543:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 base pairs

TYPE: nucleic acid

TYPE: nucleic acid

STRANDEDNESS: single

US-09-263-959-543
 1814 ATATATATATAT 1827
 1814 ATATATATATAT 1827
 05-MAR-1999
 1 ATATATGTATATAT 14
 LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 Seattle
: Washington
 linear
 US-09-263-959-545
 US-09-263-959-545
 CITY:
 RESULT 201
 δ
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RESULT 205

US-10-342-902-6011/C

Sequence 601. Application US/10342902

Sequence 601. Application US/10342902

Sequence 601. Application US/10342902

Sequence 601. Application Workston Workst
 Sequence 6085, Application US/10342902
| Sequence 6085, Application US/10342902
| Sequence 6085, Application NO. US20040054156A1
| GENERAL INFORMATION:
| APPLICANT: Blatt, Larry
| APPLICANT: Blatt, Larry
| APPLICANT: McSwiggen, Jawe
| TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
| TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
| TITLE OF INVENTION: Whethod and Reagent for Inhibiting Hepatitis B Virus Replication
| TITLE OF INVENTION: Whethod and Reagent for Inhibiting Hepatitis B Virus Replication NUMBER: US/10/342,902
| CURRENT FILING DATE: 2000-01-15
| PRIOR APPLICATION NUMBER: US 09/636,385
| PRIOR APPLICATION NUMBER: US 09/636,347
| PRIOR FILING DATE: 2000-10-24
| PRIOR APPLICATION NUMBER: US 09/620-77
 ö
 Query Match 1.2%; Score 12.4; DB 1; Length 15; Best Local Similarity 92.9%; Pred. No. 1.3e+02; Matches 13; Conservative 0; Mismatches 1; Indels
 PRIOR APPLICATION NUMBER: US 07/882,712
PRIOR FILING DATE: 1992-05-14
PRIOR APPLICATION NUMBER: US 09/436,430
 2095 AATGAACAAATGGC 2108
 ; ORGANISM: Hepatitis B virus US-10-342-902-6011
 15 ACTGAACAAATGGC 2
 셤
 RESULT 204

DESCRIPTION TO THE PROPERTY OF THE PROPERTY OF THE PUBLICATION NO. US20030068301A1

SEQUENCE 6085, Application US/0987478

PUBLICANT RIDOXYME Pharmaceuticals, Inc.

APPLICANT: Riboxyme Pharmaceuticals, Inc.

APPLICANT: Blatt, Larry

APPLICANT: McSwiggen, Jan

PRIOR PLING DATE: 2000-03-20

PRIOR PLING DATE: 1994-02-34

PRIOR PLING DATE: 1994-05-04

PRIOR PLING DATE: 1995-05-04

PRIOR PRING DATE: 1995-05-04
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 0; Gaps
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 Query Match 1.2%; Score 12.4; DB 1; Length 15; Best Local Similarity 92.9%; Pred. No. 1.3e+02; Matches 13; Conservative 0; Mismatches 1; Indels
 Query Match
1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels
PRIOR APPLICATION NUMBER: US 09/696,347
PRIOR FILING DATE: 2000-10-24
PRIOR PLING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 08/193,627
PRIOR PLING DATE: 1994-02-07
PRIOR PLING DATE: 1995-05-04
PRIOR PLING DATE: 1995-05-04
PRIOR PLING DATE: 1995-05-04
PRIOR PLING DATE: 1999-11-08
NUMBER: PRIOR PLING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6586
SOFTWARE: PATENTIN VETSION 3.0
SEQ ID NO 6011
 2095 AATGAACAAATGGC 2108
 2095 AATGAACAAATGGC 2108
 TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-6011
) ORGANISM: Hepatitis B virus US-09-877-478-6085
 15 ACTGAACAAATGGC 2
 14 ACTGAACAAATGGC 1
 TYPE: RNA
 RESULT 204
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. LOCATION: (1512879)...(1512893)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 3130
US-10-287-919-2441
 ö
 Sequence 81, Application US/10091281
Publication No. US20030490617A1
Publication No. US20030490617A1
Publication No. US20030490617A1
APPLICANT: MONTIENT
APPLICANT: MONTIENT
TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
FILE REFERENCE: 13587.338
CURRENT APPLICATION NURBER: US/10/091,281
CURRENT FILING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 463
SOFTWARE PARENT NOS: 463
SEQ ID NO 91
 Gape
 0
 ö
 Query Match
1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative, 0; Mismatches 1; Indels
 APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Methanococcus jannaschii complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION VIMBER: US/10/287,919
CURRENT PILING DATE: 2002-11-05
NUMBER OF SEQ ID NOS: 2706
SOFTWARE: Proprietary
SEQ ID NO 2441
LENGTH: 15
 Ouery Match 1.2%; Score 12.4; DB 1; Length 15; Best Local Similarity 92.9%; Pred. No. 1.3e+02; Matches 13; Conservative 0; Mismatches 1; Indels
 ORGANISM: Methanococcus jannaschii complete genome.
) OTHER INFORMATION: Putative OCTB/TST1.01 motif US-10-091-281-81
 Sequence 184, Application US/10271602B
Publication No. US20040002073A1
GENERAL INFORMATION:
APPLICANT: Alice Kiang Li
APPLICANT: Ghazala Hashmi
 US-10-287-919-2441/c
; Sequence 2441, Application US/10287919
; Publication No. US20030085830A1
; GENERAL INFORMATION:
 1867 TTTATTTTTTT 1880
 1535 AAGTGTAATTGAGA 1548
1966 ATGGATACTTATAT 1979
 1 ATGGAAACTTATAT 14
 14 AAGTGTAATTGAAA 1
 14 rrharrrrdrhan 1
 ORGANISM: Homo sapiens
 RESULT 210
US-10-091-281-81/c
 RESULT 211
US-10-271-602B-184
 ANO
 TYPE: DNA
 FEATURE:
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 ; LOCATION: (1438072)...(1438086)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 2967
US-10-287-919-2317
 LOCATION: (868160)...(868174)
CITHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 1981
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 Gaps
 Gaps
 Gaps
 sequence 2317, Application US/10287919
sequence 2317, Application US/10287919
sublication No. US20030085830A1
general information:
sublication No. US20030085830A1
sublication No. US20030085830A1
sublication No. US2002008 jannaschi complete genome.
surrarr Application Wumber. US/10/287,919
currarr Filing Date: 2002-11-05
submer of SEQ ID NOS: 2706
software: Proprietary
seQ ID NO 217
length: 15
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 ;
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0
 Sequence 1563, Application US/10287919
Publication No. U220030085830A1
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.;
TITLE OF INVENTION: Methanococcus jannaschii complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/287,919
CURRENT FILING DATE: 2002-11-05
NUMBER OF SEQ ID NOS: 2706
SOFTWARE: Proprietary
SEQ ID NO 1563
LENGTH: 15
 ch 1.2%; Score 12.4; DB 1; Length 15; 1 Similarity 92.9%; Pred. No. 1.3e+02; 13; Conservative 0; Mismatches 1; Indels
 Query Match
1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels
 Query Match
1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels
 ORGANISM: Methanococcus jannaschii complete genome.
 IYPE: DNA ORGANISM: ORGANISM: Methanococcus jannaschii complete genome.
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6592
SOFTWARE: Patentin version 3.2
SEQ ID NO 6085
LENGTH: 15
 2095 AATGAACAAATGGC 2108
 1867 TITATITITIT 1880
 TYPE: RNA
CRGANISM: Hepatitis B virus
US-10-342-902-6085
 14 rrrarrrrrrrar 1
 14 ACTGAACAAATGGC 1
 Best Local Similarity
Matches 13; Conserve
 US-10-287-919-1563/c
 US-10-287-919-1563
 Query Match
 TYPE: DNA
 FEATURE:
 RESULT 208
 RESULT 207
```

à d 2 GTACCCCAGTGAC 15

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APPLICANT: Michael Seul

TITLE OF INVENTION: MULTIPLEXED ANALYSIS OF POLYMORPHIC LOCI

TITLE OF INVENTION: BY CONCURRENT INTERROGATION AND ENZYME-MEDIATED DETECTION

TITLE OF INVENTION: BY CONCURRENT INTERROGATION AND ENZYME-MEDIATED DETECTION

CURRENT APPLICATION NUMBER: US/10/271,602B

CURRENT APPLICATION NUMBER: 60/329,427

PRIOR FILING DATE: 2001-10-14

PRIOR FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 60/329,619

PRIOR APPLICATION NUMBER: 60/329,619

PRIOR APPLICATION NUMBER: 60/329,619

PRIOR FILING DATE: 2001-10-15

NUMBER OF SEQ ID NOS: 212

SEQ ID NOS: 212

SEQ ID NOS: 212

SEQ ID NOS: 212

SEQ ID NOS: 212

SEQ ID NO 184
 ö
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 Gaps
 ; OTHER INFORMATION: Probe sequence derived from human genomic sequence US-10-271-602B-184
 ; FEATURE:
; OTHER INFORMATION: Probe sequence derived from human genomic sequence US-10-271-6028-192
 Query Match
1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels
 Query Match
1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels
 TYPE: DNA
ORGANISM: Artificial Sequence
 TYPE: DNA ORGANISM: Artificial Sequence
 1581 GTAGCCCCAGTGAC 1594
 1581 GTAGCCCCAGTGAC 1594
 2 gracccccacreac 15
```

```
US-10-2/1-602B-200

Sequence 200, Application US/10271602B

Publication No. US20040002073A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alice Xiang Li
APPLICANT: Michael Seul
TITLE OF INVENTION: BY CONCURRENT INTERROGATION AND ENZYMS-MEDIATED DETECTION
TITLE OF INVENTION: BY CONCURRENT INTERROGATION AND ENZYMS-MEDIATED DETECTION
TITLE OF INVENTION: BY CONCURRENT INTERROGATION AND ENZYMS-MEDIATED DETECTION
FILE REPERENCE: HAAP-US
CURRENT APPLICATION NUMBER: 60/329, 427
PRIOR APPLICATION NUMBER: 60/329, 427
PRIOR PILING DATE: 2001-10-15
PRIOR PILING DATE: 2001-10-15
PRIOR PILING DATE: 2001-10-15
PRIOR PILING DATE: 2001-10-14
PRIOR PILING DATE: 2001-10-15
PRIOR PILING DATE: 2001-10-15
PRIOR PILING DATE: 2001-10-15
PRIOR PILING DATE: 2001-0-15
PRIOR PILING DATE: 2001-0-10-15
PRIOR PILING DATE: 2001-0-10-15
PRIOR PILING DATE: 2001-0-10-15
PRIOR PILING DATE: 2001-0-10-15
 Sequence 207, Application US/1021602B

Publication No. US20040002073A1

GENERAL INFORMATION

APPLICANT: Alice Xiarg Li

TITLE OF INVENTION: WINTER: US/10/271,602B

FILE REFERENCE: EMAP-US

CURRENT APPLICATION NUMBER: 60/329,427

PRIOR FILING DATE: 2001-10-15

PRIOR FILING DATE: 2001-10-14

PRIOR FILING DATE: 2001-10-14

PRIOR FILING DATE: 2001-10-14

PRIOR FILING DATE: 2001-10-14

PRIOR FILING DATE: 2001-10-15

PRIOR FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 60/329,619

PRIOR FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 60/329,619

PRIOR FILING DATE: 2001-10-15

SOFTWARE: Fast SEQ ID NOS: 212

LENGTH: 15
 ö
 ; OTHER INFORMATION: Probe sequence derived from human genomic sequence
US-10-271-602B-200
 Query Match 1.2%; Score 12.4; DB 1; Length 15; Best Local Similarity 92.9%; Pred. No. 1.3e+02; Matches 13; Conservative 0; Mismatches 1; Indels
 1581 GTAGCCCCAGTGAC 1594
 TYPE: DNA
ORGANISM: Artificial Sequence
 2 GTACCCCCAGTGAC 15
 RESULT 214
US-10-271-602B-207
 ò
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COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 ATTORNEY AGENT INFORMATION:
NAME: MCMASTERS, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 92001
TELECHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 649:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
1 COPOLOGY: linear
 1814 ATATATATAT 1825
 1794 GIGIGIGIGIGI 1805
 1 Grererererer 12
 1 ATATATATAT 12
 CITY: Seattle
STATE: Washington
 US-09-263-959-649/c
 US-09-263-959-649
 RESULT 218
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 US-09-735-363A-13

Sequence 13, Application US/09735363A

Sequence 13, Application US/09735363A

Sequence 13, Application US/09735363A

Sequence 13, Application US/09735363A

SEPERCANT: Filion, Mario

APPLICANT: Filion, Mario

APPLICANT: Filion, Mario

TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides

FILE REFERENCE: 02811-0181

CURRENT FILION DATE: 2000-12-13

PRIOR APPLICATION NUMBER: 60/170,325

PRIOR FILING DATE: 1999-12-13

PRIOR FILING DATE: 2000-08-29

NUMBER OF SEQ ID NOS: 87

SOFTWARE: Patentin version 3.0

SEQ ID NO 13

LENGTH: 12
 Gaps
 ; FEATURE:
0 OTHER INFORMATION: Probe sequence derived from human genomic sequence
US-10-271-6028-207
 0; Gaps
 USS-09-735-363A-14

USS-09-735-363A-14

Sequence 14, Application US/09735363A

Patent No. USZ0010041681A1

GENERAL INFORMATION:

APPLICANT: Fillion, Mario

APPLICANT: Fillion, Mario

APPLICANT: Fillion, Mario

TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides

FILE REPRENCE: 02811-0181

CURRENT APPLICATION NUMBER: US/09/735,363A

CURRENT FILING DATE: 2000-12-12

PRIOR APPLICATION NUMBER: 60/170,325

PRIOR FILING DATE: 2000-08-29

PRIOR FILING DATE: 2000-08-29
 Query Match
1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels
 Query Match 1.1%; Score 12; DB 1; Length 12; Best Local Similarity 100.0%; Pred. No. 1.40+02; Matches 12; Conservative 0; Mismatches 0; Indels
 ; PEATURE:

OTHER INFORMATION: Synthetic Oligonucleotide

US-09-735-363A-14
 ; OTHER INFORMATION: Synthetic Oligonucleotide US-09-735-363A-13
 NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin version 3.0
SEQ ID NO 14
LENGTH: 12
 TYPE: DNA ORGANISM: Artificial Sequence
TYPE: DNA
ORGANISM: Artificial Sequence
 1580 TGTAGCCCCAGTGA 1593
 ORGANISM: Artificial Sequence
 1793 TGTGTGTGTG 1804
 1 TGTACCCCCAGTGA 14
 1 rererererere 12
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Sequence 649, Application US/09263959

Patent No. US20020150891A1

GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: KOOWEN, Lee
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry Lip
STREET: 6300 Columbia Center, 701 Fifth Avenue
 Sequence 649, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSERS: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
 Gaps
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o
 Query Match 1.1%; Score 12; DB 1; Length 12; Best Local Similarity 100.0%; Pred. No. 1.46+02; Matches 12; Conservative 0; Mismatches 0; Indels
Query Match 1.1%; Score 12; DB 1; Length 12; Best Local Similarity 100.0%; Pred. No. 1.46+02; Matches 12; Conservative 0; Mismatches 0; Indels
 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/263,959 FILING DATE: 05-MAR-1999 CLASSIFCATION:
 920010.426C2
```

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Sequence 768, Application US/09263959
Sequence 768, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITILE OF INTENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
TITILE OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: Betentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILICATION NUMBER: US/09/263,959
FILING DATE:
CONFORTER: US/09/263,959
 US-09-263-959-832/c
| Sequence 832, Application US/09263959
| Patent No. US20020150891A1
| Patent No. US20020150891A1
| APPLICANT: Hood, Leroy E.
| APPLICANT: Rowen, Lee
| APPLICANT: Rowen, Lee
| APPLICANT: Koop, Ber F.
| TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
 0; Gaps
 1.1%; Score 12; DB 1; Length 12; 100.0%; Pred. No. 1.4e+02; tive 0; Mismatches 0; Indels
 Length 12;
 0; Indels
 Query Match 1.1%; Score 12; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0;
 ATTORNEY GENERAL STATE OF TAILOR DATE: 05-WAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCMASTEREN, David D.
REGISTRATION NUMBER: 32-963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELEFROWNE: (206) 622-6031
TELEFROWNE: (206) 622-6031
INFORMATION FOR SEQ ID NO: 768:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
 1814 ATATATATAT 1825
 1814 ATATATATATAT 1825
 Conservative
 1 ATATATATAT 12
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
 Local Similarity
nes 12; Conserva
 linear
 US-09-263-959-768/c
 ;
US-09-263-959-768
 US-09-263-959-768
 Query Match
 RESULT 221
 Matches
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 g
 Sequence 768, Application US/09263959
Retent No. US20102150891A1
GENERAL INFORMATION:
APPLICANT: Rowen, Lee
APPLICANT: Seed and Berry LLP
STREET: Seed and Berry LLP
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: Seattle
CITY: Seattle
CITY: Seattle
STREET: Mashington
 ö
 0; Gaps
 Length 12;
 0; Indels
 ZII: 98104-7092

COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PE-ENDS/MS-DOS
SOFTWARE: PE-ENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 05-MR-1999
FILING DATE: 05-MR-1999
 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASS/FICATION:
 Query Match
1.1%; Score 12; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0;
 ATTORNEY AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE FOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
INFORMATION FOR SEQ ID NO: 768:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
 ATTORNEY/AGENT INFORMATION:
NAME: MOMBASEE'S, David D.
NAME: MOMBASE, 33,963
NEGISTRATION NUMBER: 33,963
NEFERENCE/DOCKET NUMBER: 920010.426C2
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 649:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 1814 ATATATATATAT 1825
 ; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-649
 Seattle
Washington
 98104-7092
 RESULT 219
US-09-263-959-768
 COUNTRY:
 COUNTRY:
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Sequence 972, Application US/09263959
Sequence 972, Application US/09263959
Patent NO. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
 Gaps
 Gapa
 ..
 Length 12;
 CITY: Seattle
STATE: Washington
COUNTRY: US
ZID: 98104-7092
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
 Score 12; DB 1; Le
Pred. No. 1.4e+02;
 DB 1; Le
1.4e+02;
 Mismatches
 Query Match
1.1%; Score 12; DB
Best Local Similarity 100.0%; Pred. No. 1.4
Matches 12; Conservative 0; Mismatches
 1.1%; Score 12;
100.0%; Pred. No.
 US-09-263-959-975/c
; Sequence 975, Application US/09263959
; Patent No. US20020150891A1
 ATTORNEY/AGENT INPORMATION:
NAME: MCMASters, David D.
REGIGTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 9200
TELEPHONE: (206) 622-4900
 Query Match
Best Local Similarity 100.0%; P:
Matches 12; Conservative 0;
 TELEPRONE: (206) 622-4900
TELERAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 972:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 83
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLIGY: linear
US-09-263-959-838
 1793 TGTGTGTGTGTG 1804
 1793 TGTGTGTGTG 1804
 12 rererererere 1
 TYPE: nucleic acid
STRANDEDNESS: single
 linear
 GENERAL INFORMATION
 CLASSIFICATION:
 US-09-263-959-972/c
 ;
US-09-263-959-972
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 유
 Georgence 838, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rood, Leroy E.
APPLICANT: Rood, Leroy E.
APPLICANT: Rood, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
 ö
 0; Indels
 CITY: SCLETAIN Washington
COMPUTRY: US
ZIP: 98104-7092
ZIP: 98104-7092
COMPUTRY READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTRY: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHILI Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
MAME: MCMASTER: 05-MAR-1999
CLASSIFICATION NUMBER: 33,963
REPERENCE/DOCKET NUMBER: 33,
 E: Seed and Berry LLP 6300 Columbia Center, 701 Fifth Avenue
 DB 1; Le:
1.4e+02;
 Query Match 1.1%; Score 12; DB Best Local Similarity 100.0%; Pred. No. 1.4 Matches 12; Conservative 0; Mismatches
 ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,928
REERENCE/DOCKET NUMBER: 921
TELECOMMUNICATION INFORMATION:
 (206) 622-4900
 1793 TGTGTGTGTG 1804
 rererererere 1
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and
 STATE: Washington COUNTRY: US
 NUMBER OF SEQUENCES:
 RESULT 222
US-09-263-959-838/c
 TOPOLOGY:
US-09-263-959-832
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OTHER INFORMATION: Description of Artificial Sequence: Primer
 REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMAUNICATION INPOPURATION:
TELESPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR ESQ ID NO: 981:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
 ; Sequence 11, Application US/09841157A; Publication No. US20020192648A1; GENERAL INFORMATION;
 REGISTRATION NUMBER: 33,963
 ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
 1814 ATATATATATAT 1825
 1793 TGTGTGTGTG 1804
 LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 1 ATATATATAT 12
 12 rerererere 1
 ; TOPOLOGY: linear
US-09-263-959-981
 RESULT 226
US-09-841-157A-11
 SEQ ID NO 11
 SEQ ID NO 11
LENGTH: 12
 TYPE: DNA
 RESULT 227
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 ଚ
 ઠે
 Sequence 381, Application US/09263959
Patent No. US20020150831A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Roop, Ben F.
TITLE OF INVANTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
 APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TILLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSE: Seed and Berry LLP
ADDRESSE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
 Gaps
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 Length 12;
 0; Indela
 ZIP: 98104-7092
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: O5-MAR-1999
CLASSIFICATION:
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
 5: Seed and Berry LLP
6300 Columbia Center, 701 Fifth Avenue
 Query Match
1.1%; Score 12; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0;
 920010.42602
 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCMARGERS, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 92001
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-6031
INFORMATION FOR SEQ ID NO: 975: SEQUENCE CHARACTERISTICS:
LENGTH: 12 Dasse pairs
TYPE: nucleic acid
STRANDENESS: single
 ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
 1793 TGTGTGTGTGTG 1804
 Hood, Leroy E.
 12 referererere 1
 Washington
 Washington
 ; TOPOLOGY: linear
US-09-263-959-975
 CITY: Seattle
STATE: Washingt
COUNTRY: US
 RESULT 225
US-09-263-959-981/c
 ADDRESSEE:
STREET: 63
APPLICANT:
 COUNTRY:
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US-09-841-157A-11/c

| Sequence | 11, Application US/09841157A |
| GENERAL INFORMATION: APPLICANT: TARGARMA, TSUTOMU |
| APPLICANT: HAWANO, KEITHH: TITLE OF INVENTION: METHODS OF IDENTIFYING AN ORGANISM BASED ON ITS GENOTYPE |
| TITLE OF INVENTION: METHODS OF IDENTIFYING AN ORGANISM BASED ON ITS GENOTYPE |
| TOTRENT APPLICATION NUMBER: US/09/841,157A |
| CURRENT FILING DATE: 2001-04-25 |
| NUMBER OF SEQ ID NOS: 44 |
| SOFTWARE: PatentIn Ver. 2.1
 APPLICANT: NISHIGAKI, KOICHI
APPLICANT: NISHIGAKI, KOICHI
APPLICANT: TAKASAWA, TSTTOMU
APPLICANT: TAKASAWA, TSTTOMU
APPLICANT: TAKASAWA, TSTTOMU
TITLE OF INVENTION: METICHI
FILE REFERENCE: 12637/P66662US0
CURRENT APPLICATION NUMBER: US/09/841,157A
CURRENT FILING DATE: 2010-04-25
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATENTIN Ver. 2.1
 Gaps
 0; Gaps
 .
 ; OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-841-157A-11
Ouery Match 1.1%; Score 12; DB 1; Length 12; Best Local Similarity 100.0%; Pred. No. 1.46+02; Matches 12; Conservative 0; Mismatches 0; Indels
 Query Match
1.1%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.46+02;
Matches 12; Conservative 0; Mismatches 0; Indels
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RESULT 230
US-09-877-478-6010/C
US-09-877-478-6010/C
Sequence 6010, Application US/09877478
Publication No. US20030068301A1
Sequence 6010, Application US/09877478
Publication No. US20030068301A1
Sequence 6100, Application No. US20030068301A1
APPLICANT: Bit of Control of Cont
 Sequence 9167, Application US/09848754A

Sequence 9167, Application US/09948754A

Publication NO. US20030073207AI

GENERAL INFORMATION:
GENERAL INFORMATION:
TYPILE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related TITLE OF INVENTION: Levels of Epidernal Growth Factor Receptors
TITLE OF INVENTION: Levels of Epidernal Growth Factor Receptors
CURRENT APPLICATION NUMBER: US/09/848,754A

CURRENT FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 9645
SOFTWARE: Patentin version 3.0

SEQ ID NOS: 9645
 ö
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 Length 15;
 Indels
 Length 12;
 0; Indels
 Score 12; DB 1; Li
Pred. No. 1.5e+02;
Query Match
1.1%; Score 12; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0;
 Query Match 1.1%; Score 12; DB Best Local Similarity 100.0%; Pred. No. 1.5 Matches 12; Conservative 0; Mismatches
 TYPE: RNA
ORGANISM: Artificial Sequence
 TYPE: RNA
CRGANISM: Hepatitis B virus
US-09-877-478-6010
 2097 TGAACAAATGGC 2108
 1794 GIGIGIGIGI 1805
 14 TGAACAAATGGC 3
 US-09-848-754A-9167/c
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 Sequence 1, Application US/10077275A

| Sequence 1, Application US/20030228A1
| Publication No. US20030032028A1
| GENERAL INFORMATION:
| APPLICANT: Dace, Gayle
| APPLICANT: Kinmerly, William
| APPLICANT: Goff, Stephen
| APPLICANT: Goff, Stephen
| APPLICANT: Oeller, Paul
| TITLE OF INVENTION: In vitro capture of nucleic acids via modified oligonucleotides a
| TITLE OF INVENTION: In vitro Capture of nucleic acids via modified oligonucleotides a
| TITLE OF INVENTION: In vitro Capture of nucleic acids via modified oligonucleotides a
| TITLE OF INVENTION: In vitro Capture of nucleic acids via modified oligonucleotides a
| TITLE OF INVENTION: Magnetic Deads.
| TITLE OF INVENTION: UNDIER: US/10/077,275A
| CURRENT PILING DATE: 2002-02-15
| PRIOR PILING DATE: 2001-06-12
| SEQ ID NO 1
| SEQ ID NO 1
| LEMOTH: 12
| LEMOTH: 12
| LEMOTH: 12
 Sequence 2, Application US/10331780

| Sequence 2, Application US/10331780
| Publication No. US20030162210A1
| GENERAL INFORMATION:
| APPLICANT: Chetverin, Alexander B. |
| APPLICANT: Kramer, Fred Rusel | APPLICANT: Kramer, Fred Rusel | TITLE OF INVENTION: NOVEL OLIGONUCLEOTIDE ARRAYS AND THEIR USE FOR SORTING, TITLE OF INVENTION: NOVEL OLIGONUCLEOTIDE ARRAYS AND THEIR USE FOR SORTING, FILE REPERROCE: 07763-004002 | CURRENT APPLICATION NUMBER: US/10/331,780 | CURRENT FILING DATE: 2002-12-31 | PRIOR PRILING DATE: 1995-06-07 | PRIOR PEPLICATION NUMBER: US (08/247,530 | PRIOR PEPLICATION NUMBER: US (08/247,530 | PRIOR FILING DATE: 1994-05-25 | PRIOR FILING DATE: 1992-02-19 | NUMBER OF SEQ ID NOS: 19 | NUMBER OF SEQ ID NOS: 19 | SOFTWARE FREEKE
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 Gaps
 Gaps
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 Length 12;
 1.1%; Score 12; DB 1; Length 12;
100.0%; Pred. No. 1.4e+02;
tive 0; Mismatches 0; Indels
 1.4e+02;
 1.1%; Score 12; DB 1;
 , OTHER INFORMATION: Synthetically derived DNA US-10-331-780-2
 Query Match 1.1%; Score 12; DB Best Local Similarity 100.0%; Pred. No. 1.4 Matches 12; Conservative 0; Mismatches
 CTHER INFORMATION: LNA Homopolymer US-10-077-275A-1
 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
 1794 GIGIGIGIGI 1805
 1814 ATATATATAT 1825
 Query Match
Best Local Similarity 1000.
Matches 12; Conservative
 1 crererererer 12
 12 ATATATATAT 1
 RESULT 229
US-10-331-780-2/c
 US-09-841-157A-11
 RESULT 228
US-10-077-275A-1
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Length 15;
 Ouery Match 1.1%; Score 12; DB 1; L Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 12; Conservative 0; Mismatches 0;
 Sequence 193, Application US/10056414
Publication No. US20030003469A1
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
Draper, Kenneth G.
MCSWiggen, James
TITLE OF INVENTION: RIBOZEASES OR CONDITIONS
RELATED TO LEVELS OF
 COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD BETECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,414
FILING DATE: 33-43a-2002
CLASSIFICATION AUMER: US/08/291,932A
PRIOR APPLICATION NUMBER: US/08/291,932A
PILING DATE: August 15, 1994
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: WATDULGY RICHARD AUGUST
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 30,327
REGISTRATION NUMBER: 30,327
 COUNTRY 20071-2066
ZIP: 90071-2066
COMPUTER READABLE FORM:
 STATE: California
COUNTRY: U.S.A.
ZIP. 210.
ZIP. SONG
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 120:
 NUMBER OF SEQUENCES: 830
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
STREET: 633 West Fifth Street
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 120:
SEQUENCE CHRARACTERISTICS:
LENGTH: 15 base pairs
 TYPE: nucleic acid
STRANDEDNESS: single
 2153 CACCTGGAAGCA 2164
 CITY: Los Angeles
STATE: California
 15 CACCTGGAAGCA 4
 RESULT 234
US-10-056-414-193/c
 US-10-056-414-120
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 and Reagent for Inhibiting Hepatitis B Virus Replication
 ; OTHER INFORMATION; Description of Artificial Sequence: Enzymatic Nucleic acid
US-09-848-754A-9167
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 Gapa
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 Length 15;
 Query Match 1.1%; Score 12; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 12; Conservative 0; Mismatches 0; Indels
 1.5e+02;
 APPLICANT: Stinchcomb, Dan T.
Draper, Kenneth G.
McSwiggen, James McSwiggen, James TREATMENT OF TITLE OF INVENTION: BISEASES OR CONDITIONS
 Query Match
1.1%; Score 12; DB 1;
Best Local Similarity 100.0%; Pred. No. 1.5e+0.
Matches 12; Conservative 0; Mismatches
 RELATED TO LEVELS OF
 APPLICANT: Draper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
FILE OF INVENTION: Method and Reagent for In
FILE REPERENCE: 400,075 (WBHB00-845-1)
CURRENT APPLICATION NUMBER: US/10/342,902
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 09/631,025
PRIOR PELLING DATE: 2000-06-08
PRIOR FILING DATE: 2000-06-08
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: US 09/636,385
PRIOR PELLING DATE: 1994-02-07
PRIOR APPLICATION NUMBER: US 09/636,347
PRIOR APPLICATION NUMBER: US 09/636,430
PRIOR APPLICATION NUMBER: US 09/436,430
PRIOR PILING DATE: 1999-11-08
PRIOR FILING DATE: 1999-11-08
 Sequence 6010, Application US/10342902 Publication No. US20040054156A1 GENERAL INFORMATION: APPLICANT: Sirna Therapeutics, Inc.
 Sequence 120, Application US/10056414
Publication No. US20030003469A1
GENERAL INFORMATION:
 NUMBER OF SEQUENCES: 830
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
 2097 TGAACAAATGGC 2108
 ; ORGANISM: Hepatitis B virus US-10-342-902-6010
 2059 TGATTTCTAGGT 2070
 14 rGAACAAArGGC 3
 US-10-056-414-120/c
 SEQ ID NO 6010
LENGTH: 15
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Strand = positive ConnectronObjectNumber =
 Sequence 590; Application US/10287919
Publication No. US20030085830A1
GRARRAL INFORMATION:
GRARRAL INFORMATION:
TITLE OF INVENTION: Methanococcus jannaschii complete genome.
FILE REFERRNCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/287,919
CURRENT FILING DATE: 2002-11-05
NUMBER OF SEQ ID NOS: 2706
SOFTWARE: Proprietary
SOFTWARE: Proprietary
 Sequence 2049, Application US/10287919
Publication No. US20030085830A1.
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Methanococcus jannaschii complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/287,919
CURRENT PILING DATE: 2002-11-05
NUMBER OF SEQ ID NOS: 2706
SOFTWARE: Proprietary
 Length 15;
 Length 15
 Indels
 Indels
 TYPE: DNA
ORGANISM: Methanococcus jannaschii complete genome
 0uery Match
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0;
 Ouery Match
1.1%; Score 12; DB 1; L
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0;
FILING DATE: August 15, 1994
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 489-1600
 TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 309:
 ; LOCATION: (174470)...(174484); OTHER INFORMATION: Chromosome = 1 US-10-287-919-590
 INFORMATION FOR SEQ ID NO: 309:
SEQUENCE CHRARACTERISTICS:
LENGTH: 15 Dase pairs
 TYPE: nucleic acid
STRANDEDNESS: single
 2153 CACCTGGAAGCA 2164
 1892 TATTTCAATGTT 1903
 15 cáccrecaagea 4
 14 TATTTCAATGTT 3
 RESULT 237
US-10-287-919-2049/c
 US-10-287-919-590/c
 US-10-056-414-309
 RESULT 236
 ð
 셤
 ö
 쉱
 ö
 Gaps
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 Length 15;
 0; Indels
 DB 1; Le
 COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOPTWARE: WORD Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,414
FILING DATE: 23-dan-2002
CLASSIFFCATION: «Unknown»
PRIOR APPLICATION DATA:
 APPLICANT: Stinchcomb, Dan T.
Draper, Kenneth G.
McSwiggen, James
TITLE OF INVENTION: RIBOZYME TREATMENT OF
 CITY: Los Angeles
STATE: California
COUNTX: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 RELATED TO LEVELS OF
 COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/291,932A
FILING DATE: August 15, 1994
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
 APPLICATION NUMBER: US/08/291,932A
 1.1%; Score 12; DB 100.0%; Pred. No. 1.5
 APPLICATION NUMBER: US/10/056,414
FILING DATE: 23-Jan-2002
CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/157
TELECOMMUNICATION INFORMATION:
 TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 193
US-10-056-414-193
 FILING DATE: December 7, 1992
 NUMBER OF SEQUENCES: 830
CORRESPONDENCE ADDRESS:
ADDRESSES: Lyon & Lyon
STREET: 633 West Fifth Street
 Sequence 309, Application US/10056414 Publication No. US20030003469A1 GENERAL INFORMATION:
 FELEPHONE: (213) 489-1600
 (213) 955-0440
 TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
 TYPE: nucleic acid
STRANDEDNESS: single
 storage
 2153 CACCTGGAAGCA 2164
 Query Match
Best Local Similarity 100.
Matches 12; Conservative
 CACCTGGAAGCA 4
 TELEFAX:
 US-10-056-414-309/c
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APPLICANT: ANGREET A.

DIV, MARGARET A.

DAVIES, MARY-ELLEN M.

FRRED, DANIEL C.

TITLE OF INVENTION: VACCINES COMPRISING SYNTHETIC GENES
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESSE: J. MARK HAND - MERCK & CO., INC.

STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
 COMPUTER READABLE FORM:

MEDLUM TYPE: RIOPPY disk

COMPUTER: IN PC Compatible

COMPUTER: IN PC Compatible

COMPUTER: IN PC Compatible

COMPUTER: IN PC COMPATIBLE

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/369,121

FILING DATE: 17-Feb-2003

FILING DATE: 17-Feb-2003

APPLICATION NUMBER: US/09/340,798A

FILING DATE: 28-Jun-1999

APPLICATION NUMBER: US/09/340,798A

FILING DATE: 28-Jun-1999

APPLICATION NUMBER: US/08/877,418

FILING DATE: COMPANION:

ATTORNEY/AGENT INFORMATION:

NAWE: HAND. J. MARK

REGISTRATION NUMBER: 19729Y

TELECOMMUNICATION INFORMATION:
 1.1%; Score 12; DB 1; L
100.0%; Pred. No. 1.5e+02;
iive 0; Mismatches 0;
 TOPOLOGY: linear

MOLECULE TYPE: other mucleic acid

BESCRIPTION: /desc = "cligonucleotide"

SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-10-369-121-51
 Search completed: April 2, 2004, 14:38:06
Job time : 4 secs
 Sequence 51, Application US/10369121 Publication No. US20030229214A1 GENERAL INFORMATION:
 TELEPHONE: 908-594-3905
 LENGTH: 15 base pairs
 INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
 TYPE: nucleic acid
STRANDEDNESS: single
 1521 ATGCCTGCTATT 1532
 STATE: NEW JERSEY
COUNTRY: US
 Best Local Similarity 100.
Matches 12; Conservative
13 ATGCCTGCTATT
 CITY: RAHWAY
 US-10-369-121-51/c
 Query Match
 ઠે
 FEATURE:

; COCATION: (1247186)...(1247200)

; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 2622

US-10-287-919-2049
 ö
 COUNTY: USE COUNTY: USE COUNTY: USE COUNTY: USE COUNTY: USE COUNTY: USE COMPUTER READALE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rclease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/041,414
FILING DATE: 08-MAY-2002
CLASSIFICATION: <UNKNOWN>
 US-10-041-414-52/c
US-10-041-414-52/c
US-10-041-414-52/c
US-10-041-414

SEQUENCE 52, Application US/10041414

Publication No. US2003008725A1

GENERAL INFORMATION:

PUBLICANT: SHIVER, JOHN W.

DAVIES, MARY ELLEN
FREED, DANIEL C.

LIU, MARGARET A.

PERRY, HELEN C.

TITLE OF INVENTION: SYNTHETIC HIV ENV GENES

NUMBER OF SEQUENCES: 53

CORRESPONDENCES: 53

CORRESPONDENCES: 126 E. LINCOLN AVE., - P.O. BOX 2000

CITY: RAHWAY

CATANAY

CONTRESSEE JOHN W.

STREET: 126 E. LINCOLN AVE., - P.O. BOX 2000

CITY: RAHWAY
 1.1%; Score 12; DB 1; Length 15; 100.0%; Pred. No. 1.5e+02; tive 0; Mismatches 0; Indels
 Query Match
1.1%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels
 TYPE: DNA
ORGANISM: Methanococcus jannaschii complete genome
 TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "oligonucleotide"

SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-10-041-414-52
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/802,368
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 19643
TELECOMMUNICATION INFORMATION:
 FELEPHONE: 732-594-3905
 TELEFAX: 732-594-4720 INFORMATION FOR SEQ ID NO: 52:
 TYPE: nucleic acid
STRANDEDNESS: single
 NAME: HAND, J. MARK
 1521 ATGCCTGCTATT 1532
 1892 TATITCAATGIT 1903
 STATE: NEW JERSEY
 Query Match
Best Local Similarity 100.0
Matches 12; Conservative
 14 ratricaardir 3
SEQ ID NO 2049
LENGTH: 15
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Gaps ö

Length 15;